

Changes of Gene Frequencies in Synthetic Corn Populations by Two Methods of Recurrent Selection and Pedigree Selection

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ABSTRACT

Forty-five F1C0 corn hybrids were derived from diallel series of 10 selected inbreds from different sources of germplasm. AgSyn1C0 was synthesized from bulked balanced seeds of 45 F1C0. The remnant seeds were tested for their yielding ability in randomized complete block design with 4 replications simultaneously, selected plants in border rows were selfed to obtain S1C0. Forty-five S1C0 from diallel set plus 4 additional S1C0 were planted in R-49 grouped replicated honeycomb design. Top-10 F1C0 (diallel selection) and top-10 S1C0 (S1 selection) were selected from each cycle. Their pedigrees were recorded and frequencies of original lines presented in pedigree of selected lines were used to calculate gene frequencies in derived populations. Pedigree selection was also conducted from each selected S1 set from each cycle. Two cycles of selection were done to obtain AgSyn1C1, AgSyn1C2. Two selected lines from pedigree selection were added to AgSyn1C2 to obtain AgSyn1C2-Sem. Changes of gene frequency patterns by the 3 methods of selection were very similar but diallel selection and pedigree selection retained more genetic diversity than S1 selection. Therefore, there was no clear advantage of recurrent selection over the pedigree selection. However, recurrent selection enhances gene recombination and accumulation of desirable genes in the population while pedigree selection is suitable for accumulation of few desirable genes in single plant. The results suggested that recurrent selection should be a supporting program to provide desirable germplasm to pedigree program. Diallel selection not only retained more genetic diversity but needs only 2 planting seasons to complete a cycle instead of 3 planting seasons as most recurrent selections now generally in use. Therefore, diallel selection should be more effective than S1 selection for the improvement of population per se from which good inbreds could be derived. The results also suggested that genetic diversity of first few cycles of selection drastically dropped when combining ability of the original lines were widely different.

Key words: S1 selection, gene frequency, diallel, corn hybrid

INTRODUCTION

Pedigree selection has been used effectively for the improvement of corn inbreds and hybrids. However, continuous selfing nature of pedigree selection limited gene recombination and accumulation of favorable genes. Eberhart *et al.*

(1995) proposed that population improvement should be used as a supporting program of pedigree method to provide desirable germplasm for the improvement of corn inbreds and hybrids. Several modifications of population improvement methods had been proposed with variable results and effectiveness. Duclos and Crane (1968) found that

S1 selection and testcross selection were equally effective for the improvement of population per se. Similar results were reported by Carrangal *et al.* (1971). Contrarily, Horner *et al.* (1969) found that testcross selection for specific and general combining ability were more effective than S2 selection for the improvement of random mated populations but S2 selection rendered inbreds with better grain yield. However, after four cycles of selection Burton *et al.* (1971) found that response to S1 selection was 10.6 % as compared to only 5.7 % from testcross selection.

Weyhrich *et al.* (1998) conducted a direct comparison of seven population improvement methods ; mass, modified ear-to-row, half-sib with inbred tester, full-sib, S1 progeny, S2 progeny and reciprocal full-sib selection and concluded that S1 and S2 progeny selections were the most effective methods for overall performance of derived populations. Genter and Alexander (1966) suggested that visual selection for desirable agronomic traits plus S1 yield evaluation offers a greater opportunity for effective early generation selection than testcross methods now generally in use. However, Genter and Eberhart (1974) concluded that sources of materials and environmental conditions under which recurrent selection trials are conducted may be as important as the selection methods used.

Despite a wide acceptance of line screening under high plant densities to get tougher inbreds and hybrids (Troyer, 1996) Tokatlidis *et al.* (2001) had proved that selection under nil competition environment in honeycomb design was very effective for the improvement of high yield corn inbreds and hybrids which could adapt to wide ranges of plant densities.

Since potential yield improvement may be counterbalanced by inbreeding depression, this experiment was conducted to study the changes of gene frequencies in responses to S1 selection under nil competition in honeycomb design as compared to diallel and pedigree selections.

MATERIALS AND METHODS

Ten inbreds from different germplasm sources, Ag17 and Ag18 (Pioneer 3012), Ag6, 25 and 26 (Pioneer 3013), Ag11 and 28 (SW 3853), Ag27 (G5445A), Ag22 (Cargill 919) and Ag24 (Uni-H9728) were intercrossed in a diallel manner. The derived 45 F1C0 were bulked and designated as AgSyn1C0 population. Remnant seeds of each 45 F1C0 were tested for their yielding ability in randomized complete block design with 4 replications, each plot comprised 4 rows of 5 meter long with 0.75 × 0.25 m plant spacing. Five plants in the border rows of each F1C0 were selfed and bulked within each family. Four selected S1C0 families were added to the derived 45 S1C0 families and planted in R-49 grouped replicated honeycomb (Fasoulas and Fasoula, 1995). Forty plants of each S1C0 family were planted in equilateral triangle of side 0.866 m. Single plant selection was done by moving circle selection with selection intensity of 14.3 % (1 out of 7 plants in the circle). Simultaneously, 1 out of 7 plants in the rows was selected by visual selection and selfed to obtained S2 seeds. Ten S1C0 families with highest selection frequencies by moving circle selection were chosen. However, instead of using S1C0 seeds, the S2C0 seeds were diallel crossed to start the following. Remnant seeds of top-10 S2 lines of each cycle were continued selfing for pedigree selection. Pedigree of 10 selected S1s and F1s from each diallel set of each cycle were recorded and the frequency of each original line presented in each population was used to estimate the gene frequencies of each selection cycle. Two cycles of selection were conducted to obtain AgSyn1C1, AgSyn1C2, F1C1, S1C1 and S5 from pedigree selection.

Ten S5s derived from the original S1C0 by pedigree selection were diallel crossed to estimate combining ability of S5 lines. Top-2 general combining ability lines were intercrossed with 10 S1C1 and designated as AgSyn1C2-Sem. (semi-

open end population). All Syn1 populations, AgSyn1C0, AgSyn1C1, AgSyn1C2, and AgSyn1C2-Sem. were tested to compare their yielding ability with SW1C12 and SW5C4.

RESULTS AND DISCUSSIONS

The original 10 inbred lines were Ag17, Ag18 (pioneer 3012), Ag6, Ag25, Ag26 (pioneer 3013), Ag11, Ag18 (SW3853), Ag27 (G5445A), Ag22 (Cargill 919) and Ag24 (Uni-H9728). Therefore, each source of germplasm contributed a frequency of 20% (2pioneer 3012), 30% (3pioneer 3013), 20% (2SW3853) and 10% (1) each for G5445A, Cargill 919 and Uni-H9728. After the first round of S1 selection, frequencies of Pioneer 3012, Pioneer 3013, SW3853, G5445A, Cargill 919 and Uni-H9728 in top-10 single crosses were 4, 7, 1, 6, 1 and 1 which equal to 20, 35, 5, 30, 5, and 5 percent, respectively and subsequently, after the second round of S1 selection, frequencies of Pioneer 3012, Pioneer 3013, SW3853, G5445A, Cargill 919 and Uni-H9728 in double crosses were 10, 14, 1, 13, 1, and 1 which equal to 25, 35, 2.5, 32.5, 2.5 and 2.5 percent, respectively (Table 1).

Simultaneously, frequencies of 10 selected F1C0 and F1C1 from diallel selection calculated from pedigrees of single crosses and double crosses were 10, 40, 15, 25, 5, and 5 percent and 15, 27.5, 5, 37.5, 10 and 5 percent, respectively.

Frequencies of Pioneer 3012, Pioneer 3013 and G5445A were increased steadily by S1 selection from S0C0 to S1C1 with the expense of SW3853, Cargill 919 and Uni-H9728. Similar trend was observed from diallel selection (Table 1). Regardless of selection methods, after one or two cycles of selection, high combining ability lines from Pioneer 3012, Pioneer 3013 and G5445A dominated the gene pool of populations. This finding may explain the previous study of Genter (1973), Duclos and Crane (1968), Ortiz (1963), and Carrangal *et al.* (1971) of which inbred line selection was as effective as testcross selection. Although, different methods of combining ability testing were used, a slightly more balance of gene frequencies by diallel selection of this study also may explain why in certain case, testcross selection was more effective than inbred selection for random mated population per se (Horner *et al.* 1973). However, Genter and Eberhart (1974) found that variable results from different

Table 1 Changes of gene frequencies by S1 selection, diallel selection, and pedigree selection.

Germplasm source	Original gene frequency (%)	Gene frequency of selected line (%)				
		S ₀ C ₀	S ₁ C ₀ ^{1]}	F ₁ C ₀ ^{2]}	S ₁ C ₁ ^{1]}	F ₁ C ₁ ^{2]}
Pioneer 3012	20	20	10	25	15	25
Pioneer 3013	30	35	40	35	27.5	20
SW 3853	20	5	15	2.5	5	5
G5445A	10	30	25	32.5	37.5	35
Cargill 919	10	5	5	2.5	10	10
Uni-H9728	10	5	5	2.5	5	5
Total	100	100	100	100	100	100

1] Gene frequencies of germplasm after each cycle of S1 selection.

2] Gene frequencies of germplasm after each cycle of diallel selection.

3] Gene frequencies of germplasm from pedigree selection.

methods of selection were largely because of different sources of material under selection and environmental conditions under which selection trials were conducted.

Yields of AgSyn1C1 and AgSyn1C2 were clearly dropped from AgSyn1C0 (Table 2). Horner *et al.* (1969). also found that population yields of the first two cycles were lower than the original population. However, population yields of the more advanced cycles were steadily increased and surpassed the original population after 5 cycles of selection. Results of present study indicated that inbreeding depression had a pronounced effect on yield in the first 1 or 2 cycles of selection. This may be because of the AgSyn1C0 derived from crossing among well selected inbred lines while AgSyn1 of the first 2 cycles were derived from narrow base of segregated S1 lines, causing expression of deleterious genes. However, accumulation of desirable genes in the more advanced cycles should increase yield of random mated populations. In fact, the ultimate purpose was to obtain strong high yield inbreds but not the high yield of random mated

population. Selection for inbred lines per se drastically increased inbreeding depression, especially when original germplasm was widely different in combining ability. The poor combining ability lines were discarded in the first few cycles and hence inbreeding among related lines. Variable results of testcross selection were also reported by Sprague *et al.* (1959), Penny and Eberhart (1971) and Genter (1973). Therefore, each selection method worked differently with different populations.

Selections in Syn2 or Syn3 may slowly decrease genetic variability and reduce inbreeding depression of selected populations but it probably needs more selection cycles to discard deleterious recessive genes and takes longer time for the population to reach the same yield level as of selection in Syn1. SW1-C12 originated from a very broad base population by S1 selection and took more than 20 years (planted 2-3 crops per year) to reach the same yield level as of only few cycles of S1 selection in highly selected narrow-base population from commercial cultivars and improved germplasm. (Table 2).

Table 2 Yield of Ag-Syn1 populations as compared to SW1-C12 and SW5-C4.

Selection cycles	Character							
	Grain yield	Percent to SW1-C12	50% silking	Shelling	Moisture	Plant height	Ear height	Foliar dis.
	kg/ha%.....	... days... % cm			0-5
C0	4,768 a	108	54 a	82 a	29 a	176 b	96 b	1.25 ab
C1	4,293 b	97	54 a	79 b	29 a	174 b	100 ab	0.50 b
C2	4,318 b	98	53 a	78 b	29 ab	177 b	103 ab	1.00 ab
C2-Sem*	4,362 b	99	54 a	79 b	29 ab	173 b	100 ab	1.00 ab
<i>Check</i>								
SW1-C12	4,381 b	100	54 a	78 b	28 ab	191 a	103 ab	0.75 ab
SW5-C4	4,406 b	100	54 a	79 b	29 b	196 a	105 a	1.50 b
Mean	4425	—	54	79	29	181	101	1.00
%CV	3.03	—	1.32	1.28	2.07	3.3	4.62	54.77

* Semi-open end population (Ag-Syn1C2-Sem) derived from diallel series of 10 S2 lines of Ag-Syn1C1 plus 2 S5 lines from Ag-Syn1C0 by pedigree selection.

Table 3 Yields at 15 percent moisture and other agronomic traits of top-10 F1 hybrids derived from S5 inbreds extracted from AgSyn1C0 by pedigree method.

Pedigree	Grain yield	% of Pion. 3012	Moisture	Shelling	50% silking	Plant height	Ear height
	kg./ha.%			dayscm.....	
Ag210/Ag205	8,144 a-c	105	35 a-g	77 f-m	54 b-d	189 c-h	107 d-f
Ag208/Ag204	7,847 a-d	101	34 a-j	78 b-I	54 c-e	185 c-k	100 f-k
Ag210/Ag204	7,532 a-f	97	33 d-m	76 f-m	53 c-f	184 c-m	100 f-k
Ag201/Ag208	7,500 a-f	97	33 d-n	81 a-d	54 c-e	181 g-p	97 h-n
Ag207/Ag203	7,404 a-f	95	36 a-d	82 a-c	53 d-g	194 a-f	110 b-e
Ag205/Ag208	7,199 b-h	93	33 d-n	75 I-n	53 c-f	183 d-m	105 d-h
Ag209/Ag203	7,190 b-h	93	32 g-p	79 b-h	52 e-g	188 c-h	110 b-e
Ag210/Ag203	7,150 b-h	92	31 I-r	77 e-l	53 d-g	186 c-j	112 a-d
Ag206/Ag205	7,141 b-h	92	33 d-n	74 k-n	53 c-f	203 a	120 a
Ag210/Ag202	7,141 b-h	92	31 h-p	78 b-j	54 b-d	194 a-f	110 b-e
<i>Check :</i>							
Pioneer 3012	7,765 a-e	100	29 n-p	82 ab	55 a-c	203 a	110 b-e
CP989	6,479 f-m	83	30 m-p	78 b-I	56 ab	196 a-c	100 f-k
Syngenta NK45	8,469 a	109	29 p	79 b-g	55 a-c	195 a-d	94 j-o
Cargill 919	8,271 ab	107	31 k-p	83 a	54 b-d	172 l-t	92 k-o
%CV	8.84	—	5	2	1	3	5

The semi-open end population (AgSyn1C2 Sem.) derived from diallel crossed of the same 10 S2 lines of AgSyn1C2 and 2 additional top combining ability S5 lines from pedigree selection yielded more or less the same as AgSyn1C2. Lack of heterosis in AgSyn1C2-Sem indicated that S1 selection accumulated the same dominant loci as of S5 lines from pedigree selection. While pedigree selection is more flexible for specific crosses, recurrent selection for inbred per se allows accumulation of additive and dominant genes within population and promotes stronger derived inbreds from advanced populations. Therefore, recurrent selection for inbred per se should be used as gene pool of desirable traits to support the pedigree program especially when single cross hybrid is the ultimate goal of breeding program.

Diallel selection rendered a more balance of germplasm and maintained more genetic variability as compared to S1 selection (Table 1). Moreover, diallel selection allowed a direct test for combining ability among selected inbreds. Therefore, combining ability of the advanced cycles should be increased. Therefore, diallel progeny testing and simultaneously selfing of the diallel set and diallel crossed of selected S1s in the following season to start new cycle of selection should be a logical method for recurrent selection. This method used only 2 seasons per cycle instead of 3 seasons per cycle for S1 and testcross selection methods now generally in use. Gene frequencies of Pioneer 3012, Pioneer 3013, SW 3853, G5445A, Cargill 919 and Uni-H9728 in 10 selected S5s from pedigree selection were 25, 20, 5, 35, 10, and 5% respectively

(Table 1). The results suggested that pedigree selection rendered a similar pattern of gene frequencies as of that obtained from S1 selection and diallel selection. However, recurrent selection provided a systematic crossing and simultaneous selection of desirable traits and allows a thorough use of germplasm. Therefore, recurrent and pedigree selections should be interplayed for the most effective use of germplasm. Table 3 showed yields and few other agronomic traits of top-10 hybrids ($S_5 \times S_5$) from pedigree selection. The top two hybrids were more or less yielded the same as of check hybrids but significantly higher yield than CP989. The experimental hybrids had higher moisture content and lower shelling percentage and there were no clear advantages on other aspects.

CONCLUSION

Regardless of selection methods, the ultimate purposes of breeding program are to eliminate of deleterious genes and accumulate desirable genes either for the improvement of pure population or heterogeneous population. However, pedigree selection is still the most widely used for the improvement of inbreds either for direct use or for hybrid production. Although recurrent selection has been proposed for the improvement of combining ability of the heterogeneous population from which good combining ability inbreds could be derived, its effectiveness is obscure because of variable results of the methods. Results from this study as well as previous studies led to the conclusion that recurrent selection in selected narrow base population could be used as supporting system to pedigree method. While pedigree method is more flexible for specific crosses and improvement of few desirable traits, recurrent selection systematically provides a more thorough use and simultaneous selection of desirable traits. Most of recurrent selections now generally in use require 3 steps per cycle but diallel selection requires only 2 steps per cycle, a simultaneous testing of diallel

progenies and selfing of the F1s from which derived S1s are diallel crossed to start the new cycle. Beside, diallel selection provides a direct testing for combining ability of selected lines. Comparatively, the present study showed that diallel selection retained more genetic diversity of derived population than S1 selection. Therefore, the method should be an effective system for inbred and hybrid improvement as well as a supporting system to pedigree method.

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Received date : 01/11/02

Accepted date : 23/12/02