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## Responses to Recurrent Selection Methods in Two Sweet Corn (*Zea mays L. saccharata*) Populations

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**Abstract:** In the present study, two cycles of Mass Selection (MS) and Selfed Progeny Selection (SPS) were conducted on two sweet corn populations (BC<sub>2</sub>-10 and BC<sub>1</sub>-10 x Syn-II). The improved populations generated from each of the two populations were evaluated in comparison with the base populations, at two locations, to determine the genetic gains, to estimate heritability and correlations among traits measured. The two base populations showed varied average realized responses to MS and SPS. In BC<sub>2</sub>-10 derived populations, the realized responses to MS were 5.1% in cycle 1 (C<sub>1</sub>) and 4.8% in cycle 2 (C<sub>2</sub>), whereas, the realized responses to SPS were 9.1% in C<sub>1</sub> and 1.2% in C<sub>2</sub>. In BC<sub>1</sub>-10 x Syn-II derived populations, the realized responses to MS were 5.5% in C<sub>1</sub> and 2.9% in C<sub>2</sub>, while the realized responses to SPS were 5.6% in C<sub>1</sub> and 2.9% in C<sub>2</sub>. The two selection methods were equally effective in improving the populations for ear length, except in C<sub>1</sub> of BC<sub>2</sub>-10, where SPS was more effective than MS. Both selection methods were also effective in increasing fresh ear yield and number of kernels per row. Response of other correlated traits depended on selection methods used and populations under selection. The improved populations generated could serve as better germplasm sources to develop vigorous inbred lines and open pollinated varieties and further selection in these populations could offer better responses.

**Key words:** Mass selection, response to selection, selfed progeny selection, sweet corn

### INTRODUCTION

Recurrent selection methods have been used to improve performance of corn populations for quantitatively inherited traits. A number of efficient intra-population improvement schemes have been developed, their operational details carefully studied and suitable modifications have been suggested to further improve their efficiency<sup>[1-4]</sup>.

Mass selection, as modified by Gardner<sup>[5]</sup>, has been used to increase number of ears<sup>[6]</sup>, to change maturity<sup>[7]</sup>, to improve grain yield<sup>[8]</sup> and to change ear length<sup>[9]</sup>. However, Salazar and Hallauer<sup>[10]</sup> reported that the increase in ear length caused undesirable changes in other agronomic traits. Yield was decreased, while plant height, ear height and days to maturity were increased with selection for increased ear length.

Selfed progeny selection is more efficient than other selection method<sup>[4,11,12]</sup> because of the effectiveness of the method in selecting for additive gene effects. Hallauer and Miranda<sup>[3]</sup> summarized early studies on SPS and reported that SPS generally gave higher genetic gain for yield than

other methods of intrapopulation improvement. However, reports since 1990s indicated that SPS has shown variable gains. Livine *et al.*<sup>[13]</sup>, Burgess and West<sup>[14]</sup> and Roger *et al.*<sup>[4]</sup> reported that two to five cycles of SP selection were effective in improving grain yield or other traits that included disease resistance. In contrast, Iglesias and Hallauer<sup>[15]</sup> and Lamkey<sup>[16]</sup> who evaluated four to eight cycles of SP selection, reported that the SPS was either effective in improving grain yield only during the initial three to four cycles or not effective at all. Thus there is a need to collect more empirical data on the effectiveness of SP selection.

In comparing different methods of selection, Sprague and Eberhart<sup>[1]</sup> reported an average gain per cycle for grain yield of 2.0, 3.1, 3.4, 3.8 and 4.6 per cycle for S-2, full-sib, mass, ear-to-row and S-1 selections, respectively. Tanner and Smith<sup>[11]</sup> compared half-sib and S-1 recurrent selection in the Krug yellow dent maize population and reported that the S-1 selection was more effective than half-sib selection method, at least in cycles one to four. Rafii *et al.*<sup>[12]</sup> reported that S-1 selection method increased fresh ear yield in Bakti-1 and Manis Madu

by 16.7 and 10.2%, respectively, while full-sib reciprocal recurrent selection increased the same trait by 5.9% in Bakti-1, but decreased by 6.4% in Manis Madu.

Most comparisons for the effectiveness of selection methods involved selection for yield, which is highly influenced by environmental factors. The ideal comparison would involve selection for highly heritable trait using different intra-population selection methods in common base populations.

In this study, two cycles of MS and SPS for ear length were conducted on two sweet corn base populations using ear length that had higher heritability and strong correlation with yield. The improved populations from each of the two sources were evaluated, in comparison with the base populations, at two locations. The objectives of this study were to estimate and compare predicted and realized responses to two cycles of mass and selfed progeny selections performed on two sweet corn populations, to estimate heritability of traits measured and to determine the correlations among traits measured on populations.

## MATERIALS AND METHODS

**Description of the base populations:** BC<sub>2</sub>-10 was developed through crossing of the local population Manis Madu with exotic germplasm, Hybrid 368, followed by mass selection and then two generations of backcrossing to the local parent. On the other hand, BC<sub>1</sub>-10 x Syn-II was developed at the initial stage of this study, by crossing of Syn-II population to BC<sub>1</sub>-10, which was an elite population obtained from just one generation of the above mentioned backcrossing to the local parent. Syn-II was an exotic population possessing genes for earliness, kernel sweetness and plant shortness, while BC<sub>1</sub>-10 was a local population possessing genes for high yield and well adapted to the local environmental conditions, but was late in maturity, with less sweet kernels and tall plants.

**Mass and selfed progeny selections:** Mass Selection (MS) was conducted on the two base populations (BC<sub>2</sub>-10 C<sub>0</sub> and BC<sub>1</sub>-10 x Syn-II C<sub>0</sub>) for two consecutive cycles at the Institute of Bioscience Farm, Universiti Putra Malaysia. The selection experiments were conducted during February 2002 to March 2004.

Selfed progeny selection was conducted on the two base populations, BC<sub>2</sub>-10 C<sub>0</sub> and BC<sub>1</sub>-10 x Syn-II C<sub>0</sub>, for two consecutive cycles from June 2002 to March 2004. Initially, each base population was planted on an area of 400 m<sup>2</sup> following the recommended cultural practices. Progenies were developed by selfing the two base

populations, following the procedures described by Singh<sup>[17]</sup>. Selected 100 progenies for each of the base population were evaluated and the he selected progenies were then recombined to form population of the first cycle (C<sub>1</sub>). Population of the second cycle (C<sub>2</sub>) was also formed following the same procedure conducted on population of C<sub>1</sub> for each of the base population. Finally, the four improved populations and the two base populations were included in the evaluation experiment.

**Evaluation of populations generated from selection:** The populations generated from two cycles of mass selection (BC<sub>2</sub>-10 MS C<sub>1</sub>, BC<sub>2</sub>-10 MS C<sub>2</sub>, BC<sub>1</sub>-10 x Syn-II MS C<sub>1</sub> and BC<sub>1</sub>-10 x Syn-II MS C<sub>2</sub>), selfed progeny selection (BC<sub>2</sub>-10 SPS C<sub>1</sub>, BC<sub>2</sub>-10 SPS C<sub>2</sub>, BC<sub>1</sub>-10 x Syn-II SPS C<sub>1</sub> and BC<sub>1</sub>-10 x Syn-II SPS C<sub>2</sub>) and the base populations (BC<sub>2</sub>-10 C<sub>0</sub> and BC<sub>1</sub>-10 x Syn-II C<sub>0</sub>) were evaluated, at the University Agriculture Park and IBS Farm, UPM. A Randomized Complete Block Design with four replications was used. Each plot consisted of five rows of 5 m long, with spacings of 0.75 x 0.25 m between and within rows, respectively. Recommended cultural practices were followed at each location. The whole experiment was conducted during December 2001 to March 2004 at UPM, Malaysia.

**Data collection and analysis:** Data collected in this experiment include husked and dehusked fresh ear yields, husked and dehusked ear lengths, husked and dehusked ear diameters, plant height, ear height, number of kernel rows per ear, number of kernels per row, total soluble solids, days to tasseling, days to silking, number of leaves and number of ears per hectare.

The data were analyzed using Statistical Analysis System computer package Version 8.2<sup>[18]</sup>. The analyses of variance were conducted first for individual location and the combined ANOVA was then conducted for traits that showed homogeneous error variances revealed by Bartlett's test.

The predicted response to selection was estimated using the formula suggested by Falconer and Mackay<sup>[19]</sup>, as follows:  $R = ih^2\sigma$ , where, R = predicted response to selection, i = the intensity of selection, h<sup>2</sup> = heritability of a trait and  $\sigma$  = phenotypic standard deviation of the parental population. The intensity of selection (I) of 1.4 was taken for 20% selection intensity. The cumulative responses to mass and selfed progeny selections were estimated as a percentage of the base population (C<sub>0</sub>), while individual cycle responses to the selections were estimated as a percentage of respective preceding parental populations.

Table 1: Parameters measured on improved sweet corn populations generated from BC<sub>2</sub>-10 and BC<sub>1</sub>-10 x Syn-II, following two cycles of mass selection

Population	Mean ear length (cm)	Standard deviation	Heritability (%)	Predicted response (%)*	
				A	B
BC <sub>2</sub> -10					
C <sub>0</sub>	13.8	3.32	73.4		
C <sub>1</sub>	16.5	3.05	72.9	24.7	
C <sub>2</sub>				18.8	47.2
SE	1.59				
BC <sub>1</sub> -10 x Syn-II					
C <sub>0</sub>	11.9	2.89	65.6	22.3	
C <sub>1</sub>	14.4	2.55	64.3	16.0	41.6
C <sub>2</sub>					
SE	1.50				

\*A: response to individual cycles, B: cumulative response

Table 2: Parameters measured on sweet corn populations generated from BC<sub>2</sub>-10 and BC<sub>1</sub>-10 x Syn-II, following two cycles of selfed progeny selection

Population	Mean ear length (cm)	Standard deviation	Heritability (%)	Predicted response (%)*	
				A	B
BC <sub>2</sub> -10					
C <sub>0</sub>	10.0	1.19	70.9		
C <sub>1</sub>	14.8	1.09	64.6	13.2	
C <sub>2</sub>				9.8	21.7
SE	1.45				
BC <sub>1</sub> -10 x Syn-II					
C <sub>0</sub>	11.8	1.25	67.3		
C <sub>1</sub>	12.4	1.14	64.3	9.9	
C <sub>2</sub>				8.3	18.7
SE	1.76				

\*A: response to individual cycles, B: cumulative response

The realized response to selection was estimated as realized response

$$(\%) = \frac{C_n - C_{n-1}}{C_{n-1}} \times 100$$

Where, C<sub>n</sub> and C<sub>n-1</sub> are mean values for improved and preceding populations, respectively.

Results of predicted and realized response to selections were compared using  $\chi^2$  test. Broad-sense heritability (h<sup>2</sup><sub>B</sub>) over locations was calculated using the variance components method as suggested by Holland *et al.*<sup>[20]</sup> and simple phenotypic correlations among plant traits studied were computed using the formula given by Gomez and Gomez<sup>[21]</sup>.

## RESULTS

**Predicted response to mass selection:** The predicted response from individual cycle in BC<sub>2</sub>-10 were 24.7 and 18.8% in cycle 1 (C<sub>1</sub>) and cycle 2 (C<sub>2</sub>), respectively, whereas, the predicted responses from individual cycles in BC<sub>1</sub>-10 x Syn-II were 22.3 and 16.0% in C<sub>1</sub> and C<sub>2</sub>, respectively (Table 1).

**Predicted response to selfed progeny selection:** The predicted responses from individual cycle in BC<sub>2</sub>-10

derived populations were 13.2% in C<sub>1</sub> and 9.8% in C<sub>2</sub>. In BC<sub>1</sub>-10 x Syn-II derived populations, the predicted responses from individual cycles were 9.9% in C<sub>1</sub> and 8.3% in C<sub>2</sub> (Table 2).

**Realized response to mass selection:** At UAP, the realized responses to mass selection from individual cycles in BC<sub>2</sub>-10 populations were 7.4% in C<sub>1</sub> to 4.0% in C<sub>2</sub>. At IBS Farm, the realized responses to mass selection were 3.3% in C<sub>1</sub> to 5.0% in C<sub>2</sub>, while the cumulative realized response was 8.4% (Table 3).

At UAP, the realized responses to mass selection in BC<sub>1</sub>-10 x Syn-II derived populations were 8.3% in C<sub>1</sub> and 2.8% in C<sub>2</sub>, while the cumulative realized response was 11.4% in C<sub>2</sub> over C<sub>0</sub>. At IBS Farm, the realized responses to mass selection were 3.1% in C<sub>1</sub> and 2.4% in C<sub>2</sub>. The average realized responses to mass selection, over the two locations, in these populations were 5.5% in C<sub>1</sub> and 2.9% in C<sub>2</sub> (Table 3).

**Realized response to selfed progeny selection:** At UAP the realized responses to SPS from individual cycles in BC<sub>2</sub>-10 derived populations were 11.7% in C<sub>1</sub> and 2.2% in C<sub>2</sub>, whereas the realized responses to SPS from individual cycles at IBS Farm were 9.1% in C<sub>1</sub> over C<sub>0</sub> and 1.2% in C<sub>2</sub> over C<sub>1</sub>. The average realized response to SPS, over the two locations, were 10.1% in C<sub>1</sub> and 1.7% in C<sub>2</sub> over the preceding cycles (Table 4).

Table 3: Response of mass selection measured on improved sweet corn populations evaluated at the University Agriculture Park and Institute of Bioscience Farm, Malaysia, 2004

Population	At UAP			At IBS			Average		
	Mean ear length (cm)	Response <sup>1</sup> (%)		Mean ear length (cm)	Response <sup>1</sup> (%)		Mean ear length (cm)	Response <sup>1</sup> (%)	
		A	B		A	B		A	B
BC <sub>2</sub> -10									
C <sub>0</sub>	16.2			15.4			15.8		
C <sub>1</sub>	17.4	7.4		15.9	3.3		16.6	5.1	
C <sub>2</sub>	18.1	4.0	11.7	16.7	5.0	8.4	17.4	4.8	10.1
Mean	17.2	5.7		16.0	4.1		16.6	3.9	
SE	0.55			0.38			0.46		
BC <sub>1</sub> -10 x Syn-II									
C <sub>0</sub>	16.7			16.1			16.4		
C <sub>1</sub>	18.1	8.3		16.6	3.1		17.3	5.6	
C <sub>2</sub>	18.6	2.8	11.4	17.0	2.4	5.6	17.8	2.9	8.5
Mean	17.8	5.5		16.7	2.7		17.2	4.2	
SE	0.57			0.26			0.41		

<sup>1</sup>A: response to individual cycles, B: cumulative response

Table 4: Response to selfed progeny selection measured on two sweet corn populations, evaluated at the University Agriculture Park (UAP) and Institute of Bioscience (IBS) Farm, Malaysia, 2004

Population	At UAP			At IBS			Average		
	Mean ear length (cm)	Response <sup>1</sup> (%)		Mean ear length (cm)	Response <sup>1</sup> (%)		Mean ear length (cm)	Response <sup>1</sup> (%)	
		A	B		A	B		A	B
BC <sub>2</sub> -10									
C <sub>0</sub>	16.2			15.4			15.8		
C <sub>1</sub>	18.1	11.7		16.8	9.1		17.4	10.1	
C <sub>2</sub>	18.5	2.2	14.2	17.0	1.2	10.4	17.7	1.7	12.0
Mean	17.6	6.9		16.4	5.1		17.0	5.9	
SE	0.71			0.50			0.59		
BC <sub>1</sub> -10 x Syn-II									
C <sub>0</sub>	16.7			16.1			16.4		
C <sub>1</sub>	17.5	4.8		17.1	6.2		17.3	5.5	
C <sub>2</sub>	18.1	3.4	8.4	17.5	2.3	8.7	17.8	2.9	8.5
Mean	17.4	4.1		16.9	4.2		17.2	4.2	
SE	0.40			0.42			0.28		

<sup>1</sup>A: response to individual cycles, B: cumulative response

Table 5: Comparison between selection methods for predicted and realized responses for ear length performed on two sweet corn populations

Populations	Predicted response (%)			Realized response (%)		
	MS	SPS	$\chi^2$	MS	SPS	$\chi^2$
BC <sub>2</sub> -10						
C <sub>1</sub>	24.7	13.2	5.35*	5.1	10.1	4.90**
C <sub>2</sub>	18.8	9.8	4.31*	4.8	1.7	2.00
Cumulative	47.2	21.7	13.78**	10.1	12.0	0.36
BC <sub>1</sub> -10 x Syn-II						
C <sub>1</sub>	22.3	9.9	6.90**	5.5	5.6	0.01
C <sub>2</sub>	16.0	8.3	3.70	2.9	2.9	0.00
Cumulative	41.6	18.7	12.60**	8.5	8.7	0.01

\*\*,\* significant at p = 0.01 and 0.05, respectively, MS = Mass Selection, SPS = Selfed Progeny Selection,  $\chi^2$  = calculated chi-square

For BC<sub>1</sub>-10 x Syn-II derived populations, at UAP, the realized responses from individual cycles were 4.8% in C<sub>1</sub> over C<sub>0</sub> and 3.4% in C<sub>2</sub> over C<sub>1</sub> whereas the realized responses to SPS at IBS Farm were 6.2% in C<sub>1</sub> over C<sub>0</sub> and 2.3% in C<sub>2</sub> over C<sub>1</sub>. The average realized response to SPS, over the two locations, were 5.6% in C<sub>1</sub> over C<sub>0</sub> and 2.9% in C<sub>2</sub> over C<sub>1</sub> (Table 4).

**Comparison of predicted and realized responses and selection methods:** Based on the results of  $\chi^2$  test, there

was a significant difference between predicted and realized responses to MS on the two base populations, where the predicted responses were significantly higher than the realized. In selfed progeny selection, on the other hand, the predicted responses to selection were not significantly different from the realized except in C<sub>2</sub> of BC<sub>2</sub>-10 population that showed significant difference between predicted and realized responses (Table 5).

There was a significant difference between MS and SPS for predicted response to selection (except in C<sub>2</sub> of

Table 6: Genetic variances ( $\sigma^2_G$ ), phenotypic variances ( $\sigma^2_{Ph}$ ) and broad-sense heritability ( $h^2_B$ ) estimates over locations

Traits	BC <sub>2</sub> -10			BC <sub>1</sub> -10 x Syn-II		
	$\sigma^2_G$	$\sigma^2_{Ph}$	$h^2_B$ (%)	$\sigma^2_G$	$\sigma^2_{Ph}$	$h^2_B$ (%)
Husked fresh ear yield	187310.00	303810.00	61.6	84930.00	186142.00	45.6
Dehusked fresh ear yield	42714.00	156397.00	27.3	132293.00	241889.00	54.7
Husked ear length	0.02	0.09	22.2	0.15	0.19	78.9
Dehusked ear length	0.30	0.40	75.0	0.21	0.32	66.6
Husked ear diameter	0.52	0.95	54.7	-0.02	0.44	-4.5
Dehusked ear diameter	-0.21	0.26	-80.8	0.56	0.90	62.2
Cob diameter	-0.20	0.57	-35.1	0.39	0.84	46.4
Plant height	8.77	16.09	54.3	12.49	20.69	60.4
Ear height	6.40	15.17	42.2	5.10	9.14	55.8
Number of rows per ear	0.01	0.08	12.5	0.06	0.09	66.7
Number of kernels per row	2.01	3.10	64.8	0.77	1.96	39.3
Total soluble solids	0.61	0.91	67.0	0.35	0.57	61.4
Days to tasseling	0.96	1.34	72.0	8.70	8.92	97.6
Days to silking	0.56	1.06	53.4	7.77	8.30	93.6
Number of leaves per plant	0.05	0.10	50.0	0.04	0.09	45.3
Number of ears/hectare	2374.20	-18519.00	-7.8	-12292.50	88891.00	-13.8

Table 7: Phenotypic correlations among traits measured on populations generated from mass and selfed progeny selections, evaluated at two locations

Traits	HFEY	DFEY	HEL	DEL	HED	DED	CD	PH	EH	RPE	KPR	TSS	DT	DS	NL	NEPH
HFEY		0.86**	0.26*	0.35**	0.24*	0.45**	0.10	0.08	0.13	0.08	0.01	0.09	-0.19	-0.20	0.01	0.02
DFEY			0.31**	0.41**	0.08	0.36**	0.15	0.09	0.24*	0.15	0.09	0.08	-0.08	-0.09	0.11	0.12
HEL				0.37**	-0.13	0.01	0.07	0.06	0.17	0.11	0.16	0.24*	-0.18	-0.27	0.06	0.13
DEL					0.03	0.19	0.16	-0.08	0.20	0.06	0.17	0.44**	-0.26*	-0.29*	0.04	0.16
HED						0.37**	0.07	-0.06	-0.25*	0.15	-0.28*	0.03	-0.10	-0.07	0.03	-0.21
DED							0.18	-0.03	-0.12	0.23*	-0.25*	0.01	-0.01	0.04	0.15	0.13
CD								-0.02	-0.03	0.02	0.01	0.09	-0.06	-0.03	0.09	0.06
PH									0.30**	0.21	0.03	-0.10	0.35**	0.37**	-0.01	0.04
EH										0.12	0.13	0.07	0.05	-0.20	0.02	0.13
RPE											0.20	0.28*	0.06	0.01	0.19	0.20
KPR												0.16	-0.02	0.01	0.01	0.03
TSS													-0.31**	-0.32**	0.11	0.04
DT														0.93**	-0.03	0.06
DS															-0.06	0.03
NL																0.24*
NEPH																

HFEY = Husked Fresh Ear Yield, DFEY = Dehusked Fresh Ear Yield, HEL = Husked Ear Length, DEL = Dehusked Ear Length, HED = Husked Ear Diameter, DED = Dehusked Ear Diameter, CD = Cob Diameter, PH = Plant Height, EH = Ear Height, RPE = Number of Kernel Rows per Ear, KPR = Number of Kernels per Row, TSS = Total Soluble Solids, DT = Days to Tasseling, DS = Days to Silking, NL = Number of Leaves per Plant and NEPH = Number of Ears per Hectare, \*\*, \* Significant at  $p \leq 0.01$  and  $0.05$ , respectively, N = 96

BC<sub>1</sub>-10 x Syn-II that revealed no significant difference between predicted response to MS and SPS (Table 6). Unlike the predicted response where there was a significant difference between MS and SPS, the two selection methods were not statistically different for realized response to selection (except in C<sub>1</sub> of BC<sub>2</sub>-10, that showed significant difference between MS and SPS, where SPS was more effective than MS) (Table 6).

**Broad-sense heritability:** In BC<sub>2</sub>-10 derived populations, high, broad-sense heritability estimates were revealed by dehusked ear length (75.0%), days to tasseling (72.0%), total soluble solids (67.0%) and number of kernels per row (64.8%), while moderate estimates were shown by husked fresh ear yield (61.6%), husked ear diameter (54.7%), plant height (54.3%), days to silking (53.4%), number of leaves (50.0%) and ear height (42.2%). On the other hand, dehusked fresh ear yield (27.3%), husked ear length

(22.2%) and number of kernel rows per ear (12.5%) showed low heritabilities, with estimates of 27.3, 22.2 and 12.5%, respectively (Table 6).

For populations derived from BC<sub>1</sub>-10 x Syn-II, broad-sense heritability estimates were high for days to tasseling (97.6%), days to silking (93.6%), husked ear length (78.9%) and dehusked ear length (66.6%), whereas, the heritability estimates were moderate for husked fresh ear yield (46.6%), dehusked fresh ear yield (54.7%), dehusked ear diameter (62.2%), cob diameter (46.4%), plant height (60.4%), ear height (55.8%), number of kernels per row (39.3%), total soluble solids (61.4%) and number of leaves per plant (45.3%). On the other hand, negative heritability estimates were found for husked ear diameter and number ears per hectare (Table 6).

**Correlations among traits measured on populations:** Husked fresh ear yield showed high ( $p \leq 0.01$ ) positive

correlations with dehusked fresh ear yield ( $r = 0.86$ ), husked ear length ( $r = 0.26$ ), dehusked ear length ( $r = 0.35$ ), husked ear diameter ( $r = 0.24$ ) and dehusked ear diameter. Dehusked fresh ear yield also showed strong ( $p \leq 0.01$ ) positive correlation with husked ear length ( $r = 0.31$ ), dehusked ear length ( $r = 0.41$ ), dehusked ear diameter ( $r = 0.36$ ) and ear height ( $r = 0.24$ ) (Table 7).

Husked ear length revealed high ( $p \leq 0.01$ ) positive correlations with dehusked ear length ( $r = 0.37$ ) and total soluble solids ( $r = 0.24$ ), whereas dehusked ear length was positively correlated with total soluble solids ( $r = 0.44$ ), however, this trait was negatively correlated with days to tasseling ( $r = -0.26$ ). On the other hand, husked ear diameter showed high ( $p \leq 0.01$ ) positive correlation with dehusked ear diameter ( $r = 0.37$ ), however, this trait was negatively correlated with ear height and number of kernels per row. Similarly, dehusked ear diameter showed positive correlation ( $r = 0.23$ ) with number of kernel rows per ear and negative correlation ( $r = -0.25$ ) with number of kernels per row (Table 7).

Plant height was highly ( $p \leq 0.01$ ) correlated with ear heat ( $r = 0.30$ ) days to tasseling ( $r = 0.35$ ) and days to silking ( $r = 0.37$ ). There was also significant and positive association between number of kernel rows per ear and total soluble solids ( $r = 0.28$ ). Total soluble solids revealed negative and significant correlation with days to tasseling ( $r = -0.31$ ) and days to silking ( $r = -0.32$ ) (Table 7). Days to tasseling also showed significant correlation with days to silking and similar positive correlation was also obtained between number of leaves and number of ears per hectare.

## DISCUSSION

The estimates of predicted and realized responses to selection varied between populations and selection methods. The predicted response to mass selection for ear length, in populations derived from the two base populations, was significantly higher than the realized. This could be attributed to the over estimation of predicted response to selection that resulted from the use of broad-sense heritability estimates, which was composed of additive and dominant variances in equal proportion<sup>[20]</sup>.

The predicted response to selfed progeny selection, on the other hand, was not significantly different from the realized ones for individual cycles (except in BC<sub>2</sub>-10 SPS C<sub>2</sub>, where the predicted was higher than the realized response). The genetic variance (used to compute broad-sense heritability estimates that were used in computing predicted response to selfed progeny selection) was composed of more of additive variance ( $1/4 \sigma^2_A$ ) than dominant variance ( $1/16 \sigma^2_D$ )<sup>[20]</sup>. The large

additive genetic variance relative to dominance variance may explain why selfed progeny method had comparable predicted and realized responses in both populations.

The two populations also showed average realized responses of varied magnitude, in response to the two methods of selection. In BC<sub>2</sub>-10 population, the realized response to selfed progeny selection was twice that of mass selection, whereas in BC<sub>1</sub>-10 x Syn-II population, comparable realized responses were obtained for the two methods of selection, indicating that BC<sub>2</sub>-10 populations had better response to MS than SPS, while BC<sub>1</sub>-10 x Syn-II populations showed similar response to the two selection methods.

Selection for ear length in this study indirectly improved fresh ear yields in both base populations by the two methods of selections. Salazar and Hallauer<sup>[10]</sup> in their study of divergent mass selection for ear length, reported that the merit of indirect selection for yield was 66%, while selecting for longer ears.

Results of broad-sense heritability ( $h^2_B$ ) estimated for various traits measured on populations developed from BC<sub>2</sub>-10 revealed that dehusked ear length, days to tasseling, total soluble solids and number of kernels per row were highly heritable, indicating that these traits were mainly influenced by genetic factors.

Other traits (husked fresh ear yield, husked ear diameter, plant height, days to silking, number of leaves and ear height) showed moderate broad-sense heritability, indicating that these traits were influenced by both genetic and environmental factors.

For populations derived from BC<sub>1</sub>-10 x Syn-II, broad-sense heritability estimates were high for days to tasseling, days to silking and dehusked ear length, showing that these three traits were influenced mainly by genetic factors, whereas all other traits (except husked ear diameter and number ears per hectare that had a negative estimate), showed moderate heritability estimates, implying that the variation for these traits were controlled both by genetic and environmental factors. These results agree with the study of Rafii *et al.*<sup>[12]</sup>.

Dehusked ear length, which was used as selection criterion in this study, showed high heritability estimates in both populations and was positively correlated with husked and dehusked fresh ear yields, implying that it was the appropriate trait for indirect selection (for husked and dehusked fresh ear yields, husked ear length, total soluble solids and earliness). Other researchers<sup>[12,22,23]</sup> also reported moderate to high heritability estimates for ear length using variance components method.

Based on data from across locations, husked and dehusked fresh ear yields were highly correlated with husked ear length, dehusked ear length, husked ear

diameter and dehusked ear diameter, indicating that plants with long ears and large ear diameters had high yield. Heritability estimate was high for ear length, while heritability estimate was negative for ear diameter, indicating that ear length can be used as a selection criterion for indirect selection to improve yield, whereas ear diameter cannot be used as it had low heritability estimate. The theory of correlated response suggests that the correlation between the primary trait and secondary trait must be high and the heritability of the trait under selection must be larger than that of primary trait for indirect selection to be preferred to direct<sup>[19]</sup>. In the present study, estimates of heritability for dehusked ear length ( $h^2_B = 75$  and 67% for BC<sub>2</sub>-10 and BC<sub>1</sub>-10 x Syn-II populations, respectively) were larger than that of dehusked fresh ear yield ( $h^2_B = 27.3$  and 54.7% for BC<sub>2</sub>-10 and BC<sub>1</sub>-10 x Syn-II populations, respectively). Besides, there was a strong correlation between ear length and dehusked fresh ear yield ( $r = 0.41$ ), indicating that indirect selection via ear length would be more effective than direct selection to improve fresh ear yield in these populations.

Dehusked ear length was also positively correlated with total soluble solids, while it was negatively correlated with days to tasseling, showing that plants with long ears also had high values of total soluble solids and low number of days to tasseling and silking. Therefore, selection for plants with longer ears could result in further improvement of sweetness of kernels and earliness in days to tasseling and silking in the succeeding generations.

Total soluble solids revealed negative and significant correlation with days to tasseling and days to silking, implying that early flowering plants would produce more total soluble solids than late flowering plants.

In conclusion, the two selection methods were effective in improving ear length and some correlated traits of the both base populations. The two selection methods showed significant progress from selection for ear length, husked fresh ear yield, dehusked fresh ear yield and number of kernels per row. Hence, continuing selection for ear length in these two populations using MS and SPS could offer further improvement. Selfed progeny selection significantly increased total soluble solids, while mass selection significantly increased earliness in BC<sub>2</sub>-10 population. In BC<sub>1</sub>-10 x Syn-II, selfed progeny selection increased husked ear diameter, lateness and reduced total soluble solids, whereas mass selection had no effect on days to tasseling, indicating that direction of response to correlated traits depended on selection methods used, populations

under selection and correlation between directly and indirectly selected traits.

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