COMPARATIVE STUDIES BETWEEN TWO SELECTION METHODS FOR IMPROVEMENT OF YELLOW MAIZE POPULATION YIELD

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ABSTRACT

Recurrent selection is the most common mean for indirectly enhancing inbred lines performance by enhancing the performance of their sources of populations. We compared the effectiveness of two intrapopulation selection methods of S_1 progeny and half-sib progeny *via* Design I mating scheme in improving the yield of Nubaria yellow maize population (NYP) (C_0). For fairer comparison, we unified germplasm used in the two methods by using S_1 seeds supposed to be kept for recombination in half-sib family selection as a germplasm of S_1 family selection. This permitted studying the outbred and inbred progeny for the same parent providing the prospect for combined selection on which selection unit is the parent family (both half-sib and S_1 families for the same parent). In recombination season, at harvest, S_1 topcrosses of each improved population were separated to examine the general combining ability of each recombined S_1. The three resulting improved populations *via* their respective S_1 topcrosses were under evaluation with the original and the check populations. Significant differences were detected among S_1 topcrosses for grain yield trait. Actual gain for grain yield (3.9 and 3.7 ard/fad for S_1 and H.S. family selection methods, respectively) were apparently one-half the predicted gain. Grain yield has improved significantly through this cycle with an increase up to 32 % than the original population. The improved population by combined selection was the highest yielding followed by the improved by S_1 family selection then the improved by half-sib family selection with non significant differences among the three improved populations.

We recommend with using the improved population resulting from the combined selection as a sub-population and combining the three improved populations seeds without those of S_1 topcrosses with low-performance in one population used for isolation and as a material for the coming improving cycles of recurrent selection.

INTRODUCTION

As a consequence of inbreeding *via* self-pollination process and forming of inbred lines, maize cultivar has been developed from open-pollinated varieties to crosses production. 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.

Recurrent selection has been widely used for enhancing populations 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 Weyhrich *et al.* (1998). Selection

effect *per se* led to increasing in alleles with favorable effects and decreasing in alleles with unfavorable effects. This 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 (1981) reported that use of different methods of recurrent selection have emphasized early testing for discriminating among progenies to determine which ones to recombine to form the next cycle of selection.

In this study we used procedures of two intrapopulation selection methods that emphasize general combining ability; i.e., S_1 and half-sib progeny for improving the yield of Nubaria yellow maize population (C_0) aiming to :

- Comparing between effectiveness of both methods in improving the yield of the population under study.
- Comparing between actual and expected gains for both selection methods.

MATERIALS AND METHODS

Genetical materials

The source of germplasm under this study (NYP) was composed at Nubaria Agricultural Research Station, Maize Department by intermating 4 local and 10 exotic sources of : ADA. Pop. (Turkey), Arify Pop. (Turkey), AE. Pop. (Turkey), Pop.21 (CIM), Pop.24 (CIM), Wistigua Pop. (CIM), Pop.33 (CIM), Pop.34 (CIM), Pop.44 (CIM), S.C. 155 – F_2, S.C. 162 – F_2, T.W.C. 351 – F_2, T.W.C. 352 – F_2 and inbred B.73 (USA).

The three steps of recurrent selection cycle plus evaluating the new improved populations were done as follows :

Forming of germplasm

The progenies required for half-sib family selection *via* Design I mating scheme as introduced by Comstock and Robinson (1948) and for S_1 family selection were produced in maize crossing field at Gemmeiza Agricultural Research Station in 2009 season. Where approximately 150 random S_0 plants of N.Y.P. were selfed and at the same time each were mated to 4 random female plants. Successful pollinations with sufficient seeds were selected, to remain with us 81 parents (S_0) group, each one consisting of one S_1 family (the selfed ear) and one half-sib family (forming from four full-sib families, i.e., each ear of female represents full-sib family) that have one parent in common. It is worthmentioning that we used S_1 seeds supposed to be kept for recombination in half-sib family selection method as a germplasm of S_1 family selection method to unify germplasm used in the two methods in order to make fairer comparison between them. This also permitted studying the outbred and inbred progeny for the same parent providing third selection method on which selection unit is the parent family (both half-sib and S_1 families for the same parent). Adequate selfed seeds was kept as recombination unit for the three selection methods.

Evaluating of germplasm

The formed progenies representing in 81 S_1 families and 324 full-sib families forming 81 half-sib families for 81 males were under evaluation as a selection unit at Gemmeiza and Sids Agricultural Research Stations in 2010 season. Two progeny evaluation trials were carried out: the first one for evaluating S_1 families and the second for evaluating full- and half-sib families. Both trials were arranged in simple lattice design as outlined by Cochran and Cox (1957) (9×9) with two replications, one ridge for plot in the first trial and 4 ridges of full sibs for plot in the second trial, ridge was 4 m in length with 0.8 m between ridges and 0.25 m spaces between hills within the ridge. Hills were thinned to one plant per hill before the first irrigation. All normal agricultural practices for maize production were applied as recommended in both trials at the proper time.

Based on the results of evaluation trials, the top yielding among S_1 families, half-sib families and parents families (on the basis of the yield of both S_1 family and half sib family that have parent in common) were selected with 10% selection intensity.

Recombination and forming of the new improved populations

For recombination, three sets of the remnant S_1 seeds for the selected families in each selection method; i.e., sets for S_1, H.S. and combined selection were planted at Gemmeiza Agricultural Research Station in 2011 season. whenever most of the S_1 had visible silks and starting pollen shedding, bulk of pollen grains was collected from S_1 ridges and pollinated the available silks. At harvest, each S_1 ridge were harvested separately with its respective label in order to evaluate each S_1 topcross separately.

Then we formed three improved populations with their separated S_1 topcrosses resulting from three selection methods.

Evaluating of the new improved populations with the original and check populations

The three resulting improved populations *via* their respective S_1 topcrosses were under evaluation with the original population and Gemmeiza yellow population (G.Y.P) as check in 2012 season at Gemmeiza Agricultural Research Station. Plot size for the three improved populations consisted of number of ridges equal to the number of S_1 topcrosses for each population; i.e., 6 ridges for the two populations resulting from S_1 family selection ($C1_{(S1)}$) and half-sib family selection ($C1_{(H.S.)}$) and 5 ridges for the population resulting from the combined selection $C1_{(S1\&H.S.)}$. Data was collected for all the ridges of the plots, each separately, and average performance was computed for the whole plot. Experimental design was Randomized Complete Block with 4 replications. Degrees of freedom were 4 for populations and $C1_{(S1\&H.S.)}$ S_1 topcrosses and 5 for ($C1_{(S1)}$) and ($C1_{(H.S.)}$) S_1 topcrosses.

Data was recorded on the following characters: days to 50% silking, plant height, ear height, ear position, ear length, ear diameter, No. of rows/ear, No. of kernels/row, and grain yield.

RESULTS AND DISCUSSION

Mean performance of the inbred and outbred families for the selected parents and inbreeding depression between them for yield trait:

Data in Table 1 shows mean performance for both types of families for the selected parents in the three selection methods, plus inbreeding depression for the selected parents which calculated by subtracting S_1 mean performance from half-sibs mean performance in each selection method.

Throughout the three selection methods, S_1 families performance decreased pointedly in half-sib family selection method; it was nearly one-half the performance in S_1 family selection method, however the differences among half-sib families performance were not of this amount among S_1 families. Consequently, this clarified in the values and percentages of inbreeding depression in each selection method where the reduction of inbreeding depression in half-sib family selection method was the largest among the three selection methods.

Table 1 : Mean performance of the inbred and outbred families for the selected parents and inbreeding depression between them over the two locations in the three selection methods for grain yield trait.

Selection method	Mean performance		Inbreeding depression	
	S_1 families	H.S. families	As value	As (%)
S_1	15.93	22.75	6.82	24
H.S.	8.08	25.56	17.48	68
S_1 & H.S.	15.35	23.92	8.58	32

It is worthmentioning that the selected parents for S_1 family selection method differed completely than the selected for half-sib family selection method. In another words, the superiority in performance of half-sib families did not accompanied by superiority in performance of corresponding S_1 families and *vice versa*. However, three of the selected were common in S_1 family selection and combined selection, and there were no selected parents for half-sib family selection within the selected for combined selection. In another words, inbreeding depression between the outbred and the inbred performance was larger for the selected in H.S. than in S_1; may this showing the important role of the non additive gene action in manifesting superiority in the outbred progeny.

Analysis of variance for evaluating populations and S_1 topcrosses inside each improved population :

Table 2 : Mean squares, errors and C.V. for analysis of variance for evaluating the five populations and S_1 topcrosses inside each improved population for all the studied traits.

Traits		Populations	C1 (S1)	C1 (HS)	C1 (S1&HS)
Days to 50% silking	Entries	6.7*	3.4*	٣,٤ NS	٠,٦ NS
	Error	1.3	0.6	١,٣	١
	C.V.	1.9	1.2	١,٩	١,٧
Plant height	Entries	175NS	480*	٢٣٧ NS	٨٦١*
	Error	90	139	١٠٠	١٩٨
	C.V.	4.6	٥,٥	٥	٧
Ear height	Entries	286*	٣٥٦*	٢١٦*	٤١٩*
	Error	11.4	٧٩	٤٦	٦٤
	C.V.	2.9	٧,٣	٦	٦,٧
Ear position	Entries	26*	٢٦ NS	٣٩*	٥,٧ NS
	Error	4.2	١٤	٨	٣,٤
	C.V.	3.7	٦,٦	٥	٣,٢
Ear length	Entries	1.8NS	٢,٧ NS	٥ NS	٣,٢ NS
	Error	0.6	٢,٦	٢	١,٧
	C.V.	4.3	٨,٨	٧,٧	٧
Ear diameter	Entries	0.15*	٠,٤٠٩*	٠,١١٦ NS	٠,٢٢٢ NS
	Error	.017٠	٠,١٨٧	٠,١٣٦	٠,٠٨١
	C.V.	2.9	٦,٥	٨	٦
Rows number /ear	Entries	0.042NS	٦*	٤*	٠,٢٤٨ NS
	Error	0.15	٠,٨	٠,٩	٠,٨٧٧
	C.V.	2.5	٥,٩	٦,٣	٦,١٥
Kernels number /row	Entries	3.3NS	٥,٨ NS	٣,٥ NS	١,٦ NS
	Error	1.6	٣,٤	٩,٦	١١,٥
	C.V.	3.5	٥,٢	٨,٦	٩
Grain yield	Entries	16.4*	١٠,٨ NS	١٨,٣*	٤٤*
	Error	2.6	٩,١	٦,٤	٩
	C.V.	10.7	١٩,٣	١٦,٥	١٩

Mean square shown in Table 2 exhibited significant differences among populations for days to 50% silking, ear height, ear position, ear diameter and grain yield, however the five populations did not differ significantly for plant height, ear length, rows number/ear and kernels number/ row traits.

Significant and non signficant differences were noticed among S_1 topcrosses in all the improved populations. All the three populations exhibited significant differences among their respective S_1 topcrosses for ear height and non significant differences for each of ear length and kernels number/row traits. However, significance varied for the other traits among the three populations: for days to 50% silking, only $C1_{(S1)}$ exhibited significant differences, whereas only $C1_{(HS)}$ exhibited non significant differences for plant height. The two populations $C1_{(HS)}$ and $C1_{(S1)}$ showed significance for ear position and ear diameter, respectively, and the same two populations

showed significance for rows number/ear. For grain yield, variation among S_1 topcrosses was significant for each of C1(HS) and C1(S1&HS), while was non significant for C1(S1).

It is also noticeable that values of C.V. for S_1 topcrosses analysis were larger than their counterparts in populations analysis especially in grain yield trait. This is maybe due to the plot size which was smaller in this evaluation.

Mean performance in Table 3 indicated that the original population was the earliest (59 days) among the improved and the check populations, and also reaped the desirable values for plant height (199cm), ear height (102cm) and ear position (51%) traits with significant differences for all mentioned traits except plant height, revealing undesirable changes happened for these traits in the improved populations. While the superiority was for the improved and the check populations over the original population for ear length and ear diameter with non significant differences for the first trait and significant differences for the second one. However, almost there was no differences for rows number/ear and kernels number/row.

Table 3 : Mean of performance and LSD values for the five populations at Gemmeiza location for all the studied traits.

Traits	Nubaria yellow maize populations				G.Y.P.	LSD at 0.05%
	C0	C1 (S1)	C1(HS)	C1 (S1&HS)		
Days to 50 % silking	59	61	60	60	63	2
Plant height (cm)	199	215	202	205	211	S
Ear Height (cm)	102	123	113	118	122	5
Ear position (%)	51	57	56	57	58	3
Ear length (cm)	16.9	18.4	18.5	18.5	18.4	NS
Ear diameter (cm)	4.2	٤,٥	٤,٧	4.7	4.8	0.2
Rows number/ear	15.4	15.5	15.3	15.2	15.5	NS
Kernels number/row	35	36	36	37	36	NS
Grain yield (ard/fad)	11.670	15.640	15.390	16.050	16.940	2.5

Concerning grain yield trait, C1(S1&HS) was the highest yielding, followed by C1 (S1) and finally C1 (HS) with significant differences than the original population, and non significant differences among the three improved populations, while no improved population exceeded the check population. Grain yield has improved significantly through this cycle by an increase up to 32 % than the original population. Generally, Unlike yield, the other studied traits did not further changed in the improved populations.

In most instances, predicted gain tended to be greater than actual one; e.g., results of Arriel and Ramalho (1993), El-Morshidy *et al.* (2002), Gamea (2005), El-Seidy *et al.* (2008), and Gamea (2010). Our case was not out of the context; i.e., on the average, actual gain (3.97 & 3.720 ard/fad for S_1 and H.S. family selection methods, respectively) were apparently one-half the predicted gain which was calculated previously in the preceding paper El-Seidy *et al* (2013 a) (Table 4). It is noticeable that actual gains of S_1 and H.S. family selection were close to each other; that was in the line with differences between predicted gains of the two methods whenever genetic variance

entirely due to additive genetic variance. But, the closest prediction value to actual gain were obtained under Sids location for half-sib family selection suggesting that, the most accurate estimate for additive genetic variance were determined under this location circumstances.

Table (4): Expected gain from selection in both locations and actual one for S_1 and half-sib progeny selection methods for yield trait (ard/fad).

Selection method	Expected gain		Actual gain
	Sids	Gemmeiza	
S_1	7.45	7.06	3.97
H.S.	4.24	6.87	3.72

Reasons of inconsistency between predicted and actual gain can be listed in the following points :
(1) Upward estimates of additive genetic variance for both selection methods.
(2) How we assure selection just for alleles of additive gene action, it is more likely that we select favorable alleles whatever what kind of gene action controlling the effect of these alleles.
(3) Missing some of S_1 families with their favorable alleles during recombination process of forming the new improved populations.

Anyway, we reaped reasonable gain from this cycle of selection for improving grain yield.

Mean performance of each S_1 topcross involved in each improved population resulting from this improvement cycle is shown in Table 5.

Evaluation of S_1 topcrosses for each improved population was to achieve full representation of all S_1 topcrosses forming each improved population in evaluation trial and to examine general combining ability of each recombined S_1 which enable us to exclude those of unfavorable performance values

It is noted that, relative performance of S_1 topcrosses differed among all the studied traits in the three improved populations; i.e., mean performance order varied among the studied traits. The improved population $C1_{(S1)}$ were the highest one in variation among its relative S_1 topcrosses in most studied traits, followed by $C1_{(HS)}$, and finally $C1_{(S1\&HS)}$.

With focus on trait of selection (grain yield), there were two significantly lower values than the highest yielding in $C1_{(HS)}$ for S_1 topcrosses 2 & 6 and one significantly lower value in $C1_{(S1\&HS)}$ for S_1 topcross 6. It can be deduced that if S_1 topcrosses with low-performance were cancelled, our gain from selection will maximize. In our case the number of S_1 topcrosses constituting each improved population is small, so inbreeding depression will magnified more if any of S_1 topcrosses were cancelled. But we can combine the three improved populations seeds without those of S_1 topcrosses with low-performance in one population.

Table 5 : Mean performance and LSD values for S_1 topcrosses (entries) inside each improved population for all the studied traits.

Ent.	Days to 50% silking	Plant height	Ear height	Ear position	Ear length	Ear diameter	Rows number /ear	Kernels number /row	Grain yield
C1(S_1)									
١	٦٠	٢٢٤	١٢٦	٥٦	١٨	٤,٥	١٤,٩	٣٥	١٥,٩٦٠
٢	٦٢	٢٢٩	١٣٥	٥٨	١٩	٤,٧	١٥,٣	٣٤	١٧,٤٢٠
٣	٦٠	٢١٨	١٣٠	٥٩	١٩,٦	٤,٨	١٤,٦	٣٧	١٧,٠٣٠
٤	٦٠	٢٠٧	١١٥	٥٥	١٧	٤,٧	١٧,١	٣٤	١٢,٨٩٠
٥	٦٠	٢٠١	١١٧	٥٨	١٧,٧	٤,٨	١٧,١	٣٧	١٤,٩٧٠
٦	٦٠	٢٠٥	١٠٧	٥٢	١٨,٥	٣,٩	١٤,٣	٣٦	١٥,٠٠٠
LSD at 0.05%	١	١٨	١٣	NS	NS	٠,٤	١,٣	NS	NS
C1(HS)									
١	٦٠	١٩٦	١٠٧	٥٤,٥	١٩	٤,٩	١٥,١	٣٦	١٧,٠٩٠
٢	٥٩	١٩٣	١١١	٥٧,٦	١٩,٥	٤,٥	١٤,١	٣٧	١٣,٢٧٠
٣	٦٠	٢٠١	١٢٢	٦١	١٩	٤,٧	١٤,٥	٣٦	١٧,٨٥٠
٤	٦١	٢١٥	١٢٢	٥٦,٨	١٩	٤,٥	١٥	35	١٥,٧٩٠
٥	٦٠	٢٠٣	١٠٩	٥٣,٦	١٧	٤,٩	١٧	٣٧	١٥,٩٦٠
٦	٦١	٢٠٤	١٠٧	٥٢,٥	١٧	٤,٦	١٥,٤	٣٥	١٢,٣٨٠
LSD at 0.05%	NS	NS	١٠	٤,٢	NS	NS	١,٥	- NS	٣,٨٢٠
C1(S_1 & HS)									
١	٦٠	٢٠٦	١١٩	٥٧,٨	١٩	٤,٩	١٥,٢	٣٨	١٨,٤١٠
٢	٦٠	٢٠٨	١٢٠	٥٧,٧	١٨	٤,٧	١٥,٤	٣٧	١٦,٩٥٠
٣	٦٠	١٨٧	١٠٧	٥٧,٢	١٩	٤,٨	١٥,٤	٣٧	١٧,٠٩٠
٤	٦١	٢٢٧	١٣٤	٥٨,٩	١٩	٤,٧	١٤,٨	٣٧	١٨,٢٩٠
٥	٦٠	١٩٩	١١١	٥٥,٦	١٧	٤,٣	١٥,٣	٣٧	١٠,٣٣٠
LSD at 0.05%	NS	٢٢	١٢	٢,٤	NS	NS	NS	NS	٤,٧٢٠

Finally, an important question arises of which one of the three improved populations is the most profitable in breeding program. maize breeding nowadays depends on two reverse processes: inbreeding in order to form inbred lines and hybridization between these inbred lines in order to form crosses. The main aim of our work is enhancing performance of inbred lines extracted from population under selection through enhancing the performance of the population *per se* by elimination the harmful alleles. Over the three improved populations, the performance enhanced with close values, but with a look to the performance of the selected in the three selection methods shown in Table 1, it is readily seen that selection among half-sib families was for the highest combining ability of parents regardless of their inbreeding depression occurred in the first self-generation. While selection among S_1 families was for the lowest inbreeding depression for parents without testing their combining ability. Whilst the combined selection gathered the two selection criterion (inbreeding depression and combining ability). With taking lines isolation process into consideration, the improved population with half-sib family selection method may not be productive because of high inbreeding depression could be done. While, in the population improved by S_1 family selection, although low inbreeding expected to be done, but perhaps the combining ability of the lines extracted from this population will be less than of those extracted from the population improved by combined selection.

Therefore, we think that combined selection method is the most profitable among
the three studied methods. This was with the line with what Goulas and Lonnquist (1976) pointed out of that combined half-sib and S_1 family selection may be useful for improving simultaneously combining ability and *per se* value. And with what mentioned by Hallauer and Miranda (1981) about, "genes contributing to heterotic behavior are more likely to be selected in half-sib evaluation than in S_1 family evaluation, where genes with favorable additive effects receive greater emphasize. Consequently, combined selection using information from both half-sib and S_1 progenies provides for an increase in frequency of desirable alleles and allelic combination more effectively than either half-sib or S_1 separately"

Conclusion

Selection succeeded in improving the yield of Nubaria yellow maize population by an increase up to 32 %, with no significant differences among the used methods of selection.

Recommendation

We recommend with :

(1) Using the improved population resulting from the combined selection as a sub-population for extracting inbred lines needed in maize breeding program for hybrids production.

(2) Combining the three improved populations seeds without those of S_1 topcrosses with low-performance in one population used for isolation and as a material for the coming improving cycles of recurrent selection.

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مقارنــة فعاليــة اثنـين مـن طـرق الانتخـاب فـي تحسـين محصـول عشـيرة مـن الـذرة الشامية

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يعتبر الانتخاب التكراري الوسيلة الأكثر شيوعا للتحسين غير المباشر لأداء السلالات المرباة داخليا من خلال تحسين أداء مصادرها من العشائر. في هذه الدراسة, تم مقارنة كفاءة طريقتي انتخاب عائلات الجيل الذاتي الأول والعائلات نصف الأخوية باستخدام تصميم نورث كارولينا الأول في تحسين عشيرة النوبارية الصفراء (الحلقة الأولى). من أجل إجراء مقارنة عادلة بين الطريقتين, تم توحيد المادة الوراثية المستخدمة فيهما باستخدام حبوب العائلات الذاتية والمفترض أن يحتفظ بها لتكوين العشيرة الجديدة في طريقة انتخاب العائلات نصف الأخوية كمادة وراثية مستخدمة في طريقة انتخاب عائلات الجيل الذاتي الأول. ذلك مكننا من دراسة الأداء للنسل الذاتي والخلطى لنفس الأب, ليكون لدنيا وحدات أخرى للانتخـاب المشترك تتمثل في العائلات الأبوية (العائلتان الذاتية ونصف الأخوية معا لنفس الأب الواحد). تألفت المواد الوراثية من ٨١ عائلة ذاتية و ٣٢٤ عائلة أخوية يشكلون ٨١ عائلة نصف أخوية. تم تقييم تلك المواد الوراثية في موقعين مختلفين بمحطة البحوث الزراعية بالجميزة والممثلة لمنطقة وسط الدلتا ومحطة البحوث الزراعية بسدس والممثلة لمنطقة مصر العليا. قد لوحظ أن العائلات نصف الأخوية المنتخبة ذات الأداء المرتفع لم يصاحبها تفوق في أداء العائلات الذاتية المقابلـة لهـا مـن نفس الأب والعكس صـحيح., فلم تكن هنـاك علاقة واضـحة بـين أداء العـائلات الذاتيـة ونصـف الأخويـة. عند الحصـاد, لموسـم تكـوين المجتمعـات الجديـدة , تم فصـل خطـوط التلقيحات القمية للعائلات الذاتية المكونة لكل عشيرة, لاختبار القدرة على التآلف لكل عائلة ذاتية مهجنه في كل عشيرة. تم تقييم الثلاث عشائر المحسنة بالخطوط الناتجة من التلقيح القمي للعائلات الذاتية الخاصـة بكل منهم مع العشيرة الأصلية وعشيرة المقارنة بمحطة البحوث الزراعية بالجميزة. لوحظ اختلافات معنوية بين خطوط التلقيحـات القميـة للعائلات الذاتيـة في صـفة محصـول الحبوب. كـان التقدم الوراثي الفعلـي (٣,٩٧ & ٣,٧٢ أردب/فدان لكل من طريقتي انتخاب الجيل الذاتي الأول ونصف الأخوية بالترتيب) تقريبا نصف قيمة المتنبأ بـه. ارتفع المحصول معنويا خلال هذه الدورة من التحسين بالانتخاب بزيادة تصل إلى ٣٢% عن محصول العشيرة الأصلية، وكانت العشيرة المحسنة بالطريقة المشتركة الأعلى محصـولا, يليها العشيرة المحسنة بطريقة انتخاب العائلات الذاتية, ثم العشيرة المحسنة بطريقة العائلات نصف الأخوية بفروق طفيفة وغير معنويـة بـين الثلاث عشائر المحسنة.

وتوصي هذه الدراسة باستخدام العشيرة المحسنة الناتجـة من الانتخـاب المشترك كعشيرة ثانويـة لعزل السلالات المرباة داخليا مع دمج حبوب الثلاث عشائر المحسنة بدون تلك الخاصـة بالتلقيحـات القميـة للعائلات الذاتية ذات الأداء المنخفض في عشيرة واحدة تستخدم لعزل السلالات وكمادة وراثية لحلقات التحسين بالانتخاب القادمة.

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