

Genetic Improvement for Yield and Yield Related Traits by Introgressive Hybridization in Sweet Corn

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ABSTRACT : Proper choice of source populations contributes to the ultimate success of selection for genetic improvement. The source population should possess the most desirable alleles at as many loci as possible for intrapopulation improvement. Such desirable alleles can be intensified by introgression of exotic germplasm into locally adapted ones through hybridization followed by selection. The objectives of this study were to determine the mean performance, genetic variability (σ^2_G) and heritability of fresh ear yield and other important traits within two sweet corn source populations, BC1-10 \times Syn-II and BC2-10. One hundred selfed progenies from each of the two source populations were evaluated in a 10 \times 10 lattice design, at the Institute of Bioscience (IBS) Farm, University of Putra Malaysia (UPM) following the recommended cultural practices. Significant differences among selfed progenies within BC1-10 \times Syn-II were observed for all traits, while differences among selfed progenies within BC2-10 were noted for fresh ear yield, ear length, ear diameter, number of kernels per row, ear height, days to tasseling and days to silking. Progenies developed from BC1-10 \times Syn-II population had higher estimates of σ^2_G than did progenies from BC2-10 population for number of kernel rows per ear, total soluble solids, plant height, days to tasseling and days to silking, showing that selection to improve these traits would be more effective in selfed progenies of BC1-10 \times Syn-II than that in BC2-10. On the other hand, progenies developed from BC2-10 population had higher estimates of σ^2_G for ear length, ear diameter and ear height, indicating that progenies from this population would have better genetic gain than BC1-10 \times Syn-II. 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 is expected to produce similar genetic gains for these two traits. Therefore, selfed progenies developed from both source populations could be used to improve the two populations for various traits and thereby develop superior genotypes for immediate use in the production system.

Keywords: Genetic, variability, response to selection, sweet corn

In plant breeding programmes, 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 & Eberhart, 1977). Such desirable alleles can be intensified in the target source populations through introgression of exotic germplasm into locally adapted ones (Russell, 1991). Exotic germplasm from similar environmental conditions would be most useful, provided that they possess favorable alleles that could complement those possessed by the adapted materials. The source populations developed this way can be improved through recurrent selection.

Recurrent selection (RS) is a process of cyclical selection in a breeding population to increase the frequency of favorable alleles, and thus improve mean performance. Selfed progeny selection is considered to be superior to other methods of RS for improvement of population *per se* (Lamkey, 1992). In this selection scheme, alleles are fixed rapidly, where deleterious homozygous alleles are exposed and eliminated early in selection (Weyhrich *et al.*, 1998).

The sweet corn 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.

The objectives of this study were to compare selfed progenies by estimating the genetic variability within two sweet corn populations, to estimate heritability of the traits and to predict gains from selection in each population.

MATERIALS AND METHODS

Parental populations

Four (two local and two introduced) sweet corn (*Zea mays*

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

Formation of base populations

Crosses were made among the four source populations at IBS Farm, UPM in the months of March to May, 2002. The populations were crossed in the North Carolina Design-II (Factorial) Mating System (Hallauer & Miranda, 1988). As a result, four sets of crosses were obtained and the seeds of each set of crosses were harvested from the female parents and then bulked within each cross separately.

The 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 (Saleh *et al.*, 2003). BC2-10 also had comparable fresh ear yield with BC1-10 × Syn-II. As a result of this, these two populations were selected as source populations to undertake selection. The F₁ seeds of the selected population cross, BC1-10 × Syn-II, were planted in isolation for intermating. The intermated population was used as a base population (C0) to generate selfed progenies.

Population BC2-10 (BC1-10 × Manis Madu) was obtained from previous breeding effort in the UPM Maize Programme. This second base population was also selected as a parent based on performance *per se* and its adaptation to the local environmental conditions.

Formation of selfed progenies

The two base populations were planted on an area of 400 m² each, following the recommended cultural practices. Within each of the two populations, 200 to 300 plants were self-pollinated at IBS Farm, UPM, following the procedures described by Singh (1987). Self pollinated ears were individually harvested and dried in the grain drier. Each ear was then shelled an ear to a bag, and seeds were put in cold storage until planting.

Evaluation of selfed progenies

Of the selfed progenies developed from each base popula-

tion, 100 progenies were taken for evaluation at IBS Farm, UPM using a 10 × 10 simple lattice design. Each progeny was planted in a 5-m long row using 0.75 m × 0.25 m between and within row spacings in 2002. Recommended rates of fertilizer and other cultural practices were followed.

Data collection

Data were collected for husked fresh ear yield, ear length, ear diameter, plant height, ear height, number of kernel rows per ear, number of kernels per row, total soluble solids, days to tasseling and days to silking.

Data Analysis

Analysis of variance (ANOVA) was employed, and mean comparisons were made using the Statistical Analysis System (SAS) Software Version 8.2, developed by SAS Institute Inc, (2001). ANOVA was used to detect the effects of progenies, blocks and replications. Phenotypic, genotypic and environmental components of variance were estimated using the observed mean squares, based on the expected mean squares for each population from the ANOVA table, as suggested by Kang (1995). Variation among selfed progenies (σ^2_G) has the expected additive genetic variance of $1/4\sigma^2_A$ and dominance genetic variance of $1/16\sigma^2_D$, assuming no epistasis and allelic frequencies of one-half ($p = q = 0.5$) for segregating alleles.

Broad-sense heritability (h^2_B) was calculated using the variance components method, as suggested by Becker (1984), as follows:

$$h^2_B = \frac{\sigma^2_G}{\sigma^2_P}$$

$$\text{where: } \sigma^2_G = \frac{(\sigma^2_e + \sigma^2_G) - \sigma^2_e}{r}$$

$$= \frac{(MS_G - MS_e)}{r},$$

$$\text{where: } \sigma^2_P = \sigma^2_G + \sigma^2_e$$

$$= \frac{(MS_G)}{r},$$

h^2_B = broad-sense heritability,
 σ^2_G = genotypic variance,
 σ^2_P = phenotypic variance,
 σ^2_e = environmental variance,
 MS_G = mean squares due to genotype,
 MS_e = error mean squares, and
 r = number of replications.

Predicted responses to selection (R) were computed using

the formula suggested by Falconer & Mackay (1996) as follows:

$$R = i\sigma_p h^2$$

where, i is the standardized selection differential, σ_p is phenotypic standard deviation and h^2 is the estimates of heritability on a selfed progeny mean basis.

RESULTS AND DISCUSSION

The overall mean values and ranges for selfed progenies developed from BC1-10 \times Syn-II and BC2-10 populations are shown in Table 1. Significant differences among selfed progenies of BC1-10 \times 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 \times Syn-II. On the other hand, selfed progenies developed from BC1-10 \times 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 \times Syn-II population for these traits. Such genetic variability in BC1-10 \times Syn-II population could be exploited through selection.

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

Trait	Population			
	BC2-10		BC1-10 \times Syn-II	
	Mean	Range	Mean	Range
Fresh ear yield (kg/plot)	1.0	0.4 to 2.2	1.4	0.95 to 2.1
Ear length (cm)	10.0	7.6 to 15.2	11.8	8.4 to 15.9
Ear diameter (mm)	36.6	30.0 to 46.6	41.7	35.8 to 47.8
Number of rows per ear	11.9	10.0 to 13.6	12.9	9.4 to 15.2
Number of kernels per row	21.0	13.2 to 32.9	25.4	16.5 to 34.7
Total soluble solids (%)	14.0	10.9 to 17.3	14.9	11.1 to 18.1
Plant height (cm)	130.9	98.7 to 167.4	158.5	119.3 to 194.4
Ear height (cm)	55.8	30.6 to 82.4	76.5	48.5 to 96.2
Days to tasseling	54.4	48.0 to 60.5	50.4	47.0 to 54.5
Days to silking	58.8	50.5 to 64.5	54.3	50.0 to 60.5

*n = 200 for all traits

Table 2. Estimates of phenotypic variance (σ_p^2), genotypic variance (σ_G^2) and heritability (h^2) for 100 selfed progenies of two sweet corn populations.

Trait	Population					
	BC2-10			BC1-10 \times Syn-II		
	σ_p^2	σ_G^2	h^2	σ_p^2	σ_G^2	h^2
Fresh ear yield (kg/ha)	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	16.2	5.83	36.0	15.99	5.51	34.4
Total soluble solids (%)	1.5	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

Estimates of phenotypic variance (σ^2_P), genotypic variance (σ^2_G), 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^2_G) were positive ($\sigma^2_G > 0$) for all traits measured in selfed progenies of BC1-10 \times 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^2_G) 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 \times Syn-II, while BC1-10 \times Syn-II progenies had higher estimates for number of rows per ear, total soluble solids and plant height than did BC2-10 progenies. Falconer & 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^2_G for ear length, ear diameter and ear height in progenies of BC2-10 population suggest that progenies developed from this population could have better genetic gains for these traits than progenies from BC1-10 \times Syn-II. On the other hand, BC1-10 \times 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 \times 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 compa-

Table 3. Estimates of predicted response to selection for traits measured in selfed progenies of two sweet corn populations.

Trait	Mean	Standard deviation	Heritability (%)	Predicted response* (%)	
				A	B
<i>BC2-10</i>					
Fresh ear yield (kg/ha)	1.0	0.28	54.7	26.4	21.0
Ear length (cm)	10.0	1.35	65.0	15.5	13.2
Ear diameter (mm)	36.6	3.37	37.0	6.0	3.7
Number of rows per ear	11.9	0.71	na	nh nh	
Number of kernels per row	29.7	4.02	36.0	8.6	6.9
Total soluble solids (%)	14.0	1.22	10.0	1.5	1.2
Plant height (cm)	158.5	14.09	na	nh	nh
Ear height (cm)	76.5	10.55	60.1	14.6	11.6
Days to tasseling	54.4	2.55	55.2	2.8	2.2
Days to silking	58.8	2.90	50.3	2.6	2.0
<i>BC1-10 \times Syn-II</i>					
Fresh ear yield (kg/ha)	1.4	0.26	43.0	14.4	11.4
Ear length (cm)	11.8	1.55	37.1	11.2	9.9
Ear diameter (mm)	41.7	2.66	50.5	5.7	4.5
Number of rows per ear	12.9	0.92	56.5	7.1	5.6
Number of kernels per row	25.4	4.00	34.4	9.6	7.6
Total soluble solids (%)	15.9	1.25	36.8	5.1	4.0
Plant height (cm)	130.9	14.08	51.1	9.6	7.7
Ear height (cm)	55.9	9.78	53.1	16.3	13.0
Days to tasseling	50.4	1.81	43.8	4.6	3.6
Days to silking	54.3	2.34	33.9	4.4	3.5

*A. at 10% selection intensity; B. at 20% selection intensity

na = estimate not available because of negative variance

nh = estimate not available because heritability estimate was not available

able 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.

Estimates of heritability for traits measured on the progenies generated from the two source populations are presented in Table 2. Heritability estimates for traits measured on the progenies generated from BC2-10 were found to be moderate for ear length (65.0%), ear height (60.1%), days to tasseling (55.2%), fresh ear yield (54.7), days to silking (50.3%), ear diameter (37.0%) and number of kernels per row (36.0%). Progenies generated from BC1-10 × Syn-II had moderate heritability estimates for all traits measured, indicating that these traits were moderately influenced by the environment.

When heritability estimates of the two source populations are compared, estimates were higher for fresh ear yield, ear length, ear height, days to tasseling and days to silking in BC2-10 than BC1-10 × Syn-II. On the other hand, higher estimates of heritability for ear diameter, number of kernel rows per ear, total soluble solids and plant height were obtained in progenies generated from BC1-10 × Syn-II than those from BC2-10.

Predicted response to selection at 10 and 20% selection intensities are presented in Table 3. For progenies developed from BC2-10 population, predicted response to selection exceeding 5% was obtained for fresh ear yield, ear length, ear diameter, number of kernels per row and ear height. Progenies generated from BC1-10 × Syn-II population, had predicted response to selection higher than 5% for fresh ear yield, ear length, ear diameter, number of kernel rows per ear, number of kernels per row, plant height and ear height.

Progenies generated from BC2-10 had higher predicted response to selection (at both 10 and 20% selection intensity) than those from BC1-10 × Syn-II for fresh ear yield and ear length, while progenies of BC1-10 × Syn-II had better predicted response to selection than those of BC2-10 for number of kernel rows per ear, total soluble solids, plant height, days to tasseling and days to silking. Progenies generated from both populations had comparable response to selection for

ear diameter, number of kernels per row and ear height.

Therefore, BC2-10 appeared to have greater potential for improvement of fresh ear yield and ear length than BC1-10 × Syn-II, whereas BC1-10 × Syn-II would be expected to have higher potential for improvement of number of kernel rows per ear, total soluble solids, plant height, ear height, days to tasseling and days to silking than BC2-10. Comparable response to selection between the two source populations could be expected for further improvements of ear diameter, number of kernels per row and ear height.

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.

Moderate estimates of heritability for fresh ear yield, ear length, ear diameter, number of kernels per row and ear height were obtained from progenies of BC2-10 and BC1-10 × Syn-II, indicating that selection for improvement of these traits would be effective in selfed progenies of the two source populations. Moreover, progenies of BC1-10 × Syn-II had moderate as well as higher estimates of heritability for number of kernel rows per ear, total soluble solids, plant height, days to tasseling and days to silking than those of BC2-10, indicating that selection for improvement of these traits would be more effective in selfed progenies of BC1-10 × Syn-II than those of BC2-10.

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.

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