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INHERITANCE AND NATURE OF SOME ECONOMIC CHARACTERISTICS IN SWEET CORN

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ABSTRACT

This study was conducted in the Experimental Farm and Germplasm Preservation Laboratory of Horticulture Department, Faculty of Agriculture, Moshtohor, Benha University, and Research Station of HYTECH Seed Company, Assuit Egypt, during the successive summer and Nily seasons of 2013 and 2014. The current study was conducted using six populations design to study the nature of inheritance of some sweet corn traits. Significant genetic variance was detected for all traits in the six crosses. Highly significant negative heterotic effects for days to 50% tasselling and silking in most of the six crosses were detected. Highly significant positive heterotic effects were detected for weight of husked ears, weight of huskless ears and plant height. The results indicated that (P) values exceeded the unity in all cases. Inbreeding depression was significantly negative for number of days to 50% tasselling and silking in the six crosses. Meanwhile, significant positive inbreeding depression was detected for all crosses except plant height, total sugars, starch% in the third cross, and Beta carotene in the second cross. Significant F2 (E1) and backcrosses deviations (E2) were obtained for most traits. The additive gene effects (a) were significant for number of days to 50% silking, plant height, total sugars, starch% and Beta carotene in the six crosses, no. of days to 50% tasseling except the fourth cross and weight of husked ears except the sixth cross. High genetic coefficient of variation was detected for weight of husked ears, weight of huskless ears, starch% and Beta carotene in the six crosses. High heritability values in broad sense heritability were detected in the six crosses except weight of huskless ears. High narrow sense heritability was detected for no. of days to 50% tasseling in the fifth cross, no. of days to 50% silking in the first, second and fifth crosses and Beta carotene in the first and sixth crosses.

Keywords: Sweet corn, Inheritance, Heterosis, Inbreeding depression, Heritability

INTRODUCTION

Sweet corn (*Zea mays* L.) is considered one of the ten most important vegetable crops. Sweet corn resulted from a mutation in chromosom 4 at the Su1 locus of the cultivated corn (*Zea mays* L.). The uniqueness of the sweet corn is manifested in accumulation of sugars and water–soluble polysaccharides in the endosperm tissue that becomes translucent and brittle by the completion of maturation. Sweet corn is produced primarily in North America, but foreign consumption has increased in many locations of the world including Egypt (Wong *et a1.* 1994, El-Seidy2001).

Sweet corn has the potentiality to be an important vegetable crop for both local consumption and export in Egypt. The most important quality characteristics of sweet corn are the high sweetness of kernels and the slow rate of sugar decrease in kernels during storage of ears after harvest. In addition, low starch content in kernels is a desirable quality characteristic.

Despite the fact that highly effective breeding program are available for other members of the *Gramineae* family (El-Ebrashy 1961, Sedhom 1984, El Hosary and Sedhom 1990, El Hosary and Abd el Sattar 1998, Abou-Deif 2007 El-Shouny et al., 2005, El Badawy 2012, Haddadi et al., 2012, El Hosary and El-Akad 2015), efforts have been limited for sweet corn breeding (Wong et al., 1994, El-Seidy 2001, Lertrat and Pulam 2007, Pajic et al., 2010, Ozlem et al., 2014).

The main objective of the present study was to estimate the different genetic parameters required to design a successful breeding program to improve yield, the sweetness of kernels at harvest time, and the rate of total sugars decrease during storage of sweet corn ears. This will lead to new sweet corn lines and /or hybrids with ears characterized by high yield and long shelf life.

MATERIALS AND METHODS

This study was conducted in the Experimental Farm and Germplasm Preservation Laboratory of Harticulture Department, Faculty of Agriculture–Moshtohor, Benha University, Moshtohor–Kalubia, Egypt and Research Station of HYTECH Seed Company, Egypt, during the successive summer and Nily seasons of 2013 and 2014 in Assuit Station. This investigation was conducted using six populations desgn to study the nature of inheritance for some traits in sweet corn.

Four inbred lines of sweet corn (*Zea mays* L.), i.e. SCIN, SC023B, SC028A, and M-2-3 were obtained from the Germplasm Preservation Laboratory, Faculty of Agriculture at Moshtohor, Kalubia, Egypt. The line SCIN is a tropical inbred from India and lines SC023B and SC028A from thailand which M-2-3 was obtained from the Germplasm preservation Laboratory Faculty of Agriculture at Moshtohor. The previously mentioned inbred lines were choosen to be used as parental genotypes in the present study based on the relatively wide morphological variation and quality characters observed among these inbred lines.

In early summer season of 2013, seeds of four Inbred lines were planted. All possible cross combinations without reciprocals were made between the four inbred lines giving a total of 6 crosses. In the Nily season 10th Augst of 2013, seeds of the four inbred line and F_1 hybrids were planted in Assuit. F_1 seeds of six crosses i.e. $P_1xP_2,$ $P_1xP_3,$ $P_1xP_4,$ P_2xP_3 $P_2xP_4,$ $P_3xP_4,$

with four inbred lines were sown and the F_1 plants of each cross were backcrossed to both parental inbred lines to produce BC_1 (F_1x P_1) and BC_2 (F_1x P_2) for each cross. In addition, the F_2 seeds were obtained by selfing of F_1-plants.

In 2014 season, the six populations involving parents, F_1, F_2, BC_1 and BC_2 of each cross were sown on 15th of March. For each cross, two rows of each inbred lines and F_1; 10 rows of each of the two backcrosses and 20 rows of each F_2 population were grown in ridges 5 m long and 70cm width in three replications. Hills were spaced by 20 cm with two kernels per hill. All recommended cultural practices for maize growing were followed.

The following readings and measurements were recorded on individual plant basis, during and at the end of the growing season: 50% tasseling date, 50% Silking date, plant height, weight of fresh husked ears, weight of fresh huskess ears, percentage of seeds total sugars, percentage of seeds starch and β-carotene.

Various biometrical parameters were calculated, only, if the F_2 genetic variance was significant. Heterosis was expressed as "the increase of F_1 above the better parent value". Inbreeding depression was calculated as "the difference between means of the F_1 and F_2 expressed as percentage of the F_1 mean". Genetic analysis of generation means for main effect parameter (m), additive (a), dominance (d), additive x additive(aa), additive x dominance (ad) and dominance x dominance (dd) effects were all calculated according to Gamble (1962). In addition, F_2 deviation (E1) and backcross deviation (E2) were determined following the method, suggested by Mather and Jinks (1971). Heritability was calculated, in both broad and narrow senses, according to the procedure of Mather (1949). The predicted genetic advance from selection was estimated using the formula presented by Johanson *et al.*(1955) , and the potence ratio was calculated according to Peter and Frey (1966).

RESULTS AND DISCUSSION

Number of plants, mean, variance, variance of mean and coefficient of variation of the studied traits of the six crosses for parents, F_1, F_2, Bc_1 and Bc_2 are presented in (Table 1). (Table 2) shows the test of significance of parental mean performance and the genetic variance among F_2 populations in each cross for all studied traits. The difference between the two parents each cross significant in each of the six crosses for all studied characters except number of days to tasseling in the six cross, number of days to silking in the first and sixth crosses, plant height in the sixth cross, weigh of husked ears in the second, third, fourth and sixth cross, weigh of huskless ears in the second, third and sixth cross, total sugars in the first cross, starch % in the first cross and beta carotene in the fifth cross. Significant genetic variance was detected for all traits in the six crosses and therefore, other genetical parameters were estimated. The existence of significant genetic variability inspit of the significant differences between the parental inbred lines which was obtained here for most traits, may suggest that the genes of like effects were not completely associated in the parents, i.e., these genes are dispersed **(Mather and Jinks, 1971).**

Table (1): Means and variance for the six generations for all studied traits in the three studied crosses.

Trait	Cross		Population					
			P1	P2	F1	F2	Bc1	Bc2
Number of days to tasseling	1x2	Mean	61.03	60.57	61.33	62.60	70.12	60.33
		Variance	0.66	0.25	1.20	10.64	8.06	7.59
	1x3	Mean	61.03	61.87	61.00	62.77	61.56	62.50
		Variance	0.66	0.33	0.56	2.72	1.52	3.04
	1x4	Mean	61.03	61.81	59.47	62.6	62.16	61.55
		Variance	0.66	1.13	0.38	2.64	2.41	2.00
	2x3	Mean	60.57	61.87	60.92	60.32	60.29	60.15
		Variance	0.25	0.33	0.38	0.87	0.60	0.75
	2x4	Mean	60.57	61.81	62.35	60.49	60.16	58.43
		Variance	0.25	1.13	1.63	5.62	4.14	3.33
	3x4	Mean	61.87	61.81	59.12	61.45	60.93	62.20
		Variance	0.33	1.13	0.53	2.13	1.57	2.23
Number of days to sliking	1x2	Mean	62.03	62.09	62.97	63.74	72.34	59.07
		Variance	0.84	0.52	1.22	4.99	3.71	2.55
	1x3	Mean	62.03	63.17	62.97	63.42	62.28	63.84
		Variance	0.84	0.49	0.17	13.54	9.21	8.07
	1x4	Mean	62.03	63.56	60.82	63.74	63.59	61.34
		Variance	0.84	1.29	0.27	3.99	2.73	3.19
	2x3	Mean	62.1	63.17	62.97	58.93	59.01	59.59
		Variance	0.58	0.49	0.60	2.39	1.67	1.92
	2x4	Mean	62.1	63.56	63.74	60.98	58.16	60.31
		Variance	0.58	1.29	1.23	5.81	3.14	4.24
	3x4	Mean	63.17	63.56	60.59	62.26	60.67	63.14
		Variance	0.49	1.29	0.31	3.83	3.38	2.35
Plant height	1x2	Mean	207.58	124.17	237.42	210.15	240.37	181.89
		Variance	59.56	13.94	117.38	390.68	223.32	372.62
	1x3	Mean	207.58	130.17	237.73	208.34	228.31	217.63
		Variance	59.56	40.49	20.08	622.86	472.75	436.69
	1x4	Mean	207.58	130.16	183.38	213.67	236.80	225.20
		Variance	59.56	13.68	25.33	529.61	380.16	375.64
	2x3	Mean	124.17	130.17	204.44	165.06	182.79	196.42
		Variance	13.94	40.49	96.83	341.25	237.82	277.02
	2x4	Mean	124.17	130.16	220.29	165.20	167.87	197.01
		Variance	13.94	13.68	298.4	805.88	668.36	582.41
	3x4	Mean	130.17	130.16	208.38	180.44	173.06	204.59
		Variance	40.49	13.68	99.58	348.42	292.87	294.24

Table (1): Continue

Trait	Cross		Population					
			P1	P2	F1	F2	Bc1	Bc2
Weight of husked	1x2	Mean	292.12	252.67	494.09	417.58	315.37	289.39
		Variance	3179.73	3275.4	3999.15	13083.11	9788.14	8855.18
	1x3	Mean	292.12	274.00	631.97	328.96	446.25	475.25
		Variance	3179.73	2142.1	2428.03	13127.92	10666.77	11323.99
	1x4	Mean	292.12	291.25	507.35	423.33	439.73	490.27
		Variance	3179.73	2269.35	6486.72	15504.07	10651.28	11243.76
	2x3	Mean	252.67	274.00	500.56	335.65	293.90	354.44
		Variance	3275.4	2142.07	2148.25	8854.73	5903.04	8322.5
	2x4	Mean	252.67	291.25	465.59	295.42	342.00	360.00
		Variance	3275.4	2269.35	5698.13	9738.14	7524.32	6707.89
	3x4	Mean	274.00	291.25	532.21	331.92	349.88	381.28
		Variance	2142.07	2269.35	7498.77	9025.56	7196.28	6397.17
Weight of huskless	1x2	Mean	182.12	153.67	367.42	291.39	220.85	185.12
		Variance	2323.48	2782.60	2601.75	6686.46	6157.90	5089.49
	1x3	Mean	182.12	188.33	485.50	241.66	316.97	348.50
		Variance	2323.48	1772.99	2079.91	9796.62	9226.78	8417.27
	1x4	Mean	182.12	187.50	353.82	288.67	301.73	345.00
		Variance	2323.48	1735.48	3630.39	9793.33	9079.39	8225.34
	2x3	Mean	153.67	188.33	379.72	234.35	190.00	247.65
		Variance	2782.64	1772.99	2374.21	5172.23	4028.95	4198.18
	2x4	Mean	153.67	187.50	348.82	198.37	234.27	254.03
		Variance	2782.64	1735.48	4078.88	6097.97	5216.68	4653.32
	3x4	Mean	188.33	187.50	395.15	229.01	260.61	263.49
		Variance	1772.99	1735.48	5935.58	5823.33	4640.36	6117.1
Total sugars	1x2	Mean	6.93	6.88	6.78	8.18	7.66	7.25
		Variance	0.53	0.36	0.04	1.51	0.60	1.50
	1x3	Mean	6.93	8.84	7.62	7.41	6.10	8.26
		Variance	0.53	0.07	0.31	3.21	2.70	2.14
	1x4	Mean	6.93	8.47	5.86	7.37	8.34	7.38
		Variance	0.53	0.12	0.06	5.83	4.83	3.07
	2x3	Mean	6.88	8.84	9.02	7.84	7.49	7.69
		Variance	0.36	0.07	0.15	1.44	1.26	1.30
	2x4	Mean	6.88	8.47	8.94	7.45	5.43	6.87
		Variance	0.36	0.12	0.18	1.85	1.98	1.12

	3x4	Mean	8.84	8.47	7.25	8.87	8.58	7.18
		Variance	0.07	0.12	0.19	2.58	2.28	1.59

Table 1): Continue

Trait	Cross		Population					
			P1	P2	F1	F2	Bc1	Bc2
Starch %	1x2	Mean	20.72	19.86	17.92	24.73	22.95	24.02
		Variance	4.30	3.36	0.33	15.64	11.52	10.44
	1x3	Mean	20.72	29.48	26.33	21.98	20.07	28.15
		Variance	4.30	0.07	15.07	47.33	31.63	35.62
	1x4	Mean	20.72	28.26	16.91	21.23	25.32	22.16
		Variance	4.30	0.29	4.95	37.41	26.57	31.22
	2x3	Mean	19.86	29.48	28.66	17.69	23.71	25.03
		Variance	3.36	0.07	7.30	30.3	24.17	21.78
	2x4	Mean	19.86	28.26	31.29	22.00	13.69	19.62
		Variance	3.36	0.29	1.20	36.88	30.31	35.61
	3x4	Mean	29.48	28.26	19.58	20.67	19.98	24.40
		Variance	0.07	0.29	1.50	70.88	50.97	62.94
β- carotene p.p.m	1x2	Mean	2.94	7.40	5.98	5.84	5.48	8.30
		Variance	0.03	1.86	1.25	5.54	2.82	4.40
	1x3	Mean	2.94	5.18	5.72	6.57	6.8	7.78
		Variance	0.03	1.52	0.37	5.34	2.66	4.78
	1x4	Mean	2.94	6.40	7.76	7.51	3.36	5.64
		Variance	0.03	7.30	1.33	5.14	4.99	4.07
	2x3	Mean	7.40	5.18	3.62	3.45	5.48	6.24
		Variance	1.86	1.52	0.48	6.22	4.99	5.73
	2x4	Mean	7.40	6.40	6.80	6.06	5.08	6.82
		Variance	1.86	7.30	0.21	9.56	6.59	7.08
	3x4	Mean	5.18	6.40	7.16	6.71	7.12	4.60
		Variance	1.52	7.30	0.23	16.21	10.11	9.54

Heterosis

Estimates of heterosis percentage for all character in six crosses are presented in Table 3 The results indicated highly significant negative heterotic effects for days to tasselling, silking, total sugars, starch % and beta carotene in some crosses of the six crosses of sweet corn under study. These results indicated to the possibility of producing ealier hybrids of sweet corn using these inbred lines.

Highly significant positive heterotic effects, were detected for all the other traits. As it well known, weigh of husked and weigh of huskless. are the main components for yield in sweet corn. Hence heterotic increase, if it is found in one or more of the, may lead to considerable yield increase in hybrids. It is worth noting that heterotic effect for yield was larger in magnitude than for any one of its components which is logically expected. The significance of heterotic effects show that non- additive genetic type of gene action affects such traits. These results were previously reported by El-Shouny *et al.* (2005) and Abou-Deif (2007).

Table (2): Mean performance of parents, t-test of difference between parents and F-test of genetic variance among F2 plants of the three crosses for the studied traits.

Traits	Cross	Mean value		T- test	F- test
		P_1	P_2		
Number of days to tasseling	1X2	61.03	60.57	2.66**	15.17**
	1X3	61.03	61.87	-4.63**	5.29**
	1X4	61.03	61.81	-3.21**	3.68**
	2X3	60.57	61.87	-9.35**	2.72**
	2X4	60.57	61.81	-5.81**	5.60**
	3X4	61.87	61.81	0.25	3.22**
Number of days to silking	1X2	62.03	62.09	-0.28	5.79**
	1X3	62.03	63.17	-5.39**	27.04**
	1X4	62.03	63.56	-5.75**	4.98**
	2X3	62.10	63.17	-5.66**	4.31**
	2X4	62.10	63.56	-5.87**	5.63**
	3X4	63.17	63.56	-1.63	5.51**
plant height	1X2	207.58	124.17	53.29**	6.14**
	1X3	207.58	130.17	42.39**	15.55**
	1X4	207.58	130.16	49.55**	16.12**
	2X3	124.17	130.17	-4.45**	6.77**
	2X4	124.17	130.16	-6.24**	7.42**
	3X4	130.17	130.16	0.01	6.80**
Weigh of husked	1X2	292.12	252.67	2.69**	3.75**
	1X3	292.12	274.00	1.36	5.08**
	1X4	292.12	291.25	0.06	3.90**
	2X3	252.67	274.00	-1.59	3.51**
	2X4	252.67	291.25	-2.84**	2.60**
	3X4	274.00	291.25	-1.42	2.27**
Weigh of huskless	1X2	182.12	153.67	2.18*	2.60**
	1X3	182.12	188.33	-0.53	4.76**
	1X4	182.12	187.50	-0.46	3.82**
	2X3	153.67	188.33	-2.81**	2.24**
	2X4	153.67	187.50	-2.76**	2.13**
	3X4	188.33	187.50	0.08	1.85**

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

Table (2): cont.

Traits	Cross	Mean value		T- test	F- test
		P_1	P_2		
Total sugars	1X2	6.93	6.88	0.29	4.88**
	1X3	6.93	8.84	-13.48**	10.61**
	1X4	6.93	8.47	-10.42**	24.39**
	2X3	6.88	8.84	-16.45**	7.53**
	2X4	6.88	8.47	-12.58**	8.49**
	3X4	8.84	8.47	4.67**	20.43**
Starch %	1X2	20.72	19.86	1.69	5.87**
	1X3	20.72	29.48	-22.94**	7.30**
	1X4	20.72	28.26	-19.28**	11.76**
	2X3	19.86	29.48	-28.44**	8.47**
	2X4	19.86	28.26	-24.09**	22.81**
	3X4	29.48	28.26	11.07**	114.40**
Beta carotene p.p.m	1X2	2.94	7.40	-17.73**	5.27**
	1X3	2.94	5.18	-9.84**	8.31**
	1X4	2.94	6.40	-7.00**	1.78**
	2X3	7.40	5.18	6.61**	4.82**
	2X4	7.40	6.40	1.81	3.06**
	3X4	5.18	6.40	-2.25*	5.37**

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

Nature and degree of dominance.

Potence ratio (P) was calculated to study the nature and degree of dominance for all studied characters (Table 3). The results indicated that (P) values exceeded the unity in most cases. Overdominance towards the higher parent was detected for weight of husked and weigh of huskless suggesting that higher parents were dominated over the lower parents in the studied characters. Overdominance towards the lower parent was detected for number of days to tasseling and silking, total sugars content and starch% suggesting that lower parents were dominated over the higher parents in the characters. Moreover, the results in (Table 3) that (P) values were less than unity in some crosses. Partial dominance for higher or lower parents were observed in some crosses. Generally, potence values followed the same trend as heterotic effects for all traits. These results are in agreement with those obtained by Sedhom 1984, El-Shouny *et al.* (2005) and Abou-Deif (2007).

Inbreeding depression:

Table 3 shows the percentages of inbreeding depression for all traits in the six studied crosses. Inbreeding depression was significantly negative for no. of days to tasselling and silking in the six crosses. Meanwhile, significant positive inbreeding depression was detected for other traits except total sugars and Starch % in the first, third and six cross and Beta carotene in the second cross. Both heterosis and inbreeding depression effects as it is well known are two coincides to a same particular phenomenon. Therefore, it is logically to expect that heterosis in F_1 will be accompanied by appreciable reduction in the F_2 performance and vice versa. Similar results were obtained by Sedhom 1984, El-Shouny et al. (2005) and Abou-Deif (2007).

Table 3 shows the epistatic deviations of F_2 (E1) and backcrosses (E2) for all the studied traits. The results indicated that significant F_2 deviation (E1) were obtained for all the studied traits except plant height in the fourth cross, starch % in the third cross and Beta carotene in the first and sixth crosses.

Significant backcrosses deviations (E2) were obtained for all traits except number of days to silking in the second and sxith crosses. Weigh of husked, huskless, total sugars sixth crosses, respectively. It is worth noting that F_2 deviation was mostly accompanied by backcross deviation of significance. Also, the presence of appreciable epistatic deviations along with the large heterotic effects and the existence of over dominance detected herein in most cases may reveal the great role of interallelic gene effects on the performance of these cases.

Nature of gene action

Nature of gene action was studied according to the relationships illustrated by Gamble (1962). Estimated values of each of the six parameters with their test of significance for all studied characters are shown in (table, 4). In all cases, estimated mean effect parameters (m) which reflects the contribution due to the overall mean plus the locus effects and interaction of the fixed loci was highly significant.

The results indicated that the additive gene effects (a) were significant for all the studied characters in the six crosses, except days to tasseling in the fourth cross, weight

Table (3): Heterosis, potence ratio, inbreeding depression, F_2 deviation and back cross deviationin the six crosses for studied traites.

Traits	cross	heterosis	potance	inbreeding	F_2	Bc
		Mp	ratio	depression	deviation E1	deviation E2
Number of dayes to tasseling	1X2	0.88*	2.31	-2.07	1.53**	8.32**
	1X3	-0.73	-1.07	-2.90**	1.54**	1.61**
	1X4	-3.18	-4.99	-5.26**	2.15**	2.82**
	2X3	-0.49	-0.46	0.98*	-0.75**	-1.70**
	2X4	1.90**	1.87	2.99**	-1.28**	-4.95**
	3X4	-4.40	-90.66	-3.95**	0.97**	2.17**
Number of dayes to silking	1X2	1.46**	30.00	-1.22**	1.22**	6.38**
	1X3	0.59**	0.65	-0.73	0.64**	0.55
	1X4	-3.14	-2.58	-4.79**	1.93**	1.30**
	2X3	0.54*	0.64	6.42*	-3.87**	-7.00**
	2X4	1.44**	1.24	4.32**	-2.30**	-8.09**
	3X4	-4.38	-14.03	-2.76**	0.28*	-0.14
plant height	1X2	43.14**	1.72	11.49**	8.50**	18.96**
	1X3	40.77**	1.78	12.36**	5.04**	39.34**
	1X4	8.60**	0.38	-16.51**	37.54**	109.75**
	2X3	60.77**	25.76	19.26**	-0.74	47.60**
	2X4	73.24**	31.10	25.01**	-8.53**	17.42**
	3X4	60.10**	7.82	13.41**	11.17**	39.11**
Weigh of husked	1X2	81.39**	11.24	15.49**	34.33**	-161.73**
	1X3	123.26**	38.51	47.95**	-128.56**	6.47
	1X4	73.94**	490.10	16.56**	23.81*	130.97**
	2X3	90.08**	22.24	32.94**	-46.29**	-115.55**
	2X4	71.20**	10.04	36.55**	-73.35**	-35.55*
	3X4	88.31**	28.94	37.63**	-75.49**	-83.67**
Weigh of huskless	1X2	118.84**	14.03	20.69**	23.73**	-129.34**
	1X3	162.11**	96.67	50.23**	-93.71**	-5.25
	1X4	91.45**	62.84	18.42**	19.35*	108.10**
	2X3	122.06**	12.04	38.28**	-41.01**	-113.07**

	2X4	104.49**	10.54	43.13**	-61.34**	-31.11*
	3X4	110.28**	493.40	42.04**	-62.52**	-58.97**

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

Table (3):cont.

Traits	cross	heterosis	potance	inbreeding	F_2	Bc
		Mp	ratio	depression	deviation E1	deviation E2
Total sugars	1X2	-1.81	-5.00	-20.64	1.34**	1.22**
	1X3	-3.33	-0.28	2.87	-0.35**	-1.15**
	1X4	-23.92	-2.40	-25.77**	0.59**	2.15**
	2X3	14.73**	1.18	13.04**	-0.60**	-1.71**
	2X4	16.39**	1.59	16.58**	-0.85**	-4.31**
	3X4	-16.21	-7.58	-22.34**	0.92**	-0.15
Starch %	1X2	-11.68	-5.54	-38.00**	5.62**	8.76**
	1X3	4.92	0.28	16.54	-3.74**	-3.21**
	1X4	-30.95	-2.01	-25.58**	0.54	6.08**
	2X3	16.17**	0.83	38.26**	-8.97**	-4.58**
	2X4	30.06**	1.72	29.70**	-5.68**	-22.04**
	3X4	-32.19	-15.26	-5.56**	-3.56**	-4.07**
Beta carotene p.p.m	1X2	15.67**	0.36	2.34**	0.27	2.63**
	1X3	40.89**	1.48	-14.86**	1.68**	4.80**
	1X4	66.17**	1.79	3.22**	1.30**	-3.43**
	2X3	-42.45	-2.41	4.70**	-1.51**	1.81**
	2X4	-1.45	-0.20	10.88	-0.79**	-1.80**
	3X4	23.66**	2.25	6.28**	0.24	-1.23**

of huskless in the sixth cross. These results are in agreement with those obtained by Sedhom 1984, El-Shouny *et al.* (2005) and Abou-Deif (2007).

The dominance gene effect (d) was highly significant for all traits in the six crosses except number of the days to silking in the second cross, total sugars in the third and fourth crosses, starch % in the third and sixth crosses and Beta carotene in the fifth and sixth crosses. Dominance effects were higher in magnitude than additive gene effect. The negative value of dominance demonstrates that the smaller mean value parent had the dominant genes responsible for these characters.

Additive x additive (aa) epistatic type of gene action was significant for all traits, except number of days to tasseling in the fourth and sixth crosses, Number of days to silking and total sugars in the second cross, Plant height in the first cross, weight of husked and Beta carotene in the fifth cross. Also, additive x dominance gene effects were significant for all traits except number of days to silking, weight of husked in the first and fifth and crosses, weight of huskless in the fifth and sixth crosses and Beta carotene in the second and third crosses. Dominance x dominance gene effects were significant for all traits in the six crosses except number of days to tasseling and silking in the second cross, weight of husked and huskless and total sugars in the first cross, starch % in the second and sixth crosses. The majority of dominance x dominance gene effects were of negative values for most traits. The absolute relative magnitudes of the epistatic gene effects to mean effects were somewhat variable depending on the cross and traits studied. Generally, the absolute magnitude of the epistatic effects were larger than mean effects and approach the dominance effects for most cases. Therefore, it could be concluded that epistatic effect was important as a major contributor in the performance of these traits. These results agree with the idea that the inheritance of a quantitative characters is generally more complex than qualitative characters. The significant values of epistasis in the six crosses were accompanied by significant estimates for E1 and E2.

The non-additive gene effects appears to be of primer importance in the inheritance of most traits, the large magnitude of both dominance and epistatic effects revealed that both types contribute in the expression of heterosis in most traits. These results well agree with those reported by Gamble (1962) from crosses between some inbred lines. Sentz (1971) reported that dominance effects tended to be more important, and Fadhi (1978) stated that dominance gene effects had the first rank of gene action and (aa) type of epistasis had the second rank with regard to grain yield. On the other hand, some researchers stated that both additive and dominance effects had similar magnitude Sedhom 1984, El-Shouny *et al.* (2005) and Abou-Deif (2007). Most investigators reported that additive effects tended to be more important in the inheritance of yield (Gardner 1967, Hallauer 1971, El-Rouby and Galal 1972 and Shehata and Dawan 1975).

Table (4): Parameters of gene effects relating to studied traites in the six crosses.

Traits	cross	gene action six parameters (Gamble producre)					
		main effect	additive a	Dominance d	add. X add.	add.xdom. (ad)	Dom.xdom.
Number of dayes to tasseling	1X2	62.60**	9.79**	11.04**	10.50**	9.56**	-27.14**
	1X3	62.77**	-0.94**	-3.39**	-2.94**	-0.52**	-0.29
	1X4	62.60**	0.61**	-4.92**	-2.97**	1.00**	-2.67**
	2X3	60.32**	0.14	-0.70	-0.40	0.79**	3.80**
	2X4	60.49**	1.73**	-3.62**	-4.78**	2.35**	14.69**
	3X4	61.45**	-1.27**	-2.28**	0.45**	-1.30**	-4.78**
Number of dayes to silking	1X2	63.74**	13.27**	8.78**	7.87**	13.30**	-20.64**
	1X3	63.42**	-1.56**	-1.09	-1.45	-0.99**	0.35
	1X4	63.74**	2.25**	-7.08**	-5.11**	3.01**	2.50**
	2X3	58.93**	-0.58**	1.82**	1.48**	-0.05	12.52**
	2X4	60.98**	-2.15**	-6.07**	-6.98**	-1.42**	23.17**
	3X4	62.26**	-2.47**	-4.19**	-1.41**	-2.27**	1.70*
plant height	1X2	210.15**	58.48**	75.46**	3.91	16.77**	-41.82**
	1X3	208.34**	10.69**	127.36**	58.50**	-28.02**	-137.18**
	1X4	213.67**	11.60**	83.86**	69.34**	-27.11**	-288.85**
	2X3	165.06**	-13.63**	175.45**	98.18**	-10.63**	-193.38**
	2X4	165.20**	-29.15**	162.11**	68.97**	-26.15**	-103.82**
	3X4	180.44**	-31.53**	111.77**	33.55**	-31.54**	-111.77**
Weigh of husked	1X2	417.58**	25.98**	-239.10**	-460.79**	6.25	784.25**
	1X3	328.96**	-29.00**	876.08**	527.17**	-38.06**	-540.11**
	1X4	423.33**	-50.54**	382.34**	166.67**	-50.97**	-428.60**
	2X3	335.65**	-60.55**	191.29**	-45.93	-49.88**	277.02**
	2X4	295.42**	-18.00*	415.93**	222.30**	1.29	-151.21**
	3X4	331.92**	-31.40**	384.20**	134.62**	-22.78*	32.73
Weigh of huskless	1X2	291.39**	35.73**	-154.10**	-353.62**	21.51*	612.31**
	1X3	241.66**	-31.53**	664.60**	364.32**	-28.42**	-353.82**
	1X4	288.67**	-43.27**	307.81**	138.80**	-40.58**	-355.00**
	2X3	234.35**	-57.65**	146.64**	-62.08**	-40.32**	288.22**

	2X4	198.37**	-19.76**	361.36**	183.12**	-2.84	-120.89**
	3X4	229.01**	-2.88	339.38**	132.15**	-3.30	-14.22

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

Table (4): cont.

Traits	cross	gene action six parameters (Gamble producre)					
		main effect	additive a	Dominance d	add. X add.	add.xdom. (ad)	Dom.xdom.
Total sugars	1X2	8.18**	0.41**	-3.04**	-2.91**	0.39**	0.47
	1X3	7.41**	-2.17**	-1.16*	-0.90	-1.22**	3.20**
	1X4	7.37**	0.96**	0.11	1.95**	1.73**	-6.26**
	2X3	7.84**	-0.20**	0.13	-1.03**	0.78**	4.45**
	2X4	7.45**	-1.44**	-3.96**	-5.22**	-0.65**	13.85**
	3X4	8.87**	1.39**	-5.38**	-3.97**	1.21**	4.27**
Starch %	1X2	24.73**	-1.08**	-7.34**	-4.97**	-1.50**	-12.56**
	1X3	21.98**	-8.08**	9.75**	8.52**	-3.70**	-2.09
	1X4	21.23**	3.16**	2.45	10.03**	6.94**	-22.20**
	2X3	17.69**	-1.32**	30.71**	26.72**	3.49**	-17.55**
	2X4	22.00**	-5.93**	-14.13**	-21.36**	-1.73**	65.44**
	3X4	20.67**	-4.42**	-3.21	6.09*	-5.03**	2.05
Beta carotene p.p.m	1X2	5.84**	-2.82**	5.01**	4.20**	-0.59**	-9.46**
	1X3	6.57**	-0.98**	4.54**	2.88**	0.14	-12.48**
	1X4	7.51**	-2.28**	-8.95**	-12.04**	-0.55	18.90**
	2X3	3.45**	-0.76**	6.97**	9.64**	-1.87**	-13.26**
	2X4	6.06**	-1.74**	-0.54	-0.44	-2.24**	4.04**
	3X4	6.71**	2.52**	-2.03	-3.40**	3.13**	5.86**

Genetic coefficient of variability.

Table 5 shows high values for genetic coefficient of variation for ear position, weight of husked, weight of huskless, total sugare, starch% and Beta carotene in all crosses. However, moderate values were obtained for plant height in all crosses. Number of days to silking and tasseling in all crosses, had low values of G.C.V.% .

By using the genetic coefficient of variation alone, however, it is impossible to estimate the magnitude of heritable variation. The heritable portion of the variation could be found out with the help of heritability estimates and genetic gain under selection (Swarup and Chaugale, 1962).

Heritability and genetic advance.

Table 6 shows heritability % in broad and narrow sense and genetic advance for all traits in six crosses. High heritability values in broad sense were detected for six crosses except weight of huskless in P_3 x P_4 (45.94%) and beta carotene in P_1 x P_4 (43.87%). These results are in agreement with those obtained by Sedhom 1984, El-Shouny et al. (2005) and Abou-Deif (2007).

Estimates of narrow sense heritability for all characters in all crosses under study are presented in (Table, 5). Heritability in narrow sense was computed according to Mather's procedure on the basis of F_2 and back crosses. High heritability in narrow sense was detected for total sugare in the third cross, number of days to tassling in the fifth cross, number of days of sillking in the first, second and fifth crosses, and beta carotene in the sixth crosses Moderate to low heritability values in narrow sense were detected for the other cases.

For number of days to tassling in the fifth cross, number of days to sillking in the first, second and fifth crosses, total sugars in the third cross and beta caroten in the sixth cross in the third cross, heritability values in narrow sense were high in magnitude and nearly equal its corresponding value in broad sense. This revealed that the genetic variance was mostly attributed to the additive effects of genes for these traits. As previously reported, non-additive gene effects were found to be the major contributing factor for these traits (Table 3). Based on these assumptions, heritability in narrow sense was excepted to be low, the exception which was not relized in the present study. Comstock (1955), stated that the presence of epistatic gene effects will cause an upward bias in the estimate of additive genetic variance. Gamble (1962) also reported that genetic model assuming negligible epistasis may be an important source of bias in the estimate of additive genetic variance and inclusion of epistasis in such models would perhaps decrease the amount of additive one.

For remaing traits of the six crosses, narrow sense heritability values were much lower than those of broad sense indicating that most of genetic variance was due to non-additive effects i.e., dominance and/ or epistasis. This finding ascertained the previous studies on the nature of gene action where the non-additive gene effects were found to have a great role for these traits (Table 3). Such results are in agreement with that obtained by several investigators, Sedhom 1984, El-Shouny et al. (2005) and Abou-Deif (2007) who obtained high to moderate heritability values for date of tasselling and silking and plant height. Warner (1952), El- Ebrashy (1961) and Fadhi (1978) reported low values of heritability in narrow sense for grain yield per plant.

Genetic advance upon selection:

Table, 5 shows the genetic advance upon selection as the percentage of F_2 for all the studied traits in all crosses under study With the exception of number of days to tasseling and silking and plant height in most crosses, the results indicated that the predicted genetic advance expressed as the percentage of the mean was moderate to high for all the studied traits. For the exceptional cases, low GA% was low (Table, 4). Johanson et al. (1955) reported that heritability estimates along with genetic gain are usually more useful than the heritability values alone in predicting the resultant effect for selecting the best individuals. On the other hand, heritability is not always associated with high genetic advance, but to make effective selection, high heritability should be associated with high genetic gain. In the present work relative high genetic gain was found to be associated with rather moderate heritability estimates for plant height in the first and third cross. Therefore, selection for these cases in these particular population should be effective and satisfactory for successful breeding purposes.

For weight of husked and weight of huskless, high genetic gain was associated with low heritability values. In spite of the relative moderate heritability in narrow sense computed in both traits, estimates of additive and additive x additive genetic effects were highly significant therefore, it could be suggested that selection for these traits in subsequent generations will be relatively more effective than in the early F_2 generation. It could be concluded that the highest genetic advance detected for both traits, in spite of low heritability estimates, may be due to a relatively range of variability in these populations.

For number of days to tasselling and sillking low genetic gain was accompanied by high or moderate heritability values. As it well known, expected improvement of selection is directly proportional to heritability. Also, the expected response to selection varies with the phenotypic standred deviation of population means. This figure is a measure of the total variability in the trait and therefore, reflect, the total response that could be realized by breeding techniques. It is possible to visualize a situation where the heritability is high, but because of little potential for improvement (low

δ^2 ph) little response can be expected. On this basis this situation could be explained.

Table (5): Heritability percentage in broad and narrow sense for studied in the six crosses.

Cross	Parameters	Number of dayes to tasseling	Number of dayes to silking	Plant height	Weight of husked
1X2	h. broad	93.41	82.73	83.71	73.36
	h. narrow	52.94	74.51	47.46	57.5
	delta g	3.56	3.43	19.32	135.49
	Genetic advanc%(Delta g%)	5.68	5.38	9.2	32.45
	G.S %	5.68	5.38	9.2	32.45
	G.C.V%	5.04	3.19	8.61	23.46
1X3	h. broad	81.1	96.3	93.57	80.32
	h. narrow	32.8	72.45	53.99	32.49
	delta g	1.12	5.49	27.76	76.68
	Genetic advanc%(Delta g%)	1.78	8.66	13.32	23.31
	G.S %	1.78	8.66	13.32	23.31
	G.C.V%	2.37	5.69	11.59	31.22
1X4	h. broad	72.79	79.93	93.8	74.34
	h. narrow	33.19	51.55	57.29	58.78
	delta g	1.11	2.12	27.16	150.77
	Genetic advanc%(Delta g%)	1.78	3.33	12.71	35.61
	G.S %	1.78	3.33	12.71	35.61
	G.C.V%	2.22	2.8	10.43	25.36
2X3	h. broad	63.18	76.79	85.23	71.52
	h. narrow	43.94	49.72	49.13	39.35
	delta g	0.84	1.58	18.7	76.27
	Genetic advanc%(Delta g%)	1.4	2.69	11.33	22.72
	G.S %	1.4	2.69	11.33	22.72
	G.C.V%	1.23	2.3	10.33	23.71
2X4	h. broad	82.16	82.25	86.52	61.52
	h. narrow	67.2	72.95	44.8	53.85
	delta g	3.28	3.62	26.2	109.47
	Genetic advanc%(Delta g%)	5.43	5.94	15.86	37.06

	G.S %	5.43	5.94	15.86	37.06
	G.C.V%	3.55	3.58	15.98	26.2
3X4	h. broad	68.93	81.84	85.29	56.01
	h. narrow	21.1	50.34	31.49	49.39
	delta g	0.63	2.03	12.11	96.66
	Genetic advanc%(Delta g%)	1.03	3.26	6.71	29.12
	G.S %	1.03	3.26	6.71	29.12
	G.C.V%	1.97	2.84	9.55	21.42

Table (5): cont.

cross	**Parameter**	**Weight of huskless**	**Total sugare**	**Starch %**	**Beta caroten p.p.m**
1X2	h. broad	61.57	79.52	82.98	81.03
	h. narrow	31.79	61.14	59.58	69.64
	delta g	53.55	1.55	4.85	3.38
	Genetic advanc%(Delta g%)	18.38	18.92	19.63	57.79
	G.S %	18.38	18.92	19.63	57.79
	G.C.V%	22.02	13.4	14.57	36.27
1X3	h. broad	78.98	90.58	86.31	87.97
	h. narrow	19.9	49.39	57.91	60.73
	delta g	40.57	1.82	8.21	2.89
	Genetic advanc%(Delta g%)	16.79	24.63	37.34	44
	G.S %	16.79	24.63	37.34	44
	G.C.V%	36.4	23.03	29.08	32.99
1X4	h. broad	73.83	95.9	91.5	43.87
	h. narrow	23.3	64.31	45.54	23.92
	delta g	47.5	3.2	5.74	1.12
	Genetic advanc%(Delta g%)	16.46	43.38	27.03	14.88
	G.S %	16.46	43.38	27.03	14.88
	G.C.V%	29.46	32.07	27.55	20
2X3	h. broad	55.34	86.71	88.19	79.25
	h. narrow	40.94	21.39	48.39	27.54
	delta g	60.65	0.53	5.49	1.41
	Genetic advanc%(Delta g%)	25.88	6.73	31.01	41.01
	G.S %	25.88	6.73	31.01	41.01
	G.C.V%	22.83	14.22	29.22	64.34
2X4	h. broad	53.01	88.22	95.62	67.32
	h. narrow	38.14	32.44	21.26	56.91
	delta g	61.36	0.91	2.66	3.62
	Genetic advanc%(Delta g%)	30.93	12.2	12.09	59.8
	G.S %	30.93	12.2	12.09	59.8
	G.C.V%	28.66	17.15	27	41.85
3X4	h. broad	45.94	95.1	99.13	81.38
	h. narrow	15.27	50.42	39.29	78.73

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وراثة وطبيعة توريث بعض الصفات الإقتصادية في الذرة السكرية

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الملخص العربى

أجريت هذه التجربة الحقلية خلال الموسم الصيفى و النيلى لعامى 2013 و 2014 بمزرعة و ومعمل حفظ الأصول الوراثية بقسم البساتين بكلية الزراعة بمشتهر - جامعة بنها–محافظة القليوبية- وكذلك بمركز بحوث شركة هايتك لانتاج التقاوى-أسيوط-مصر بغرض دراسة وراثة وطبيعة توريث بعض الصفات الإقتصادية في الذرة السكرية لستة هجن. التحليل الوراثى للعشائر الستة للهجن الستة تحت الدراسة كان التباين الوراثى معنويا فى معظم الصفات فى الست هجن.كانت قوة الهجين معنوية و سالبة لعدد الايام حتى ظهور 50% من النورة المذكرة و المؤنثة فى معظم الهجن الستة . بينما كانت قوة الهجين معنوية و موجبة لوزن الكوز بأغلفة وبدون الأغلفة و ارتفاع النبات. بالنسبة لتحليل السيادة فقد كانت السيادة فائقة فى اتجاه الاب المبكر لصفات التبكير و لجهة الاب الاعلى لصفات المحصول و مكوناته. بالنسبة لتأثير التربية الداخلية فقد ظهر نقصا سالبا و معنويا لصفات التزهيرلمعظم الهجن الستة. بينما كان هناك نقصا موجبا ومعنويا لكل الصفات الاخرى عدا ارتفاع النبات والسكر والنشا فى الهجين الثالث والبيتا كاروتين فى الثانى. أظهرت نتائج دراسة التفوق ان انحراف متوسط الجيل الثانى عن القيمة المتوقعة له و كذلك انحراف متوسط الهجن الرجعية عن القيمة المتوقعة لها معنوية لمعظم الصفات. اوضحت النتائج ان الفعل المضيف للجينات كان معنويا لصفة عدد الايام حتى ظهور 50% من الحراير وارتفاع النبات ووزن الكوز بأغلفة ونسبة السكريات والنشا والبيتا كاروتين فى الحبوب لست هجن وعدد الايام حتى ظهور 50% من النورات المذكرة عدا الهجين الرابع ووزن الكوز بدون أغلفة عدا الهجين السادس. بينما كان فعل السيادة للجينات كان معنويا لصفة عدد الايام حتى ظهور 50% من النورة المذكرة وارتفاع النبات ووزن الكوز بأغلفة ووزن الكوز بدون أغلفة للست هجن وعدد الايام حتى ظهور 50% من النورات المؤنثة عدا الهجين الثانى ونسبة السكرعدا الهجين الثالث والرابع ونسبة النشا عدا الهجين الثالث والسادس والبيتا كاروتين عدا الهجين الخامس والسادس. كان معامل الاختلاف الوراثى معنويا لصفات الوزن الكيزان بأغلفة ووزن الكيزان بدون الأغلفة ونسبة النشا والبيتا كاروتين فى الهجن الستة. كانت قيمة الكفاءة الوراثية بمعناها العريض عالية لكل الصفات فى الست هجن عدا صفة وزن الكيزان بدون أغلفة و كانت قيمة الكفاءة الوراثية بمعناها الضيق عالية لصفات وعدد الايام حتى ظهور 50% من النورات المذكرة فى الهجين الخامس وعدد الايام حتى ظهور 50% من النورات المؤنثة فى الهجين الأول والثانى والخامس و البيتا كاروتين فى الأول السادس و متوسطه الى منخفضة للصفات المتبقية.