



Asian Journal of Plant Sciences

ISSN 1682-3974

science
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Genetic Variability and Responses to Two Methods of Recurrent Selection in Two Sweet Corn (*Zea mays* L. *Saccharata*) Populations

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Abstract: The objectives of this study were to determine the genetic variability (σ^2_g) and thereby estimate the genetic gain after two cycles of selection within two sweet corn source populations, BC1-10×Syn-II and BC2-10. Selfed progenies from each of the two source populations were evaluated following the recommended cultural practices. As the progenies derived from the two source populations had sufficient genetic variability for most traits, two cycles of mass selection (MS) and selfed progeny selection (SPS) were conducted on the two sweet corn populations (BC2-10 and BC1-10×Syn-II). The two base populations showed varied average realized responses to MS and SPS. In BC2-10 derived populations, the realized responses to MS were 5.1% in cycle 1 (C1) and 4.8% in Cycle 2 (C2), whereas the realized responses to SPS were 9.1% in C1 and 1.2% in C2. In BC1-10×Syn-II derived populations, the realized responses to MS were 5.5% in C1 and 2.9% in C2, while the realized responses to SPS were 5.6% in C1 and 2.9% in C2. The two selection methods were equally effective in improving the populations for ear length, except in C1 of BC2-10, 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 and further selection in these populations could offer better responses.

Key words: Genetic variability, response to selection, sweet corn

INTRODUCTION

The sweet corn (*Zea mays* L. *saccharata*) germplasm in Malaysia contains many advanced populations with interesting adaptation traits. However, these advanced populations show limitations such as lateness, excessive plant and ear heights and low total soluble solids (Saleh *et al.*, 2003). Introgression of exotic germplasm to these locally advanced populations could result in populations with broad genetic variation that are useful to initiate selection to improve the performance of the local populations.

In plant breeding programs, success of selection for genetic improvement is partly determined by proper choice of source populations. The source populations used by breeders for genetic improvement include local or exotic germplasm so that the source populations possess the most desirable alleles at as many loci as possible to undertake selection (Sprague and Eberhart, 1977). Such desirable alleles can be intensified in the target source populations through introgression of exotic germplasm into locally adapted ones (Russell, 1991).

In this study, two local and two exotic sweet corn populations were crossed and the resulting crosses were evaluated. From the evaluation experiment two promising populations were selected and under went two cycles of mass and selfed progeny selection for 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 with the objectives of estimating the genetic variability, heritability and compare predicted and realized responses.

MATERIALS AND METHODS

Two local (BC1-10, BC1-9) and two introduced (Syn-I and Syn-II) sweet corn populations were selected as parents in making crosses. The locally advanced materials had low total soluble solids, tall plants and late in maturity, but with good yield and are well adapted to the local conditions. On the other hand, the two introduced populations had high total soluble solids in kernel, low ear placement and were earlier maturing than

the local populations (Saleh *et al.*, 2001). Crosses were made among the four source populations at Institute of Bioscience (IBS) Farm, University Putra Malaysia (UPM) in 2002. The populations were crossed in the North Carolina Design-II (Factorial) Mating System (Hallauer and Miranda, 1988).

The resulting four crosses, their parents and two checks were evaluated at Share Farm, UPM, following the recommended cultural practices. BC1-10×Syn-II, which was a product of the cross between the local and exotic germplasm, had superior overall performance for most traits. BC2-10 also had comparable fresh ear yield with BC1-10×Syn-II. Hence, these two populations were selected as source materials to undertake selection. Within each of the two source populations, 300 to 500 plants were self-pollinated of which 100 progenies were evaluated at IBS Farm, UPM using a 10×10 simple lattice design following recommended cultural practices to determine genetic variability and heritability of the breeding population. Finally, Mass selfed progeny selections were conducted on the two base populations for two consecutive cycles at the IBS Farm, UPM following the procedures suggested by Gardner (1961) and later on modified by Singh (1987).

The populations generated from two cycles of mass selection, selfed progeny selection and the base populations were evaluated, at Share and IBS Farms, UPM. A randomized complete block design with four replications was used. Each plot consisted of five rows of 5 m long, with spacings of 0.75×0.25 m between and within rows, respectively. Recommended cultural practices were followed at each location.

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 (SAS Institute, 2001). The analyses of variance were conducted first for individual location and the combined ANOVA was then conducted for traits that showed homogeneous error variances.

The predicted response to selection was estimated using the formula suggested by Falconer and Mackay (1996), as follows: $R = ih^2\sigma$, where: R = predicted response to selection, I = the intensity of selection, h^2 = heritability of a trait and σ = phenotypic standard deviation of the parental population. The realized response to selection was estimated using the formula suggested by Simmonds (1979), as follows:

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

where C_n and C_{n-1} are mean values for improved and preceding populations, respectively. Results of predicted and realized response to selections were compared using χ^2 test as suggested by Townend (2002).

RESULTS AND DISCUSSION

The overall mean values and ranges for selfed progenies developed from BC1-10×Syn-II and BC2-10 populations are shown in Table 1. Significant differences among selfed progenies of BC1-10×Syn-II were noted for all the traits measured, whereas significant differences among selfed progenies of BC2-10 were observed for fresh ear yield, ear length, ear diameter, number of kernels per row, ear height, days to tasseling and days to silking.

Selfed progenies developed from BC2-10 had wider ranges for fresh ear yield, ear diameter, days to tasseling and days to silking than progenies developed from BC1-10×Syn-II. On the other hand, selfed progenies developed from BC1-10×Syn-II had wider ranges for number of rows per ear, total soluble solids and plant height than progenies developed from BC2-10, suggesting that greater variability exists in BC1-10×Syn-II population for these traits. Such genetic variability in BC1-10×Syn-II population could be exploited through selection.

Estimates of phenotypic variance (σ_p^2), genotypic variance (σ_g^2), heritability (h^2) and predicted response to selection in selfed progenies within each of the two populations are shown in Table 2. Estimates of genetic components of variance (σ_g^2) were positive ($\sigma_g^2 > 0$) for all traits measured in selfed progenies of BC1-10×Syn-II, while BC2-10 progenies had positive estimates for fresh ear yield, ear length, ear diameter, number of kernels per row, ear height, days to tasseling and days to silking.

When selfed progenies developed from the two source populations were compared, higher estimates of components of genetic variance (σ_g^2) for ear length, ear diameter, ear height, days to tasseling and days to silking were obtained from BC2-10 progenies than those from BC1-10×Syn-II, while BC1-10×Syn-II progenies had higher estimates for number of rows per ear, total soluble solids and plant height than did BC2-10 progenies. Falconer and Mackay (1996) suggested that such genetic variances are dependent on the allelic frequencies within the populations and genetic variances of this sort could provide the opportunity to increase the allelic frequency towards the desirable direction.

The higher estimates of σ_g^2 for ear length, ear diameter and ear height in progenies of BC2-10 population suggest that progenies developed from this population

Table 1: Mean values and ranges of 10 traits measured on selfed progenies developed from two sweet corn populations

Traits	Population			
	BC2-10		BC1-10×Syn-II	
	Mean	Range	Mean	Range
Fresh ear yield (kg plot ⁻¹)	1.0	0.4-2.20	1.4	0.95-2.1
Ear length (cm)	10.0	7.6-15.2	11.8	8.4-15.9
Ear diameter (mm)	36.6	30.0-46.6	41.7	35.8-47.8
Number of rows per ear	11.9	10.0-13.6	12.9	9.4-15.2
Number of kernels per row	21.0	13.2-32.9	25.4	16.5-34.7
Total soluble solids (%)	14.0	10.9-17.3	14.9	11.1-18.1
Plant height (cm)	130.9	98.7-167.4	158.5	119.3-194.4
Ear height (cm)	55.8	30.6-82.4	76.5	48.5-96.2
Days to tasseling	54.4	48.0-60.5	50.4	47.0-54.5
Days to silking	58.8	50.5-64.5	54.3	50.0-60.5

Table 2: Estimates of phenotypic variance (σ^2_p), genotypic variance (σ^2_g) and heritability (h^2) for 100 selfed progenies of two sweet corn populations

Traits	Population					
	BC2-10			BC1-10×Syn-II		
	σ^2_p	σ^2_g	h^2	σ^2_p	σ^2_g	h^2
Fresh ear yield (kg ha ⁻¹)	0.08	0.04	54.7	0.07	0.03	43.0
Ear length (cm)	1.82	1.18	65.0	2.39	0.90	37.1
Ear diameter (mm)	11.37	4.25	37.0	7.10	3.58	50.5
Number of rows per ear	0.50	-0.03	na	0.85	0.48	56.5
Number of kernels per row	16.20	5.83	36.0	15.99	5.51	34.4
Total soluble solids (%)	1.50	0.11	10.0	1.55	0.57	36.8
Plant height (cm)	198.67	-22.47	na	198.47	101.45	51.1
Ear height (cm)	111.31	66.89	60.1	95.63	50.76	53.1
Days to tasseling	3.29	1.44	43.8	6.51	3.59	55.2
Days to silking	5.47	1.86	33.9	8.40	4.23	50.3

na = Estimate not available because of negative variance estimate

could have better genetic gains for these traits than progenies from BC1-10×Syn-II. On the other hand, BC1-10 ×Syn-II population had higher σ^2_g estimates for number of kernel rows per ear, total soluble solids plant height, days to tasseling and days to silking, showing that there is a greater potential to improve these traits in selfed progenies of BC1-10×Syn-II than selfed progenies of BC2-10. Similar genetic variance for eating quality was reported by Azanza *et al.* (1996), upon studying variation in sweet corn kernel characteristics after introgression of exotic germplasm to local population.

Progenies from both source populations revealed comparable estimates of components of genetic variance for fresh ear yield and number of kernels per row. Higher estimates of components of genetic variance were expected in BC1-10×Syn-II (a cross between local and exotic) progenies, as it was a cross between parents of divergent growth habits. The low genetic variance for ear length, ear diameter, ear height, days to tasseling and days to silking in BC1-10×Syn-II progenies could be due to linkage disequilibrium present in the BC1-10×Syn-II populations which could have hindered the release of some genetic variation. The other reason for higher genetic variance in BC2-10 populations for these traits than that in BC1-10×Syn-II could be that, BC2-10 had

undergone two cycles of mass selection and hence, the frequency of favorable alleles would be expected to be higher for those traits.

The higher estimates of σ^2_g for ear length, ear diameter and ear height in BC2-10 populations, indicate that progenies developed from this population could have better genetic gains for these traits than progenies from BC1-10×Syn-II. On the other hand, the higher estimates σ^2_g for number of kernel rows per ear, total soluble solids plant height, days to tasseling and days to silking in BC1-10×Syn-II population, showed that there could be higher genetic gains for these traits in selfed progenies of BC1-10×Syn-II than those of BC2-10. Comparable estimates of genetic variance were found for fresh ear yield and number of kernels per row, indicating that genetic improvement of the two source populations could lead to similar genetic gains for fresh ear yield and number of kernels per row.

Comparison of predicted and realized responses and selection methods: Results of comparison between the predicted and realized responses to mass and selfed progeny selections for ear length conducted on the two sweet corn base populations are presented in Table 3. Based on the results of χ^2 test, there was a significant

Table 3: Comparison between selection methods for predicted and realized responses to selection for dehusked ear length performed for two cycles on BC2-10 and BC1-10×Syn-II sweet corn populations, University Putra, 2003

Populations	Predicted response (%)			Realized response (%)		
	MS	SPS	χ^2	MS	SPS	χ^2
BC2-10						
C1	24.7	13.2	5.35*	5.1	10.1	4.90**
C2	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
BC1-10×Syn-II						
C1	22.3	9.9	6.90**	5.5	5.6	0.01
C2	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 $p \leq 0.01$ and 0.05 , respectively; MS = Mass selection; SPS = Selfed progeny selection; χ^2 = Calculated chi-square; C1, C2 = Cycle 1 and Cycle 2, respectively

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 C2 of BC2-10 population that showed significant difference between predicted and realized responses.

Results of the comparison between MS and SPS performed for the two cycles and the cumulative showed that here was a significant difference between MS and SPS for predicted response to selection (except in C2 of BC1-10×Syn-II that revealed no significant difference between predicted response to MS and SPS). 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 C1 of BC2-10, that showed significant difference between MS and SPS, where SPS was more effective than MS).

CONCLUSION

The improved populations derived from selection showed average realized responses of varied magnitude, in response to the two methods of selection. In BC2-10 population, the realized response to selfed progeny selection was twice that of mass selection, whereas in BC1-10×Syn-II population, comparable realized responses were obtained for the two methods of selection, indicating that BC2-10 populations had better response to MS than SPS, while BC1-10×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 (1986), 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.

For selection to improve ear length, ear diameter and ear height, BC2-10 seems to be the appropriate source population, whereas in selection to improve number of kernel rows per ear, total soluble solids, plant height, days to tasseling and days to silking, BC1-10×Syn-II seems to be the appropriate one. There was no clear distinction between the effectiveness of the use of progenies of BC2-10 or BC1-10×Syn-II to select for ear diameter and number of kernels per row, as progenies from both populations had comparable genetic variances. Therefore, selfed progenies developed from both source populations with elite progenies could be used to improve quantitative (like earliness and shortness) as well as qualitative traits (like high eating quality) and thereby develop superior genotypes with desirable traits.

Results of present study indicated the success of two selection methods in improving ear length and some correlated traits of the base populations. The two selection methods showed significant progress from selection for ear length. Hence, continuing selection for ear length in these two populations using MS and SPS could offer further improvement.

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