

## Effectiveness of S<sub>1</sub> Families Selection For Improving Grain Yield In Two Yellow Maize Populations

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**Abstract:** This investigation was conducted to determine the effectiveness of S<sub>1</sub> progenies to improve the breeding value of two yellow maize populations, i.e., Tuxpeno Corn Belt and Puerto Rico for grain yield, yield components and other traits. A total of 81 S<sub>1</sub> lines from each population were used in this study. Results revealed that mean squares due to S<sub>1</sub> lines of both populations were significant or highly significant for all the studied traits. On the other hand, mean squares due to S<sub>1</sub> x locations were significant or highly significant for all the studied traits of the two populations, except ear length of pop. A, no. of kernels/row and 100-kernel weight of pop. B and ear diameter of both populations. Genotypic variances for days to 50% silking, no. of rows/ear, no. of kernels/row, 100-kernel weight and grain yield of pop. B were higher than those of pop. A. Genotypic x locations interaction variances for traits of pop. A were higher than those of pop. B for plant height, ear height, no. of rows/ear, no. of kernels/row and 100-kernel weight. Genotypic coefficient of variability for plant height, ear height, ear length and

ear diameter for S<sub>1</sub> lines of pop. A were higher than those for S<sub>1</sub> lines of pop. B., while it was higher for days to 50% silking, no. of rows/ear, no. of kernels/row, 100-kernel weight and grain yield for S<sub>1</sub> lines of pop. B than for S<sub>1</sub> lines of pop. A. Mean grain yield of pop. A ranged from 0.76 to 2.41 with an average of 1.54 kg/plot and broad sense heritability estimate of 44.74%. Mean grain yield of pop. B ranged from 0.83 to 3.06 with an average of 1.56 kg/plot and broad sense heritability estimate of 68.00%. Expected gain for grain yield (kg/plot) was 23.58 and 31.87% and actual gain was 17.12 and 8.06% for pop. A. and pop. B, respectively. Expected gain from S<sub>1</sub> *per se* in Pop B. was higher than those of pop. A. 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, Corn, Genetic variance and Genetic gain.

### Introduction:

Developing improved hybrids mainly depends on the improvement of the breeding source populations. S<sub>1</sub> progeny selection

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scheme subsequently imposed to improve population *per se*. It helps eliminate deleterious recessive alleles that become homozygous due to inbreeding followed by selection, which leads to increase the gene frequency of favorable alleles at all loci.

Theoretically, selection based on  $S_1$  is expected to utilize additive genetic variance better than intrapopulation selection methods as reported by Tanner and Smith 1987, Hallauer and Miranda 1988, Soliman 1991 and Vasal *et al* 1995. In this respect, Sullivan and Kannenberg 1987, Soliman 1991, Burgess and West 1993, found that a linear genetic gain for yield and other traits through two to eight cycles of selection. Heritability estimates from  $S_1$  lines are higher than the other selection methods due to that the component of genetic variance is additive genetic effects. 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 and El-Morshidy *et al* 2002. Saini and Malhi (2001) they indicated that  $S_1$  family selection was more effective than full-sib (FS) and half sib (HS) 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 quit 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 and earliness of two different maize populations i.e., Tuxpeno Corn Belt and Puerto Rico. (ii) estimate the genetic components of variance and heritability and (iii) calculate the expected and observed gain from selection after one cycle of  $S_1$  line *per se* selection method.

#### **Materials and Methods**

This study was carried out during the period from 2007 to 2010 at Malloway and Sakha Agricultural Research Stations, A.R.C., Egypt. Two exotic yellow maize populations i.e., Tuxpeno Corn Belt and Puerto Rico were used in the present study. The two populations were provided by National Maize Program. The two populations were planted in the summer season of 2007 at Malloway Agricultural Research Station. From each population, 81 plants were selected and selfed to produced  $S_1$  lines. In 2008 season, the  $S_1$  lines from each population were evaluated in a sets within reps (9x9) with two replications as explained by (Hallauer and Miranda 1988). In each trial, the experimental plot size was one row, 4 meters length and 70 cm apart and 25 cm between hills within a row. Seedlings were thinned to one plant/hill before the first irrigation (three weeks after sowing). Fertilizer was applied at the rate of 120 kg nitrogen/fed. in two doses before the first and the second irrigations. Normal cultural practices were applied as rec-

ommended. Ten  $S_1$  lines were selected based on two selection criteria, i.e, grain yield and earliness from each trial of the two populations. The selection intensity which used was 12.34 % for both selection criteria. Equal number of seeds from the selected  $S_1$  was carefully bulked to form the base of the first cycle of the two selection criteria. Four populations of the selected families were formed as follows:

- 1- Pop. A  $C_1$  ( $S_1$  *per se*) for grain yield
- 2- Pop. A  $C_1$  ( $S_1$  *per se*) for earliness
- 3- Pop. B  $C_1$  ( $S_1$  *per se*) for grain yield
- 4- Pop. B  $C_1$  ( $S_1$  *per se*) for earliness

In 2009 season, the four groups of the selected families were planted in non-replicated plots at Mallawy Agric. Res. Station. The plot size was 30 rows, 5 m length, 70 cm apart and 25 cm 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 from each selection criterion were harvested,

dried, and shelled together to form the first cycle seed. In 2010 season, the first cycle of selection ( $C_1$ ); for each population was evaluated against the original populations to measure the actual gain from selection at Mallawy and Sakha Agric. Res. Station. ARC. Randomized Complete Block Design (RCBD) with 4 replications was used in the two locations. The experimental plot size was 4 rows, 6 meters length and 70 cm between rows. Planting was in hills spaced 25 cm apart. Seedlings were thinned to one plant/hill before the first irrigation (three weeks after sowing). Fertilizer was applied at the rate of 120 kg nitrogen/fed. in two doses; before the first and second irrigations. Normal agricultural practices were applied as recommended. Data were collected from the inner two rows. Data were recorded for days to 50 % silking, plant and ear height (cm), ear length (cm), ear diameter (cm), number of rows/ear, number of kernels/row, 100-kernel weight (g.) and adjusted grain yield (kg./plot) to 15.5 % moisture content was measured from each plot. Separate as well as combined analysis over location, after testing homogeneity of error mean squares, according to Gomez and Gomez (1984).

Expected mean squares and degrees of freedom were combined for  $S_1$  family across the two locations are presented in Table 1.

Table 1. Combined analysis of variance for S<sub>1</sub> family over two locations.

S.O.V	D.F.	M.S.	E.M.S.
Locations (l)	(l-1)		
Reps/locations	l (r-1)		
Set (s)	(s-1)		
Set x Loc.	(s-1) (l-1)		
Set x reps/Loc.	(s-1) (r-1) l		
S <sub>1</sub> families/sets	s (f-1)	M <sub>3</sub>	$\sigma^2e + r \sigma^2gL + r L \sigma^2g$
S <sub>1</sub> families/sets x loc.	S (f-1) (l-1)	M <sub>2</sub>	$\sigma^2e + r \sigma^2gL$
Error	sl (r-1) (f-1)	M <sub>1</sub>	$\sigma^2e$

The expected mean squares were used to estimate the following genetic parameters according to Singh and Chaudhary (1985).

$$\text{Genotypic variance } (\sigma^2g) = \frac{M_3 - M_2}{rL}$$

$$\text{Genotypic x location interaction variance } (\sigma^2gL) = \frac{M_2 - M_1}{r}$$

$\sigma^2e$  = error variance

$$\text{Phenotypic variance } (\sigma^2ph) = \sigma^2g + \frac{\sigma^2gL}{r}$$

$$\text{Heritability } (h^2) = \frac{\sigma^2g}{\sigma^2ph} \times 100$$

$$\text{Genotypic coefficient of variability (g c v \%)} = \frac{\sigma g}{X} \times 100$$

$$\text{Phenotypic coefficient of variability (g c v \%)} = \frac{\sigma ph}{X} \times 100$$

Expected gain from selection  $\Delta G\% = K. h^2. \sigma ph$

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

The four new populations (C<sub>1</sub>) resulted from selection were evaluated in comparison with original populations and analyzed over locations as presented in Table 2.

Table 2. Form of the combined analysis of variance for evaluation trials over locations.

S.O.V	d.f
Locations (L)	(l-1)
Reps/L	l (r-1)
Genotypes (G)	(g-1)
G x L	(l-1) (g-1)
Error	l (g-1) (r-1)

## **Results and Discussion**

### **Analysis of variance**

Analysis of variance for the studied traits of both populations are presented in Table 3. Mean squares of the combined data showed that, mean squares due to locations for all the studied traits of both populations were highly significant. Mean squares due to  $S_1$  lines of both populations were significant or highly significant for all the studied traits, except ear diameter of pop. B and no. of rows/ear of pop. A. On the other hand, mean squares due to  $S_1$  x locations were significant or highly significant for all the studied traits of the two populations, except ear length for pop. A, no. of kernels/row and 100-kernel weight of pop. B and ear diameter for both populations. These results are in good agreement with those obtained by Mahmoud *et al* 1999 and El-Morshidy *et al* 2002.

### **Variance components and heritability:**

Genetic and phenotypic variance and broad sense heritability (H) are presented in Table 4. Results showed that genetic variance for all the studied traits were less than phenotypic variance. This is due to that the genetic variance

depend upon the effect of additive and non-additive, but the phenotypic variance is due to the effect of both genetic and environmental variances. Genotypic variances for plant height, ear height, ear length and ear diameter of pop. A were higher than those of pop. B. While genotypic variances for days to 50% silking, no. of rows/ear, no. of kernels/row, 100-kernel weight and grain yield of pop. B were higher than those of pop. A. Genotypic x locations interaction variances for traits of pop. A were higher than those of pop. B for plant height, ear height, no. of rows/ear, no. of kernels/row and 100-kernel weight. While, genotypic x location variances for days to 50% silking, ear length and grain yield of pop. B were higher than those of pop. A. Meaning that the genotypes were affected by change of locations. Phenotypic variances for plant height, ear height, ear length, ear diameter, no. of rows/ear and no. of kernels/row for  $S_1$  lines of pop A. were higher than those of pop. B. On the other hand, the opposite was true for days to 50% silking, 100-kernel weight and grain yield for  $S_1$  lines of pop. B were higher than those of pop. A.

Table 3. Mean squares of the S<sub>1</sub> lines for all the studied traits of the two populations, combined across locations.

S.O.V	df	MS					
		Days to 50% silking		Plant height (cm)		Ear height (cm)	
		Pop. A	Pop. B	Pop. A	Pop. B	Pop. A	Pop. B
Loc.	1	344.31**	30.25**	92686.42**	80403.75**	58833.20**	89367.78**
Reps/Loc.	2	2.28	3.94	1843.22	155.07	462.25	146.42
Sets	8	45.08**	49.91**	3245.39**	1876.82**	871.94**	1043.73**
Sets x Loc.	8	10.91	5.21	867.57	576.06*	273.45	270.59*
Sets x reps/Loc.	16	5.70	2.89	694.93	194.97	244.93	76.44
S <sub>1</sub> lines/Sets	72	19.18**	21.67**	1222.37**	986.28**	698.01**	479.22**
S <sub>1</sub> lines/Sets x Loc	72	5.87*	4.28**	216.88*	228.61*	217.02**	147.68**
Error	144	4.17	2.47	141.80	169.69	117.07	78.25
		Ear length (cm)		Ear diameter (cm)		No. of rows/ear	
Loc.	1	179.56**	136.63**	33.96**	23.25**	29.16**	35.47**
Reps/Loc.	2	3.87	6.22	0.73	0.30	3.68	1.05
Sets	8	9.66**	2.84	0.38	0.21	6.46	3.03*
Sets x Loc.	8	2.77	2.90	0.08	0.38	3.47	1.24
Sets x reps/Loc.	16	1.51	2.80	0.33	0.24	3.48	1.15
S <sub>1</sub> lines/Sets	72	8.04**	5.53**	0.38**	0.21	3.96	3.55**
S <sub>1</sub> lines/Sets x Loc	72	2.31	2.90*	0.20	0.16	3.21*	1.31**
Error	144	2.57	1.97	0.17	0.13	2.45	0.74
		No. of kernels/row		100-kernel weight (g.)		Grain yield (Kg/plot)	
Loc.	1	943.85**	543.93**	3006.69**	3474.45**	87.30**	67.21**
Reps/Loc.	2	3.59	9.58	239.14	244.67	0.12	0.06
Sets	8	32.08	16.18	34.94*	36.87	1.19**	0.78**
Sets x Loc.	8	6.13	13.55	28.37*	57.53	0.55*	0.33
Sets x reps/Loc.	16	13.82	11.94	14.91	37.22	0.20	0.14
S <sub>1</sub> lines/Sets	72	22.03*	16.46*	48.22*	49.03**	0.38**	0.75**
S <sub>1</sub> lines/Sets x Loc	72	14.98**	9.11	29.96**	23.80	0.21**	0.24**
Error	144	6.16	10.54	16.36	21.61	0.10	0.08

Genotypic (GCV%) and phenotypic (PCV%) coefficient of variability for all the studied traits for the two populations are shown in Table 4. The phenotypic coefficient of variability for plant height, ear height, ear length, ear diameter, no. of kernels/row and 100-kernel weight of S<sub>1</sub> lines derived from pop. A were 7.85, 9.68, 9.09, 6.66, 7.17 and 13.07% which were higher than those of S<sub>1</sub> lines from pop. B with values of 7.07, 8.26, 7.40, 5.27, 6.35 and 12.11% for the same traits, respectively. On the other hand, the opposite was true for days to 50% silking, no of rows/ear and grain yield. Genotypic coefficient of variability for plant height, ear height, ear length and ear diameter for S<sub>1</sub> lines of pop. A were 7.12, 8.04, 7.67 and 4.85% and higher than those from S<sub>1</sub> lines from pop. B with values of 6.19, 6.87, 5.10 and 2.57% for the same traits, respectively. On the other hand the opposite was true for day to 50% silking, no of rows/ear, no of kernels/row, 100-kernel weight and grain yield. These results agreement with those reported by Dora *et al.* (1999) who found that the pcv was slightly larger than gcv for the nine 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. PCV values for plant and ear height, ear diameter, no. of

kernels/row and grain yield/plant of S<sub>1</sub> family were 6.68, 8.43, 11.72, 14.44 and 26.99% and GCV values were 6.62, 10.30, 6.63, 12.01 and 24.14%, respectively. Broad sense heritability for S<sub>1</sub> lines of pop. A was high, 69.40% for days to 50% silking, 68.91% for ear height, 71.27% for ear length, 82.26% for plant height and moderate for ear diameter (47.37%), no of kernels/row (32.00%), 100-kernel weight (37.87%) and grain yield (44.74%) and low for no. of rows/ear (18.94%). For S<sub>1</sub> lines of pop. B broad sense heritability was high for plant height (76.82%), ear height (69.18%), no. of rows/ear (63.10%), 100-kernel weight (51.46%) and grain yield (68.00%), and days to 50% silking (80.25%) and moderate for ear length (47.56%), ear diameter (23.81%) and no. of kernels/row (44.65%). 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 no. of rows/ear, grain yield and 100-kernel weight in pop. A, while it was intermediate in pop. B. The opposite was true for ear length. The low heritability estimates may be due to the small genetic variance or high environmental variance in the concerned population. Our results agreement with those obtained by Galal *et al.* (1984) who showed 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. Sadek *et al.* (1986) found that estimates in broad sense heritability were 49.2, 22.9, 25.0, 13.6, 18.0 and 23.4 for days to 50% silking, plant height, grain yield, 100-kernel weight, no. of rows/ear and ear length, respectively. Soliman (1991) found that heritability estimates

Table 4. Genetic variance of S<sub>1</sub> lines for all the studied traits of the two populations combined across locations

Parameters	Traits					
	Days to 50% silking		Plant height (cm)		Ear height (cm)	
	Pop. A	Pop. B	Pop. A	Pop. B	Pop. A	Pop. B
$\sigma^2_g$	3.33	4.35	251.37	189.42	120.25	82.89
$\sigma^2_{gl}$	0.85	0.91	37.54	29.46	49.98	34.72
$\sigma^2_e$	4.17	2.47	141.80	169.69	117.07	78.25
$\sigma^2_{ph}$	4.80	5.42	305.59	246.57	174.50	119.81
G.C.V	2.90	3.41	7.12	6.19	8.04	6.87
P.C.V	3.48	3.80	7.85	7.07	9.68	8.26
H%(BS)	69.40	80.25	82.26	76.82	68.91	69.18
	Ear length (cm)		Ear diameter (cm)		No. of rows/ear	
$\sigma^2_g$	1.43	0.66	0.05	0.01	0.19	0.56
$\sigma^2_{gl}$	-0.13	0.47	0.02	0.02	0.38	0.29
$\sigma^2_e$	2.57	1.97	0.17	0.13	2.45	0.74
$\sigma^2_{ph}$	2.01	1.38	0.10	0.05	0.99	0.89
G.C.V	7.67	5.10	4.58	2.57	2.75	5.52
P.C.V	9.09	7.40	6.66	5.27	6.32	6.95
H%(BS)	71.27	47.56	47.37	23.81	18.94	63.10
	No. of kernels/row		100-kernel weight (g.)		Grain yield (Kg/plot)	
$\sigma^2_g$	1.76	1.84	4.57	6.31	0.04	0.13
$\sigma^2_{gl}$	4.41	-0.72	6.80	1.10	0.06	0.08
$\sigma^2_e$	6.16	10.54	16.36	21.61	0.10	0.08
$\sigma^2_{ph}$	5.57	4.12	12.06	12.26	0.10	0.19
G.C.V	4.06	4.25	8.04	8.69	13.39	22.89
P.C.V	7.17	6.35	13.07	12.11	20.01	27.76
H%(BS)	32.00	44.65	37.87	51.46	44.74	68.00

were high for flowering date, plant and ear height, but it was low for grain yield. In this respect, Abou El-Saad *et al.* (1994) found 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. El-Morshidy

*et al.* (2002), Ibrahim (2004) and Garbuglio *et al.* (2009) obtained high heritability estimates for ear height and grain yield/plant. Shah *et al.* (2007) found moderate and high heritability estimates were manifested for grain yield.

**Means and coefficients of variability:** Mean, environmental error, coefficient of variability

and range for different characters for S<sub>1</sub> lines of both pop. A and pop. B combined across locations are presented in Table 5. Results showed that mean values for days to 50% silking, plant height, ear height, ear length, ear diameter, no. of rows/ear, no. of kernels/row, 100-kernel weight and grain yield of pop. A were 62.86, 222.80, 136.40, 15.60, 4.63, 15.74, 32.73, 26.57 and 1.54 for S<sub>1</sub> Pop. A, respectively. The coefficient of variability ranged from 3.25 for days to 50% silking to 20.53% for grain yield. For Pop. B, mean values for the above mentioned traits were 61.22, 222.18, 132.50, 15.89, 4.35, 13.56, 31.93, 28.90 and 1.56, respectively. The coefficient of variability ranged from 2.58 for days to 50% silking to 18.13 % for grain yield.

**Expected and actual gain from selection:**The genetic gain from selection has been one of the most important contribution of quantitative genetics to maize breeder. One of its direct application is the extent to which a given population is suitable for breeding purpose for either a given environment or set of environments. 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 used as selection criterion of S<sub>1</sub> family selection method in both populations are given in Table 6. Expected gain for grain yield (kg/plot) were 23.58 and

31.87% and actual gain were 17.12 and 8.06% for pop. A. and pop. B, respectively. These results could be attributed to the presence of more additive genetic variance in Pop. A than in Pop. B. Expected gain in the two populations was higher than the actual gain from selection because the expected gain was calculated from genetic variance which included both additive and non-additive components. The same results were obtained by Soliman (1991) and El-Morshidy et al (2002) they reported that the expected gain from selection was higher in magnitude than the actual one., Galal *et al* (1984) reported that S<sub>1</sub> line *per se* selection was superior and the expected gain from selection ranged from 19 -24%. Tanner and Smith (1987) compared the changes in grain yield after eight cycles of half-sib and S<sub>1</sub> progeny recurrent selection. They found that the genetic gain per cycle for grain yield in the Population *per se* for C<sub>0</sub> to C<sub>4</sub> were significantly larger than for half sib. Walters *et al* (1991) showed significant increases in grain yield with S<sub>1</sub> lines from (BSSSC0) Population. Saini and Malhi (2001) they indicated that S<sub>1</sub> family selection was more effective than FS and HS selection in improving Populations, expected responses were 22.73, 12.70 and 9.04%, respectively. Ruize and Alvarez (2007) concluded that S<sub>1</sub> selection is effective in improving the yield and reducing loading in both synthetics. Peng *et al* (2007) who

reported that modified S<sub>1</sub> was better than modified S<sub>1</sub>-HS and Modified HSRRS to improve Synthtic-4 maize Populations, where the grain yield of S<sub>1</sub> progeny of the Population increased by 10.9%, 9.8% and 10.8%, respectively. Shah et al(2007) suggested that S<sub>1</sub> recurrent selection was quit effective in improving grain yield. Expected gain for days to 50% silking was 4.03 and 5.09 % in Pop. A and Pop. B. for S<sub>1</sub> per se, respectively. On the other hand, the actual gain from selection of improved Pop. A was 0.40 %, while it was -1.3 % for improved Pop. B for S<sub>1</sub> per se, respectively. Expected gain from

S<sub>1</sub> per se in Pop B. was higher than those of Pop. A. Also the actual gain from selection in improved Pop. B was better than those in Pop. A. These results could be attributed to the presence of more additive genetic variance in Pop. B than in Pop. A. for earliness. Yield improvement of pop. A was more suitable than the pop. B for S<sub>1</sub> per se causing the more variability of pop. A. Also, the S<sub>1</sub> per se selection method was more effective in population improvement. For earliness improvement, pop. B was more suitable than pop. A. indicating that pop. B was include more variability than pop. A for this trait.

Table 5: Mean (X), environmental error variance ( $\sigma^2_e$ ), coefficients of variability (CV) and the range for grain yield and the other studied trait for S<sub>1</sub> line per se of Pop. A and B combined across locations.

Traits	Pop.A.				Pop.B			
	X—	$\sigma^2_e$	CV	Range	X—	$\sigma^2_e$	CV	Range
Days to 50% silking	62.86	4.17	3.25	57-67	61.22	2.48	2.58	55-66
Plant height (cm)	222.80	141.80	5.34	167-276	222.18	169.69	5.86	189-259
Ear height (cm)	136.40	117.07	7.93	93-172	132.50	78.25	6.68	101-167
Ear length (cm)	15.60	2.57	10.28	11.60-18.25	15.89	1.97	8.83	13.15-18.70
Ear diameter (cm)	4.63	0.17	8.90	3.90-5.45	4.35	0.13	8.29	3.90-4.85
No. of rows/ear	15.74	2.45	9.94	13.10-18.60	13.56	0.74	6.34	11.60-16.50
No. of kernels/row	32.73	6.16	7.58	26.15-36.95	31.93	10.54	10.17	27.85-35.70
100-kernel weight (g.)	26.57	16.36	15.22	21.00-39.75	28.90	21.61	16.08	19.50-37.25
Grain yield (kg/plot)	1.54	0.10	20.53	0.76-2.41	1.56	0.08	18.13	0.83-3.06



Our results indicate that,  $S_1$  *per se* selection are effective in improving grain yield and its components of the two studied maize populations. The same results were obtained by Mahdy *et al* (1987) who reported that  $S_1$  selection significantly increased grain yield/plant and ear length. Verderio *et al* (1988) reported that mean yield were significantly improved by both methods, but  $S_1$  selection *per se* was the more effective, giving increases of 11.3% when random  $S_1$  lines were used and 5.6% when testcrosses to an inbred tester were used Menkir and Kling (1999) they found that the reciprocal recurrent selection was effective in improving grain yield and other traits of inter populations crosses 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 demonstrate that the three recurrent methods were effective for increasing grain yield in testcrosses and improvement of general combining ability in maize populations.

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

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أجري هذا البحث لاختبار وتقييم عائلات الجيل الذاتي الأول بهدف تحسين القيمة التربوية لعشيرتين من الذرة الشامية الصفراء هما (Pop-Tuxpeno Corn Belt (Pop-A) and Puerto Rico (Pop-B) وذلك لصفة محصول الحبوب ومكوناته. استخدم في هذه الدراسة ٨١ عائلة من عائلات الجيل الذاتي الأول من كلا العشيرتين وأوضحت نتائج تقييم عائلات الجيل الذاتي الأول وجود فروق معنوية لجميع الصفات المدروسة لكلا العشيرتين. كان تباين التفاعل بين عائلات الجيل الذاتي الأول والمناطق معنويا لجميع الصفات المدروسة ما عدا صفة طول الكوز في العشيرة A و صفات عدد الحبوب بالصف ووزن ١٠٠ حبة في العشيرة B و صفة قطر الكوز في كلا العشيرتين. كان التباين الوراثي لصفات عدد الايام حتى ظهور ٥٠% من الحرابر، عدد الصفوف بالكوز، عدد الحبوب بالصف، وزن ١٠٠ حبة ، ومحصول الحبوب في العشيرة B أعلى من العشيرة A .

كانت تباينات التفاعل بين التراكيب الوراثية والمواقع لجميع صفات العشيرة A عاليا عن مثيلتها في العشيرة B لصفات ارتفاع النبات والكوز ، عدد الصفوف بالكوز، عدد الحبوب بالصف، وزن ١٠٠ حبة. كانت قيم معامل الاختلاف الوراثي عاليا لصفات ارتفاع النبات والكوز وطول الكوز وقطر الكوز في العشيرة A عاليا عن العشيرة B ، بينما كان عاليا في العشيرة B لصفات عدد الايام حتى ظهور ٥٠% من الحرابر ، عدد الصفوف بالكوز ، عدد الحبوب بالصف ، وزن ١٠٠ حبة ومحصول الحبوب .

تراوحت متوسطات العشيرة A من ٠.٧٦ الى ٢.٤١ كجم للخط بمتوسط قدرة ١.٥٤ ودرجة توريث ٤٤.٧٤% ، بينما تراوحت متوسطات العشيرة B من ٠.٨٣ الى ٣.٠٦ كجم للخط بمتوسط قدرة ١.٥٦ ودرجة توريث ٦٨% . كان التقدم المتوقع من الانتخاب ٢٣.٥٨ و ٣١.٨٧% بينما كان التقدم المشاهد من الانتخاب ١٧.١٢ و ٨.٠٦% في العشيرة A والعشيرة B على التوالي . وهذا يدل على أن العشيرة A تحتوي على جزء كبير من التباينات الاضافية عن العشيرة B.