

COMPARISON OF S₁ AND TEST CROSS EVALUATION IN MAIZE

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ABSTRACT

The present investigation was carried out at the Agricultural Experiment station, Faculty of Agriculture, Alexandria University, during 1996,1997 and 1998 seasons.

In this study two methods have been used for the early evaluating of inbred lines. These methods are S₁ per se and test cross performance.

The Following results were obtained :

1. The mean of S₁ was smaller than the test cross for all the characters under study. This reduction is function of inbreeding depression. It ranged between 5.8 for 100-kernel weight to 30% for grain yield .
2. Highly significant difference were obtained among the two methods of selections for all character. Also the interaction between methods and S₁ lines were significant for all characters except ear width, moisture percent and days to mid-silking. This would indicate that testing of S₁ lines would be similar for either methods of evaluation for ear width, moisture percent and days to mid-silking only.
3. Heritability estimates were in general higher for test cross evaluation. The heritability values for the combined evaluation was less than from single method.
4. Magnitude of heritability would be reflected on the expected genetic gain from selection which was 12.6% for S₁ per-se and 15.1% for test cross.
5. The interaction was highly significant for all characters except ear width, moisture % and days to mid-silking. The association between the two methods would be weak for the significant characters.
6. The phenotypic correlation between the means of lines for both methods was significantly for grain yield , ear width, 100-kernel weight and moisture content. However their values were less than 0.5 indicating that the degree of association were weak. Only six lines were common in both methods, while 8 lines were common between S₁ and the combined evaluation and 12 lines between the test cross and the combined evaluation among the best 20% of lines. Therefore it was concluded that the two methods were different in the identification of superior lines.

INTRODUCTION

Two methods have been extensively used by maize breeders for evaluation of early generation inbred lines. These methods are S₁ performance for superior S₁ per-se (Genter and Alexander 1962), and the performance of these inbred lines in top cross (test cross).

Several reports have been presented to compare the performance of S₁ lines per-se and in test cross as a basis for selection. For example (Koble and Rinke 1963) found significant correlation between S₁ and top cross for related and unrelated testers for yield and several other traits. Genter and Alexander 1966 showed that in inbred lines obtained from the population

selected on the basis of S_1 progeny performance showed an increase of 31.4% in yield after two cycles, however, yield increase after two cycle of top cross of S_1 lines (two unrelated single-cross testers) was 17.9% . In another study Duclos and Crane (1968) evaluated one cycle of selection of S_1 lines in top cross performance. The yield of S_1 lines from the original population, from derived population based on S_1 lines, and on top cross (double cross as a tester) performance was 31.9% , 40.7% and 36.92 of the check, respectively. Results showed that after one cycle of selection , S_1 lines produced the best yielding S_1 lines and selection based on top cross performance (double cross as a tester) produced the best top cross yields.

Burton et al (1971), after four cycles of selection in Krug Hi I Synthetics 3, found that S_1 lines from the population derived by the two methods (S_1 and test cross) that the selfing series had a better increase (38.7%) than for the test cross series based on unrelated double cross as a tester (12%) . Also, Genter 1973 found that the increase in top cross was significant (2.7%) in comparison of the S_1 (14.3%) over two cycles.

The goal of this study is to compare the genetic and environmental variations for S_1 and their corresponding test cross in order to compare the relative efficiency of selection based on both methods. Another objective was to detect the correlation between the two versions.

MATERIALS AND METHODS

The experiment was conducted at the Experiment Farm of Alexandria University, during 1996,1997and1998 seasons. The population used in this study was Alex 3 (white kernel synthetic) produced by Dr. El-Rouby, Crop Sci. Dep., Alexandria University.

In 1996 two hundred plants were selfed and at harvest 105 selfed ears with enough seeds were saved . One row of each of these S_1 lines were planted (in 1997) under isolation in intercrossing blocks with tester rows planted with seeds from the D.C. Hybrid Taba (unrelated tester). The S_1 rows were detasseled before pollen shedding. Ears from the S_1 rows were harvested and were bulked to represent the test cross entries. In 1998 , S_1 lines and their corresponding test cross were evaluated in two separate experiments one for S_1 and the second for test cross. Each experiment consisted of 105 entries repeated three times in R.C.B.D Plot size was a single row of five meters in length by 70 cm in width.

Data were statistically analyzed for each method and their combined analysis over the two methods as outlined by Steel and Torrie (1980). Estimates of genetic variance (σ_{LM}^2), heritability (h^2) and expected genetic advance (Δg) were calculated as given by Hallauer and Miranda (1981). Phenotypic correlation coefficient between the means of the S_1 and their test cross for various characters were calculated using the SAS (1988). Also correlation coefficients were calculated between the different characters for the S_1 and test cross.

RESULTS AND DISCUSSION

Summary of analysis of variance for the evaluation of the 105 lines as lines per se and test crossed with Taba double cross as a tester are given in Table 1. The mean squares for error was smaller for S₁ lines than those for test cross. Also M.S for lines for S₁ perse was smaller. These were significant variation for grain yield, 100-kernel weight, plant and ear height and days to mid-silking for both methods of evaluation. Test cross evaluation showed also significant variation to both ear length and ear width. Moisture percent was not significant for both methods. The above finding would suggest that selection among the tested lines would be effective for most characters except moisture percent at harvest.

Table 1. Pertinent part of ANOVA for 105 S₁ lines evaluated as S₁ per se and test cross with D.C. hybrid.

Character	M.S.		M.S.	
	S ₁ lines	Error	Test cross	Error
Grain yield (kg/plot)	0.28**	0.06	0.69**	0.09
Ear length	0.45	0.41	1.39**	0.47
Ear width	0.015	0.014	0.06**	0.02
100-kernel weight	0.82**	0.45	2.63**	0.53
Plant height	2.74**	1.09	104.0**	2.38
Ear height	3.04**	0.97	17.42**	0.79
Moisture %	0.53	0.49	0.39	0.60
Days to mid-silking	0.51**	0.30	0.98*	0.73

*.** Indicate significant at the 0.05 and 0.01 level probability respectively.

Means of S₁ and their test cross are summarized in Table 2. As expected the mean of S₁ lines was smaller than the test cross for all the characters under study. This reduction is function of inbreeding depression. It is expected that the mean of test cross would be equal of the parental population (A) in addition to the average heterosis between Alex 3 x Taba D.C. Therefore the calculated inbreeding depression would be overestimated . The inbreeding depression ranged between 5.8 for 100- kernel weight to 30% for grain yield. Inbreeding depression for 50% homozygsity was less than 10% for 100-kernel weight, plant height, moisture percent and days to silking and was between 10-20%, for ear height and ear width and length. It reached the 30% for grain yield. Hallauer and Miranda (1981) summarized the percent of inbreeding depression at different levels of homogyposity . The percent of inbreeding depression at 50% homozygosity was the highest of 25.5% for yield, intermediate for plant height ear height, ear length; low for ear diameter, kernel weight and none of days to silking. Theoretically inbreeding is function of the dominance effect of genes. The present result would indicate that dominance would play an important role in the inheritance of grain yield in addition to additive effect.

Table 2: Overall mean (X) of 105 S₁ lines and their test crosses and inbreeding depression (I) for different characters

Character	Mean X		% inbreeding depression
	S ₁ line	Test cross	
Grain yield (kg/plot)	2.675 ^b	3.820 ^a	30.0 ^{**}
Ear length (cm)	14.80 ^b	18.20 ^a	18.7 ^{**}
Ear width (cm)	4.10 ^b	4.80 ^a	14.6 ^{**}
100-kernel weight (g)	29.2 ^b	31.0 ^a	5.8 ^{**}
Plant height (cm)	234 ^b	249 ^a	6.0 ^{**}
Ear height (cm)	124 ^b	138 ^a	10.1 ^{**}
Moisture content %	19.1 ^b	19.8 ^a	3.5 ^{**}
Days to mid-silking	51.7 ^b	56.2 ^a	8.0 ^{**}

**** significant at 0.01 level.**

Means followed by different letter are significantly different at the 0.05 level of significant.

Combined analysis over the two methods of evaluation is summarized in Table 3 . Although the two environmental errors of the two separate analysis of variance were heterogenous , the significance level would be considered at the 0.01 level only. Highly significant difference were obtained among the two methods of selections for all characters. This difference is due mainly to inbreeding depression. Differences between lines were significant for only grain yield, ear width, 100-kernel weight and days to silking . However, the interaction between methods and S₁ lines were significant for all characters except ear width, moisture percent and days to mid silking. This would indicate that testing of S₁ lines would be similar for either methods of evaluation for ear width moisture percent and days to silking only.

Because of the significance of the interaction estimates, the genetic parameters were calculated for each method and were combined over the two methods and are given in Table 4.

Significant genetic variance was detected for grain yield, 100-kernel weight, plant and ear height and days to silking from the evaluation of S₁ line per se. On the other hand, all the studied characters showed significant genetic variance for all characters except moisture % for test cross evaluation. Heritability estimates were in general higher for test cross evaluation.

Magnitude of heritability would be reflected on both Δg and G% . Selection would be effective for grain yield only. For the other characters selection would be ineffective. The expected gain was 12.6% for S₁ line and 15.1% for test cross.

The heritability values for the combined evaluations was less than the single evaluation. This would be expected because of the significant interaction between method and lines (Table 5). Consequently the expected advance from selection dropped to 7.2%.

To compare the relative efficiency of selection of both methods, S_1 per se and test crosses, three criteria should be considered. First the amount of interaction σ_{LM}^2 would indicate the association between the two methods. If σ_{LM}^2 is significant, the association between the two methods would be weak. The values of σ_{LM}^2 for the different characters are given in Table 5.

The interaction was highly significant for all characters except ear width, moisture %, and days to mid-silking. The second measure for the resemblance of both methods is the phenotypic correlation between the mean of lines for both methods. Only the phenotypic correlation for grain yield, ear width, 100 kernel weight and moisture content were significant. However their values were less than 0.5 indicating that the degree of association were weak.

The third criterion to express the association between the two methods was the no. of common lines among the highest yielding 20% lines selected by both methods. Only six S_1 lines were common in both methods, while 8 S_1 lines were common between S_1 and the combined evaluation and 12 S_1 lines between the test cross and the combined evaluation.

Reviewing the previous three criteria it is clear that the two methods of evaluations are not similar in the evaluation of S_1 lines. This might be due the presence of dominance in the original population. The variance component for lines σ_{LM}^2 is function of both additive and dominance. Therefore the presence of dominance would affect the reliability of the evaluation .

On the other hand, for the test cross methods evaluation, the existence of heterotic effect between Alex 3 and the tester D.C. Taba would mask the additive effect of the lines. Therefore, the association between both methods would be weak.

In order to overcome the presence of both bias (dominance, and heterotic effect) the combined evaluation of S_1 and test cross would be more reliable and selection based on both would be more reliable. However the expected advance would be smaller and less than single evaluation. In the present result Δg for combined evaluated was 7.2%. This value is free from bias due to the interaction.

Goulas and Lonquist 1976 used combination selection based upon half-sib families and S_1 progenies. After two cycles they obtained a significant increase of 24% over the original population.

Results presented in this study are in agreement with the results suggested by Lonquist (1968), that selection based on inbred families (S_1 , S_2) has been less effective than expected. Horner et al (1973) compared results of five cycles of selection based on evaluation of test cross with two broad base testers, inbred tester, and S_2 progeny methods. Selection based on inbred tester was significantly more effective than the two other methods showing a gain in grain yield of 4.4% per cycle. The broad base testers and S_1 progeny methods showed gains of 2.4% and 2.0% respectively. The S_2 progeny method, is theoretically more effective method for changing frequencies of genes having additive effects than are the test cross methods (Horner *et al* 1969).

However, Koble and Rinke (1963) found significant correlation between S₁ lines and test cross performance for related and unrelated testers for yield and several other traits. Also, Carangal et al 1971 evaluated two cycles of selection based on two types of families. In the first, a superiority of 42.6% was obtained in favor of test cross over S₁ line for yield because difference of inbreeding was involved. The other population the yields of S₁ lines were not different from selection based on test cross.

Table 5. Variance component for (line X method) interaction σ_{LM}^2 and phenotypic correlation between line per-se and their test cross (r) for different characters.

Character	σ_{LM}^2	r
Grain yield	0.0818**	0.382**
Ear length	0.166**	-0.032
Ear width	0.016	0.423**
100-kernel weight	0.303**	0.226
Plant height	17.58**	-0.067
Ear height	2.98**	0.076**
Moisture content	0.00	0.267
Days to mid-silking	0.028	0.188

*,** indicate significance at the 0.05 and 0.01 levels of probability respectively.

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مقارنة بين تقييم السلالات النقية والهجن القمية في الذرة الشامية
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أجرى هذا البحث بمحطة بحوث كلية الزراعة - جامعة الإسكندرية خلال مواسم النمو ١٩٩٦ , ١٩٩٧ , ١٩٩٨ . وقد أستخدم في هذه الدراسة طريقتين لتقييم الأجيال المبكرة للسلالات النقية . وهذه الطرق هي سلوك سلالات جيل للتلقیح الذاتي الأول وسلوك هذه السلالات في الهجن القمية .
وقد يلى ملخص لأهم النتائج :

- 1- كان متوسط السلالات النقية أقل من متوسط الهجن القمية لجميع الصفات تحت الدراسة وكان هذا الانخفاض دالة للتربية الداخلية وتراوح هذا الانخفاض ما بين ٥,٨% لوزن مائة حبة و ٣٠% لمحصول الحبوب.
- 2- كانت هناك فروق عالية المعنوية بين طرق الانتخاب لجميع الصفات . أيضاً كان التفاعل بين طرق التقييم وسلالات الجيل الأول ذاتية التلقیح معنوياً لجميع الصفات ما عدا عرض الكوز ونسبة الرطوبة وميعاد طرد الحريرة . وهذا يعني أن تقييم سلالات الجيل الأول ذاتية التلقیح بأي من الطريقتين متماثل بالنسبة لصفات عرض الكوز ونسبة الرطوبة وميعاد طرد الحريرة.
- 3- تقديرات معامل التوريث كانت مرتفعة بصفة عامة لتقييم الهجن القمية وكانت تقديرات معامل التوريث للتقييم المشترك لكلا الطريقتين أقل من المحسوبة لطريقة واحدة.
- 4- ينعكس تقدير معامل التوريث على كل من التحسين الوراثي المتوقع من الانتخاب (Δg) والنسبة المئوية للتحسين (G%) حيث بلغت ١٢,٦% لسلالات التلقیح الذاتي و ١٥,١% للهجن القمية.
- 5- لمقارنة الكفاءة النسبية لطريقتي التقييم استخدم ثلاثة مقاييس الأول منها مكونات التباين للتفاعل بين السلالات والطرق (O² LM) وكان التفاعل معنوياً لجميع الصفات ما عدا عرض الكوز ونسبة الرطوبة وميعاد طرد الحريرة وقد كان التلازم بين الطريقتين ضعيف . وذلك في حالة التفاعل المعنوي والمقياس الثاني هو الارتباط بين متوسطات السلالات لكلا الطريقتين وقد كان معامل الارتباط المظهري معنوياً بالنسبة لصفات محصول الحبوب وعرض الكوز ووزن مائة حبة ونسبة الرطوبة ولكن قيمته كانت أقل من ٠,٥ مما يدل على ضعف العلاقة والمقياس الثالث هو عدد السلالات المشتركة عند انتخاب أعلى ٢٠% من السلالات بكلا الطريقتين وقد كانت ٦ سلالات فقط مشتركة في كلا الطريقتين بينما كان ٨ سلالات مشتركة بين طريقة التقييم للسلالات ذاتية التلقیح لمدة جيل واحد والتقييم المشترك لكلا الطريقتين و ١٢ سلالة مشتركة بين طريقة الهجن القمية والتقييم المشترك.
- 6- استنتج أيضاً أن طريقتي التقييم كانتا مختلفتين في تميز السلالات المنفوقة.

Table 3 Significance level for the combined ANOVA of S₁ lines under two methods of evaluation.

S.O.V	DF	Significance level							
		Grain yield	Ear length	Ear width	100-k weight	Plant height	Ear height	Moisture %	Days to mid silking
Methods (M)	1	**	**	**	**	**	**	**	**
S ₁ lines (L)	104	**	ns	**	*	ns	ns	ns	*
L X M	104	**	**	ns	**	**	**	ns	ns

ns,*,** indicate non significance and significance at the 0.05 and 0.01 levels of probability, respectively.

Table 4. Estimates of genetic variance (σ_g^2) heritability (h^2) and expected genetic advance upon selecting 20% of the lines Δg and relative advance (G%) for each method of evaluation and combined over the two methods.

	S ₁ line				Test cross				Combined			
	σ_g^2	h^2	Δg	G%	σ_g^2	h^2	Δg	G%	σ_g^2	h^2	Δg	G%
Grainyield (kg/plot)	0.073**	0.79	0.336	12.6	0.198**	0.89	0.58	15.1	0.055**	0.51	0.235	7.2
Ear length (cm)	0.013	0.08	0.044	0.2	0.307**	0.66	0.63	3.4	0.00	0.00	0.000	0.0
Ear width (cm)	0.000	0.05	0.005	0.1	0.013**	0.58	0.38	7.9	0.048**	0.53	0.071	1.6
100-kernel weight (g)	0.123**	0.45	0.328	1.1	0.700**	0.80	1.04	3.3	0.110*	0.33	0.271	9.0
Plant height (cm)	0.547**	0.60	0.800	0.3	33.8**	0.98	8.04	3.2	0.00	0.00	0.000	0.0
Ear height (cm)	0.689**	0.68	0.954	0.8	5.54**	0.95	3.20	2.3	0.128	0.06	0.112	0.1
Moisture content %	0.014	0.08	0.045	0.2	0.00	0.00	0.28	1.4	0.000	0.00	0.000	0.00
Days to mid-silking	0.070**	0.41	0.236	0.5	0.08*	0.26	0.06	0.1	0.050	0.33	0.179	0.3

** Indicate significant at the 0.05 and 0.01 level probability respectively.