



## EFFECTIVENESS OF $S_1$ FAMILIES SELECTION FOR IMPROVING GRAIN YIELD IN TWO MAIZE POPULATIONS

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### ABSTRACT

This investigation was conducted to determine the effectiveness of  $S_1$  progenies to improve the breeding value of two maize populations, for grain yield, yield components and other traits. A total of 81  $S_1$  lines from each population were used in this study. Results showed that mean squares due to  $S_1$  lines of both populations were highly significant for all the studied traits. Genotypic variances for no. of rows/ear, ear diameter, 100-kernel weight, grain yield/plant and grain yield/plot of Pop A were higher than those of Pop B. Genotypic coefficient of variability for no. of rows/ear, ear diameter, 100-kernel weight, grain yield/plant and grain yield/plot for  $S_1$  lines of Pop. A were higher than those obtained by  $S_1$  lines of Pop. B. Average of grain yield/plant for Pop. A ( $C_1$ ) were 138.47g., compared to 127.05 g. of the original Pop. A. The differences between the  $C_1$  cycle, and the original Pop. A was significant. For Pop. B average grain yield/plant of  $C_1$  was 141.15g., compared to 131.30 g. of the original Pop. B. The differences between the  $C_1$  cycle and the original Pop. B was significant. Expected gain for grain yield/plant was 21.61 and 10.17 and actual gain was 8.99 and 7.50% for Pop A and Pop B, respectively. Expected gain from selected in Pop A was higher than those of Pop B. Also the actual gain from selection in improved Pop A was better than those in Pop B. These results could be attributed to the presence of more additive genetic variance in Pop A than in Pop B.

**Key Words:** Maize, recurrent selection, Genetic variance and Genetic gain.

## INTRODUCTION

Production of maize since the last century mostly depends on hybrid vigor resulting from crossing among inbred lines. Obtaining high hybrid vigor requires obtaining superior inbred lines that endure inbreeding depression with high combining ability; that in turn requires enhancing our different sources of isolation. Reciprocal recurrent selection, originally proposed by Comstock *et al.* (1949), recurrent selection has been widely used for enhancing population's performance. It is a cyclical process, which, except for mass selection includes three phases: (1) development of progenies, (2) progeny evaluation, and (3) recombination of selected progenies. Selection effect *per se* led to increase in alleles with favorable effects and decreasing in alleles with unfavorable effects. These create a new recombination of alleles inside the target population led to improving in the performance of its extracted lines. Relating to this Hallauer and Miranda (1988) reported that use of different methods of recurrent selection have emphasized early testing for discriminating among progenies to determine which ones to recombine to from the next cycle of selection. Tanner and Smith (1987) reported that selection based on  $S_1$  is expected to utilize additive genetic variance. However, heritability estimates differed according to population (genetic variance) traits, selection methods and environmental conditions as reported by Coors (1988), Soliman

(1991), Walters *et al.* (1991), Mahmoud *et al.* (1999), El-Morshidy *et al.* (2002) and Saini and Malhi (2001) they indicated that  $S_1$  family selection was more effective than full-sib and half-sib selection in improving populations, expected responses were 22.73, 12.70 and 9.04%, respectively. Shah *et al.* (2007) suggested that  $S_1$  recurrent selection was quite effective in improving grain yield. The main objectives of this investigation were to: (i) evaluate the 1<sup>st</sup> cycle of  $S_1$  families' selection, for improving grain yield of two different maize populations i.e., Pop A (IW5.Leguma) and Pop B (IW154NL.5). (ii) estimate the genetic components of variance and heritability and (iii) calculate the expected and actual gain from selection after one cycle of  $S_1$  lines *per se* selection method.

## MATERIALS AND METHODS

This study was carried out during the period from 2012 to 2014 at Experimental Farm, Faculty of Agricultural, El-Minia Univ., El-Minia, Egypt. Two maize populations i.e., Pop. A (IW5.Leguma) and Pop. B (IW154 NL.5) was used in the present study. The two populations were providing by National Maize Program. The two populations were planted in the summer season of 2012 at Experimental Farm, Faculty of Agricultural, El-Minia Univ. From each population, 200 plants were selected and selfed to produce  $S_1$  lines. At harvest, 81 $S_1$  lines which had sufficient seed for evaluation were selected from each population. In 2013

summer season, the S<sub>1</sub> lines of each population were evaluated in sets within replication (9x9) with two replications, as explained by Hallauer and Miranda 1988. These sets were arranged in randomized incomplete block design with two replications, each set of 9 S<sub>1</sub> groups were randomly arranged. Therefore, two experiments were conducted to evaluate S<sub>1</sub> families of both populations A and B. In each trail, the experimental plot size was one row, 3 meters' length and 70 cm

wide and 30 cm between hills within a row. Seedlings were thinned to one plant/hill before the first irrigation (three weeks after sowing). Nitrogen fertilizer was applied at the rate of 120 kg/fed. in two doses before the first and the second irrigations. Normal cultural practices were applied as recommended. The expected mean squares and degrees of freedom for S<sub>1</sub> family evaluation are presented in Table1.

Table 1. Analysis of variance for S<sub>1</sub> family.

S.O. V	D.F	M.S	E.M. S
Reps (r)	r-1		
Sets (s)	s-1		
Sets x Reps	(s-1) (r-1)		
S <sub>1</sub> families/sets	s(f-1)	M <sub>2</sub>	$\sigma^2_e + r \sigma^2_g$
Error	s(r-1) (f-1)	M <sub>1</sub>	$\sigma^2_e$

The expected mean squares were used to estimate the following genetic parameters:

1. Genetic variance  $\sigma^2_g = (M_2 - M_1 / r)$ .
2. Phenotypic variance  $\sigma^2_{ph} = \sigma^2_g + (\sigma^2_e / r)$ .
3. Genotypic coefficient of variability (gcv) =  $(\sqrt{\sigma^2_g} / X) 100$ .
4. Phenotypic coefficient of variability (pcv) =  $(\sqrt{\sigma^2_{ph}} / X) 100$ .
5. Heritability in broad sense  $h^2 = (\sigma^2_g / \sigma^2_{ph}) 100$ .
6. Expected gain from selection  $\Delta G = K. h^2. \sigma_{ph}$ .

Where: K is selection differential for selection intensity (12.34%) = 1.667.

Ten S<sub>1</sub> lines were selected based on, grain yield from each trail of the

two populations. The selection intensity which used was 12.34%. Equal number of seeds from the selected S<sub>1</sub> was carefully bulked to obtain the base of the first cycle of selection. Two Populations of the selected families were formed as follows:

- 1- Pop. A C<sub>1</sub> (S<sub>1</sub> *per se*) yields.
- 2- Pop.B C<sub>1</sub> (S<sub>1</sub> *per se*) yields.

In 2013 autumn season, the two groups of the selected families were planted in non-replicated plots at Experimental Farm, Faculty of Agricultural, El-Minia Univ. The plot size was 30 rows, 3m length, 70cm apart and 30cm between hills within a row. Before silking, the ears were covered by glycine bags to prevent cross-pollination. At 50-60% silking,

pollen grains were collected from all plants in each plot and bulked. The bulked pollen grains of a plot were used to pollinate the plants of the same plot. Pollinated ears were harvested, dried, and shelled together to form the first cycle seed.

In 2014 season, the first cycle of selection ( $C_1$ ) for each population were evaluated against the original populations to measure the actual gain from selection at Experimental Farm, Faculty of Agricultural, El-Minia Univ. Randomized complete block design with four replications was used. The experimental plot size was 4 rows, 3m length and 70cm between rows. Planting was in hills spaced 30cm apart. Seedlings were thinned to one plant/hill before the first irrigation. Nitrogen fertilizer was applied at the rate of 120 kg/fed. in two doses; before the first and second irrigation. Normal agricultural practices were applied as recommended. Data were collected from the inner two rows.

Data were recorded for plant and ear height (cm), ear length (cm), ear diameter (cm), number of rows/ear, 100-kernel weight (g.), grain yield/plant (g.) and adjusted grain yield (kg. /plot) to 15.5% moisture content was measured from each plot.

The experimental design used for evaluation was a set within reps (9x9) with two replications (Hallauer and Miranda 1988). The expected mean squares for families ( $\sigma^2_g$ ) was estimated by Empig *et al.* (1972) to be ( $\sigma^2_A + C$ ) where (C) is a function of dominance and gene frequency. The expected value of ( $\sigma^2_g$ ) will reduce to

$\sigma^2_A$  if dominance or epistasis is lacking in the population or when the gene frequency for the segregation loci equal 0.5. Accordingly, the additive genetic variance was assumed to be  $\sigma^2_A = \sigma^2_g$ .

## RESULTS AND DISCUSSION

### A- Evaluation of $S_1$ *per se*.

Analysis of variance for the studied traits of  $S_1$  lines for both populations are presented in Table 2. Highly significant differences among  $S_1$  lines were detected in both populations for all studied traits.

### Variance components and heritability

Genetic and phenotypic variance and broad sense heritability (H) are presented in Table 3. Results showed that genetic variance for all studied traits were less than phenotypic variance. This is due to that the genetic variances depend upon the effect of additive and dominance but the phenotypic variance is due to the effect of both genetic and environmental variances. Genetic and phenotypic variance of no. of rows/ear, ear diameter, 100-kernel weight, grain yield/plant and grain yield/plot for  $S_1$  lines derived from Pop. A were higher than those of  $S_1$  lines derived from Pop. B, indicating the presence of more variability in the base Pop A for these traits.

On the other side, genetic and phenotypic variance values of Pop. B was more than those obtained from Pop. A for plant height and ear height

indicating that more variability was existed in the base Pop. B for these traits. Heritability is considered to be one of the most important parameters to express relative genetic variability whether on a broad or narrow sense. Broad sense heritability (H) for S<sub>1</sub> lines of Pop. A was high for plant height (86.46%), no. of rows/ear (90.91%), grain yield/plant (88.06%), grain yield/plot (88.91%), ear diameter (80.00), 100-kernel weight (82.52%) and ear height (78.68%) and moderate for ear length (56.24%). On the other hand, broad sense heritability for S<sub>1</sub> lines of Pop. B was high for plant height (89.53%), 100-kernel weight (86.16%), grain yield/plot (86.15%), ear height (82.76%), ear length (82.56%), ear diameter (83.33%), no. of rows/ear (77.04%), grain yield/plant (72.18%).

Generally, it could be seen that heritability estimates for the studied traits varied greatly from Pop. A to Pop. B. Heritability estimates were low for plant height, ear height, ear length, ear diameter and 100-kernel weight in Pop. A, while it was high in Pop. B. The opposite was true for no. of rows/ear, grain yield/plant and grain yield/plot. These results are in agreement with those obtained by Galal *et al.* (1984) who reported that heritability estimates were 58-92% for grain yield, 84-86% for days to 50% silking, 83-91% for plant height and 79-87% for ear height. Dawoud (1984) found that heritability estimates ranged from 46.13% for grain yield to 83.81% for ear height, higher estimates were obtained for number of

rows/ear, plant height, number of kernels/row, 100-kernel weight and ear length, moderate estimates were recorded for the other studied traits. Sadek *et al.* (1986) showed that heritability estimates in broad sense were 49.20, 22.90, 25.00, 13.60, 18.00 and 23.40 for days to 50% silking, plant height, grain yield, 100-kernel weight, no. of rows/ear and ear length, respectively. Soliman (1991) reported that heritability estimates were high for flowering date, plant and ear height, but it was low for grain yield. Abouel-Saad *et al.* (1994) showed that heritability estimates were 63.2, 42.3, 49.0, 60.6, and 35.2% for grain yield/fed. and grain yield/plant, days to 50% silking, plant height and ear height, respectively. Mahmoud *et al.* (1999) found that heritability estimates were 74.3% for grain yield and 89.5% for no. of days to 50% silking. El-Morshidy *et al.* (2002), Ibrahim (2004) and Garbuglio *et al.* (2009) obtained high heritability estimates for ear height and grain yield/plant.

Estimates of genotypic (GCV%) and phenotypic (PCV%) coefficient of variability for S<sub>1</sub> lines for all studied traits of the two populations are presented in Table 3. Results showed that GCV and PCV were high for S<sub>1</sub> of Pop. A compared to Pop. B for no. of rows/ear, ear diameter, 100-kernel weight, grain yield/plant and grain yield/plot, indicating more variability in the base population A for these traits. The opposite was true for plant height and ear height for Pop. B, indicating more variability in the base Pop. B for these traits, while, GCV for

ear length in Pop. A is lower than GCV recorded for Pop. B, but PCV of this trait in Pop. A is higher than these in Pop. B. Genotypic coefficient of variability for no. of rows/ear, ear length, ear diameter, 100-kernel weight, grain yield/plant and grain yield/plot for S<sub>1</sub> lines of Pop. A were 10.16, 10.57, 7.19, 10.97, 15.16 and 3.42 higher than those S<sub>1</sub> lines from Pop. B with values of 7.78, 11.12, 5.79, 8.24, 7.54 and 2.46 for the same traits, respectively. On the other hand, the opposite was true for plant height and ear height. On the other hand, phenotypic coefficient of variability for no. of rows/ear, ear length, ear diameter, 100-kernel weight, grain yield/plant and grain yield/plot for S<sub>1</sub> lines of Pop. A were 10.66, 14.10, 8.03, 12.07, 16.16 and 3.62 higher than those S<sub>1</sub> lines from Pop. B with values of 8.87, 12.26, 6.53, 8.88, 8.88 and 2.65 for the same traits, respectively.

The same results were obtained by El-Morshidy *et al.* (2002) who found that pcv was higher than gcv for all studied traits. Ibrahim (2004) found that phenotypic coefficient of variability (pcv) for various traits were relatively higher than genotypic coefficient of variability (gcv) for S<sub>1</sub> families derived from different populations.

#### **Means (X) and coefficients of variability (C. V%)**

Mean and coefficients of variability for different for S<sub>1</sub> lines *per se* both Pop. A and Pop. B is presented in Table 4. Mean performance values for plant height (cm), ear height (cm), no. of rows/ear, ear length (cm), ear diameter(cm), 100-kernel weight (g.), grain yield/plant (g.) and grain yield/plot (kg.) for S<sub>1</sub> lines of Pop. A were 169.58, 85.16, 12.83, 15.36, 3.94, 30.36, 111.06 and 2.23, respectively. Mean performance values for plant height (cm), ear height (cm), no. of rows/ear, ear length (cm), ear diameter(cm), 100-kernel weight (g.), grain yield/plant (g.) and grain yield/plot (kg.) for S<sub>1</sub> lines of Pop. B were 162.20, 81.89, 12.45, 15.64, 3.85, 31.73, 115.20 and 2.34, respectively. It is clear that half of the studied traits (plant and ear height, no. of rows/ear and ear length) in Pop. A possessed higher mean performance than Pop. B and the another half (ear diameter, 100-kernel weight and grain yield/plant and plot) took the opposite trend. The coefficient of variability (C.V. %) for Pop. A ranged from 4.43% for ear diameter to 9.30% for ear length, while it ranged from 4.19% for ear diameter to 9.03% for ear height for Pop. B.

Table 2. Mean squares of the S<sub>1</sub> lines for the studied traits of the Pop. A and B.

S.O.V	DF	MS									
		Plant height (cm)		Ear height (cm)		No. of rows/ear		Ear length (cm)		Ear diameter (cm)	
		PopA	PopB	PopA	PopB	PopA	PopB	PopA	PopB	PopA	PopB
Reps.	1	1570	423.4	366.6	182.6	6.5	2.9	10.0	13.2	0.63	2.23
Sets	8	347.9**	1112**	87.9**	289**	4.2**	2.5**	8.0**	19.2**	0.12**	0.17**
SetsxReps.	8	9.4	6.3	3.8	2.2	0.2	0.2	0.3	0.1	0.06	0.03
S <sub>1</sub> lines/Sets	72	601**	1006.7**	156.4**	317.3**	3.7**	2.5**	9.4**	7.4**	0.19**	0.13**
Error	72	81.4	105.4	33.3	54.7	0.3	0.6	4.2	1.3	0.03	0.26

  

S.O.V	DF	MS					
		100-kernel weight (g.)		Grain yield/plant (g.)		Grain yield/plot (kg.)	
		PopA	PopB	PopA	PopB	PopA	PopB
Reps.	1	183.9	312.02	1655.23	2808.25	14897.10	23870.13
Sets	8	24.15**	38.12**	217.33**	343.08**	1955.94**	2916.21**
SetsxReps.	8	2.72	1.57	24.47	14.18	220.26	120.54
S <sub>1</sub> lines/Sets	72	26.96**	15.90**	242.63**	143.16**	2183.65**	1216.94**
Error	72	4.75	2.20	51.77	39.82	242.94	168.49

\*\* , Highly significant at 0.01 levels of probability.

Table 3. variance components and heritability of S<sub>1</sub> lines for the studied traits of the Pop. A and B.

S.O.V	MS									
	Plant height (cm)		Ear height (cm)		No. of rows/ear		Ear length (cm)		Ear diameter (cm)	
	PopA	PopB	PopA	PopB	PopA	PopB	PopA	PopB	PopA	PopB
$\delta^2_g$	259.79	450.67	61.53	131.32	1.70	0.94	2.63	3.03	0.08	0.05
$\delta^2_e$	81.39	105.36	33.33	54.69	0.34	0.57	4.18	1.30	0.03	0.02
$\delta^2_{ph}$	300.48	503.35	78.20	158.66	1.87	1.22	4.68	3.67	0.10	0.06
G.C.V	9.50	13.08	9.21	13.94	10.16	7.78	10.57	11.12	7.19	5.79
P.C.V	10.22	13.83	10.38	15.38	10.66	8.87	14.10	12.26	8.03	6.53
H%(BS)	86.46	89.53	78.68	82.76	90.91	77.04	56.24	82.56	80.00	83.33

  

S.O.V	MS					
	100-kernel weight (g.)		Grain yield/plant (g.)		Grain yield/plot (kg.)	
	PopA	PopB	PopA	PopB	PopA	PopB
$\delta^2_g$	11.10	6.85	190.85	51.66	970.5	524.22
$\delta^2_e$	4.75	2.20	51.77	39.82	242.94	168.49
$\delta^2_{ph}$	13.45	7.95	216.74	71.57	1091.5	608.46
G.C.V	10.97	8.24	15.16	7.54	3.42	2.46
P.C.V	12.07	8.88	16.16	8.88	3.62	2.65
H%(BS)	82.52	86.16	88.06	72.18	88.91	86.15



Table 4. Mean (X) and coefficient of variability (CV%) for all studied traits for S<sub>1</sub> lines (Pop.A&B).

Traits	X		$\delta^2 e$		CV%	
	PopA	PopB	PopA	PopB	PopA	PopB
Plant height (cm)	169.58	162.20	81.39	105.35	5.32	6.33
Ear height (cm)	85.16	81.89	33.33	54.69	6.78	9.03
No. of rows/ear	12.83	12.45	0.34	0.57	4.54	6.09
Ear length (cm)	15.36	15.64	4.18	1.30	9.30	7.28
Ear diameter (cm)	3.94	3.85	0.03	0.03	4.43	4.19
100-kernel weight (g.)	30.36	31.73	4.75	2.20	4.86	4.67
Grain yield/plant (g.)	111.06	115.20	51.77	39.82	6.47	5.47
Grain yield/plot (kg.)	2.23	2.34	242.94	168.49	6.98	5.54

### A- Evaluation of the first cycle of selection (C<sub>1</sub>):

#### Analysis of variance

Mean squares for studied traits for the improved Populations, which formed from the selected S<sub>1</sub> lines of the two original populations are presented in Table 5. Significant and highly significant differences were detected for all studied traits, except no. of rows/ear and ear diameter, indicating the presence of variation among populations.

#### Mean performance

Average performances of all studied traits for original and S<sub>1</sub> *per se* of Pop. A and B are presented in Table 6. Average of grain yield/plant for S<sub>1</sub> of Pop. A was (138.47g.) compared to (127.05g.) of the original Pop. A. The differences between the C<sub>1</sub> cycle and the original Pop. A was significant. For Pop. B average grain yield/plant was (141.15g.) compared to (131.30g.) of the original Pop. B. The differences between the C<sub>1</sub> cycle and the original Pop. B was significant.

Average of grain yield/plot for Pop. A was (2.78kg.) for C<sub>1</sub> compared to 2.54kg. of the original Pop. A. The differences between the C<sub>1</sub> cycle and the original Pop. A was significant. For Pop. B average grain yield/plot of the S<sub>1</sub> selection method was (2.83 kg.) for S<sub>1</sub> compared to 2.63kg. of the original Pop. B. The differences between the C<sub>1</sub> cycle and the original Pop. B was significant. Generally, the yield of the first cycle<sup>-1</sup> of Pop. A was more than those of Pop. B, indicating wide of the variability of Pop. A than the Pop. B.

The genetic gain from selection has been one of the most important contributions of quantitative genetics to maize breeder. Another important application is concerned with comparison of different selection procedures. Estimates of the expected and actual gain from selection for the best 10% families for the characters studied as selection criterion through S<sub>1</sub> families' selection method in both Populations are given in Table 7. Expected gain for grain yield/plant

was 21.61 in Pop. A and 10.17 in Pop. B for  $S_1$  *per se* method. On the other hand, the actual gain from selection of improved Pop. A was 8.99%, while it was 7.50% for improved Pop. B for  $S_1$  *per se* method of selection. In Pop. B it was lower than those of Pop. A. Expected gain for grain yield/plot was 0.04 in Pop. A and 0.03 in Pop. B for  $S_1$  *per se* method. On the other hand, the actual gain from selection of improved Pop. A was 9.45%, while it was 7.60% for improved Pop. B for  $S_1$  *per se* method of selection in Pop. B. was lower than those of Pop. A. Also the actual gain from selection in improved Pop. A was better than those in Pop. B for the two selection methods. These results could be attributed to the presence of more additive genetic variance in Pop. A than in Pop. B. the same results were obtained by Betran and Hallauer (1996) who indicated that reciprocal recurrent selection was more effective than intrapopulation recurrent selection in reducing ear height and days from planting to silking. Yield improvement of Pop. B was suitable

than the Pop. A for  $S_1$  *per se* causing the more variability of Pop. B. The present results indicate that the  $S_1$  method of selection and reciprocal recurrent selection are effective in improving grain yield and its components of the two studied maize populations. The same results were obtained by Schnicker and lamkey (1993) who indicated that reciprocal recurrent selection has been effective in increasing the mean performance of the population cross maintain genetic variance. Menkir and Kling (1999) found that the reciprocal recurrent selection was effective in improving grain yield and other traits of interpopulations cross without a loss in genetic variance. Peng *et al* (2007) studied three recurrent selection methods i.e., modified  $S_1$  family selection, modified  $S_1$  – HS and MHRRS. They indicated that the three recurrent methods were effective for increasing grain yield in testcrosses and improvement of general combining ability in maize populations.

Table 5. Mean squares of the studied traits for the 1<sup>st</sup> cycle Populations.

S.O. V	DF	MS							
		Plant height	Ear height	No. Rows/Ear	Ear Length	Ear Diameter	100-kernel Weight	Grain Yield/Plant	Grain Yield/Plot
Reps.	3	80.47	71.34	0.18	0.41	0.04	9.92	6.55	0.09
Genotypes	5	401.87**	318.75**	0.45	14.62**	0.014	6.03**	98.87**	0.45*
Error	15	15.95	11.38	0.39	1.61	0.016	1.14	3.86	0.12

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

Table 6. Mean performance of the studied traits for the 1<sup>st</sup> cycle populations in two maize populations.

Pop.	Plant height	Ear height	No. Rows/Ear	Ear Length	Ear Diameter	100-kernel Weight	Grain Yield/Plant	Grain Yield/Plot
Pop. A	269.06	161.48	13.00	20.10	4.50	35.04	138.47	2.78
Original	250.60	149.05	13.37	19.20	4.40	33.52	127.05	2.54
Pop. A								
PopB	260.82	156.37	13.95	22.08	4.42	35.30	141.15	2.83
Original	251.72	148.00	13.77	19.20	4.35	32.97	131.30	2.63
Pop. B								
LSD	6.01	5.08	0.94	1.91	0.19	1.60	2.96	0.52
0.05								

Expected (Ex.) and actual (Ac.) gain from selection:

Table 7. Expected (Ex.) and actual (Ac.) % gain from the original populations of S<sub>1</sub>-line selection in two maize populations.

Pop.	Plant height		Ear height		No. Rows/Ear		Ear Length	
	Ex.	Ac.	Ex.	Ac.	Ex.	Ac.	Ex.	Ac.
Pop A	24.98	7.37	11.59	8.34	2.07	-2.77	2.28	4.68
PopB	33.48	3.61	17.37	5.65	1.41	1.31	2.63	15
Pop.	Ear Diameter		100-kernel Weight		Grain Yield/Plant		Grain Yield/Plot	
	Ex.	Ac.	Ex.	Ac.	Ex.	Ac.	Ex.	Ac.
Pop. A	0.42	2.27	5.04	4.53	21.61	8.99	0.04	9.45
Pop. B	0.34	1.61	4.04	7.07	10.17	7.50	0.03	7.60

Gain percentage based on the original (C<sub>0</sub>).

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### الملخص العربي

#### كفاءة انتخاب عائلات الجيل الذاتي الأول لتحسين محصول الحبوب في عشيرتين من الذرة الشامية

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أجري هذا البحث لاختبار وتقييم عائلات الجيل الذاتي الأول بهدف تحسين القيمة التربوية لعشيرتين من الذرة الشامية البيضاء هما (Pop. B (IW154 NL.5), Pop. A (IW5.Leguma) وذلك لصفة محصول الحبوب ومكوناته. أستخدم في هذه الدراسة 81 عائلة من عائلات الجيل الذاتي الأول من كلا العشيرتين، أوضحت نتائج تقييم عائلات الجيل الذاتي الأول وجود فروق معنوية لجميع الصفات المدروسة لكننا العشيرتين. كان التباين الوراثي لصفات عدد الصفوف/كوز وقطر الكوز ووزن الحبة ووزن محصول النبات ووزن المحصول/القطعة في العشيرة A أعلى من العشيرة B. كانت تباينات التفاعل بين التركيب الوراثية والمجموعات لنفس الصفات السابقة في العشيرة A عاليا عن مثيلتها في العشيرة B. كانت قيم معامل الاختلاف الوراثي عاليا لصفات عدد الصفوف/كوز وقطر الكوز ووزن الحبة ووزن محصول النبات ووزن المحصول/القطعة في العشيرة A عاليا عن العشيرة B.

كان متوسط محصول النبات الفردي للدورة الأولى للعشيرة A هو 138.47 جم مقارنة بالعشيرة الأصلية 127.5 جم. وكانت الفروق معنوية بين الدورة الأولى والعشيرة الأصلية A. وعلى الجانب الآخر كان متوسط محصول النبات الفردي للعشيرة B هو 141.15 جم مقارنة بالعشيرة الأصلية B 131.30 جم. وكانت الفروق بينهما معنوية.

كان التقدم المتوقع لصفة محصول النبات الفردي 21.61 و 10. والحقيقي 8.99 و 7.50% للعشيرتين A و B على التوالي، وكان التقدم المتوقع والحقيقي للعشيرة A أعلى من العشيرة B وهذا يدل على ان العشيرة A استجابتها للتحسين أعلى من العشيرة B.