

Heritability and Response to Recurrent Selection in Two Sweet Corn Varieties

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ABSTRAK

Kajian pemilihan berulang mudah dan pemilihan berulang salingan penuh-sib di dalam pusingan pertama telah dijalankan ke atas dua varieti jagung manis, Manis Madu dan Bakti-1, di Universiti Pertanian Malaysia. Objektif kajian ini ialah untuk membandingkan kesan kedua-dua prosedur pemilihan tersebut, dan menganggarkan kebolewarisan untuk ciri-ciri penting dalam kedua-dua populasi. Kewujudan varian genetik yang lebih tinggi di dalam populasi Bakti-1 S_1 (BIS_1) berbanding dengan populasi Manis Madu S_1 (MMS_1) menunjukkan bahawa BIS_1 mengandungi variabiliti genetik yang lebih tinggi dari MMS_1 . Anggaran kebolewarisan-luas untuk ciri-ciri yang dikaji adalah sederhana hingga tinggi (42.6% hingga 65.7%) dalam populasi progeni penyendirian, tetapi rendah hingga sederhana (20.0% hingga 49.2%) dalam populasi progeni kacukan. Selepas satu pusingan pemilihan, pemilihan berulang mudah didapati lebih berkesan di dalam meningkatkan hasil dalam kedua-dua populasi. Pemilihan berulang mudah telah meningkatkan hasil tongkol segar dalam Bakti-1 dan Manis Madu, masing-masing sebanyak 16.7% dan 10.2%, manakala pemilihan berulang salingan penuh-sib telah meningkatkannya dalam Bakti-1 sebanyak 5.9%, tetapi mengurangkannya dalam Manis Madu sebanyak 6.4%.

ABSTRACT

One cycle of simple and full-sib reciprocal recurrent selection programme was conducted on two sweet corn varieties, Manis Madu and Bakti-1, at Universiti Pertanian Malaysia. The objectives of the study were to compare the response to the two selection procedures, and to estimate heritability of some important characters in the two populations. The presence of higher genetic variance in Bakti-1 S_1 population (BIS_1) compared to that of Manis Madu (MMS_1) showed that BIS_1 possessed higher genetic variability than MMS_1 . Broad-sense heritability estimates for the characters studied were moderate to high (42.6% to 65.7%) in the selfed progeny populations, but were low to moderate (20.0% to 49.2%) in the crossed progeny populations. After one cycle of selection, simple recurrent selection was found to be more effective in increasing yield in both populations. Simple recurrent selection increased fresh ear yield in Bakti-1 and Manis Madu by 16.7% and 10.2% respectively, while full-sib reciprocal recurrent selection increased it in Bakti-1 by 5.9%, but decreased it in Manis Madu by 6.4%.

INTRODUCTION

In Malaysia, growing of corn (*Zea mays* (L.)) for human consumption of the fresh ears started with the use of field corn varieties, Local Flint and Metro. The beginning of the utilization of sweet corn varieties in the country was marked by the

introduction of the variety Chinta in the sixties. Subsequently, many varieties were introduced, developed and selected for local utilization, among which were Bakti-1, Manis Madu and Mas Madu. The country's average yield production, however, has been low i.e. less than 5 metric tons of fresh

ears per ha. (Abdul Rahman *et al.* 1987). Research efforts are continuously carried out to develop high yielding varieties, with acceptable eating quality and suitable to the local conditions.

Selection based on S_1 progeny performance in simple recurrent selection was found effective in increasing the frequency of favourable genes in corn populations by Comstock (1964) and Wright (1980). The full-sib reciprocal recurrent selection was found effective in population improvement involving crosses between two diverse populations (Hallauer 1967). West *et al.* (1980) found that after two cycles, selection based on S_1 progeny performance was more effective than that based on full-sib progeny performance in increasing yield of selfed populations; but both methods gave the same effects in populations developed from crosses between the improved populations. In another study, after five cycles, selection based on the S_1 progeny performance was found to be more effective in increasing yield in crossed populations between the improved populations (Odhiambo and Compton 1989).

This study was conducted to compare the response to one cycle of simple recurrent selection (S_1 progeny) and full-sib reciprocal recurrent selection in improving the base population of each of the two sweet corn varieties, Manis Madu and Bakti-1, and to determine the genetic variation and heritability of some important traits in the populations.

MATERIALS AND METHODS

The study was conducted at the Faculty of Agriculture Research Farm, Universiti Pertanian Malaysia, Serdang, Selangor. The source populations were two open-pollinated local sweet corn varieties, Bakti-1 and Manis Madu.

One cycle of simple recurrent selection based on the S_1 progeny performance and reciprocal recurrent selection based on the full-sib progenies was performed on the two source populations, involving four phases of planting: selfing and full-sib crossing in the first phase; evaluation of S_1 and full-sib progenies in the second; intermating among the selected S_1 families based on the S_1 or full-sib progeny performance in the third; and evaluation of the improved populations in the fourth phase. In the first phase about 200 selfed and 200 full-sib families were formed from each population. After the second phase, 20% of the

S_1 families in each evaluation (the male S_1 families in case of full-sib evaluation) were selected based on their superiority in fresh largest ear weight per plant, for intermating in the third phase. At the end of the first cycle, four improved populations were formed, i.e. two from simple recurrent selection: B1SC₁ from Bakti-1 and MMSC₁ from Manis Madu, and two from the full-sib reciprocal recurrent selection: B1RFSC₁ from Bakti-1 and MMRFSC₁ from Manis Madu. Evaluations of the improved populations were conducted in comparison with the respective source populations Bakti-1 (B1C₀) and Manis Madu (MMC₀) to determine the improvement in performance of each population *per se*. The randomised complete block design was used in all evaluations. The S_1 and the full-sib progeny evaluations in the second phase were conducted separately, each in two replications at one environment, Field 2. Each progeny family was planted in three-metre-long, one-row plots, with a planting density of 0.75 m x 0.25 m. Six plants were sampled randomly from each plot for the measurements. The improved population evaluations in the fourth phase were conducted in four replications each at two environments, Field 2 and Field 10B. Each plot comprised eight four-meter-long rows of plants, with the same planting density as in the progeny evaluations. Plants in the middle portion of the inner six rows in each plot were used for data collection.

Broad-sense heritability was estimated using the variance components in the analysis of variance table in the selfed and full-sib progeny evaluations following the equation:

$$h_B^2(\%) = \frac{\hat{\sigma}_F^2}{(\hat{\sigma}_e^2 + r\hat{\sigma}_F^2)/r} \times 100;$$

where h_B^2 , $\hat{\sigma}_F^2$, $\hat{\sigma}_e^2$ and r are broad-sense heritability, variance among families, error variance and number of replications, respectively.

Response to selection was calculated using the following equation:

$$\text{Selection response (\%)} = \frac{C_1 - C_0}{C_0} \times 100;$$

where C_1 and C_0 are means for the respective improved and source populations, respectively.

TABLE 1
Genotypic and phenotypic variances, and heritability (h_B^2) for characters measured in BIS₁ and MMS₁ populations

Character	Population	Mean squares		Variance		h_B^2 (%)
		Family	Error	$\hat{\sigma}_g^2$	$\hat{\sigma}_p^2$	
Fresh largest-ear weight per plant (g)	BIS ₁	2641.2**	1376.7	632.3	1320.6	47.9
	MMS ₁	na	na	na	na	na
Fresh dehusked largest-ear weight per plant (g)	BIS ₁	na	na	na	na	na
	MMS ₁	1244.8**	553.9	345.4	622.4	55.5
Days to tasselling (days)	BIS ₁	6.1**	2.2	1.9	3.1	63.3
	MMS ₁	6.1**	2.7	1.7	3.0	55.3
Ear diameter (mm)	BIS ₁	14.0**	5.6	4.2	7.0	60.1
	MMS ₁	15.5**	6.4	4.6	7.7	58.9
Ear length (cm)	BIS ₁	4.2**	2.2	1.1	2.1	48.3
	MMS ₁	7.3**	2.8	2.2	3.6	61.6
Plant height (cm)	BIS ₁	468.1**	268.6	99.8	226.0	65.7
	MMS ₁	na	na	na	na	na
Ear height (cm)	BIS ₁	240.6**	122.1	59.3	120.3	49.3
	MMS ₁	261.5**	100.3	80.6	130.8	61.7

$\hat{\sigma}_g^2$, $\hat{\sigma}_p^2$, h_B^2 = genotypic variance, phenotypic variance, and broad-sense heritability, respectively.

** Significant at $p < 0.01$.

na =Data not available.

TABLE 2
Genotypic and phenotypic variances, and heritability (h_B^2) for characters measured in MMB1 and B1MM populations

Character	Population	Mean squares		Variance		h_B^2 (%)
		Family	Error	$\hat{\sigma}_g^2$	$\hat{\sigma}_p^2$	
Fresh largest-ear weight per plant (g)	MMB1	2379.2*	1654.3	362.4	1189.6	30.5
	B1MM	4281.2**	2567.8	856.7	2140.6	40.0
Fresh dehusked largest-ear weight per plant (g)	MMB1	1214.6*	866.8	173.9	607.3	28.6
	B1MM	1953.2*	1413.0	270.1	976.6	27.7
Days to tasselling (days)	MMB1	4.7**	2.4	1.2	2.4	49.2
	B1MM	10.2**	6.6	1.8	5.1	35.4
Ear diameter(mm)	MMB1	34.7**	48.4	6.9	24.2	28.4
	B1MM	14.2**	8.8	2.7	7.1	38.2
Ear length (cm)	MMB1	4.9**	2.6	1.2	2.5	47.7
	B1MM	7.9**	4.2	1.9	4.0	47.1
Plant height (cm)	MMB1	453.8 ^{ns}	363.3	45.3	226.9	20.0
	B1MM	709.4**	357.1	176.2	354.7	49.7
Ear height (cm)	MMB1	211.5**	120.7	45.4	105.7	42.9
	B1MM	318.8**	175.9	71.5	159.4	44.8

$\hat{\sigma}_g^2$, $\hat{\sigma}_p^2$, h_B^2 = genotypic variance, phenotypic variance, and broad-sense heritability, respectively.

** ; * ; ^{ns} = Significant at $p < 0.01$; significant at $p < 0.05$; and non-significant, respectively.

RESULTS

Heritability

A summary of the results of the analyses of variance and estimates of broad-sense heritability from the S_1 and full-sib progeny evaluations is shown in Tables 1 and 2. Broad-sense heritability values estimated from the $B1S_1$ progeny population were high for days to tasselling (63.3%) and ear diameter (60.1%); moderate for ear height (49.3%), ear length (48.3%) and fresh largest ear weight per plant (47.9%). In MMS_1 progeny population, estimates of broad-sense heritability were high for plant height (65.7%), ear height (61.7%), ear length (61.6%), ear diameter (58.9%), fresh dehusked largest ear weight per plant (55.5%) and days to tasselling (55.3%) (Table 1).

Broad-sense heritability estimates in the $MMB1$ progeny population were moderate for days to tasselling (49.2%), ear length (47.7%), ear height (42.9%), fresh largest ear weight per plant (30.5%) and fresh dehusked largest ear weight per plant (28.6%). Heritability for plant height was, however, low (20.0%). In the $B1MM$ progeny population, all traits showed moderate broad-sense heritability estimates, ranging from 27.7% to 49.7% (Table 2).

Response to Selection

Selection responses on fresh ear yield, fresh dehusked ear yield and number of ears per hectare are shown in Table 3.

TABLE 3
Response to one cycle of simple and full-sib reciprocal recurrent selection on populations $B1C_0$ and MMC_0 , for yield characters

Population	At Field 2		At Field 10B		Average Response (%)
	Mean	Response (%)	Mean	Response (%)	
Fresh ear yield (ton/ha)					
$B1C_0^{\#}$	6.11c		6.60a		
$B1SC_1$	8.21a	34.2	6.55a	-0.8	16.7
$B1RFSC_1$	7.63ab	24.8	5.74a	-13.1	5.9
$MMC_0^{\#}$	7.12abc		5.59a		
$MMSC_1$	7.35abc	3.2	6.56a	17.2	10.2
$MMRFSC_1$	6.61bc	-7.2	5.29a	-5.5	-6.4
Mean	7.17		6.05		
Fresh dehusked ear yield (ton/ha)					
$B1C_0^{\#}$	4.12c		4.55a		
$B1SC_1$	5.76a	39.8	4.69a	3.2	21.5
$B1RFSC_1$	5.25ab	27.6	3.96a	-12.9	7.4
$MMC_0^{\#}$	5.17abc		3.97a		
$MMSC_1$	5.07abc	-2.0	4.56a	14.6	6.3
$MMRFSC_1$	4.55bc	-12.1	3.87a	-2.7	-7.4
Mean	4.99		4.27		
Number of ears/ha					
$B1C_0^{\#}$	34223b		40148ab		
$B1SC_1$	42667a	24.7	41926ab	4.4	14.6
$B1RFSC_1$	41556a	21.4	33778b	-15.9	2.8
$MMC_0^{\#}$	40222a		36741ab		
$MMSC_1$	39889a	-0.8	43408a	18.1	8.7
$MMRFSC_1$	39445a	-1.9	36000ab	-2.0	-2.0
Mean	39667		38667		

[#] source population

Means followed by the same letter in the same column of each character are not significantly different at $p < 0.05$, following DNMR. T.

Fresh Ear Yield

Evaluation at Field 2 showed that both populations B1SC₁ and B1RFSC₁ had fresh ear yield significantly higher than that of the source population, B1C₀, with increases of 34.2% and 24.8%, respectively. Evaluation at Field 10B, however, showed that both populations had lower yields than the source population, with decreases of 0.8% and 13.1%, respectively. The mean of both locations for fresh ear yield indicated that there were increases of 16.7% and 5.9% in B1SC and B1RFSC₁, respectively, over the source population B1C₀.

For Manis Madu, results at Field 2 showed that population MMSC₁ had a fresh ear yield 3.2% higher than the source population MMC₀, but population MMRFSC₁ had a fresh ear yield 7.2% lower than the source population. At Field 10B, fresh ear yield of MMSC₁ was 17.2% higher, but fresh ear yield of MMRFSC₁ was 5.5% lower than that of MMC₀. The means of both locations for MMSC₁ and MMRFSC₁ increased by 10.2% and decreased by 6.4% respectively, compared with the yields of the source populations.

Fresh Dehusked Ear Yield

For the Bakti-1 population, evaluation at Field 2 showed that both B1SC₁ and B1RFSC₁ had higher yields than the source population, B1C₀, with 39.8% and 27.6% increases, respectively. At Field 10B, however, fresh dehusked ear yield of B1SC₁ was 3.2% higher than that of the source population, but the yield of B1RFSC₁ was 12.9% lower than that of the source population. The means of the yield increments were 21.5% in B1SC₁ and 7.4% in B1RFSC₁.

For selection on Manis Madu, from evaluation at Field 2, it was found that both MMSC₁ and MMRFSC₁ had a fresh dehusked ear yield lower than that of the source population, MMC₀, with decreases of 2.0% and 12.1%, respectively. At Field 10B, fresh dehusked ear yield was 14.6% higher in MMSC₁, but was 2.7% lower in MMRFSC₁, compared to the yield of the source population. The means were 6.3% higher in MMSC₁ but 7.4% lower in MMRFSC₁.

Number of Ears per Hectare

For selection on Bakti-1, evaluation at Field 2 showed that both B1SC₁ and B1RFSC₁ had a higher number of ears per hectare than the source population, B1C₀, with increases of 24.7% and

21.4%, respectively. At Field 10B, the number of ears per hectare was 4.4% higher in B1SC₁, but was 15.9% lower in B1RFSC₁, compared to that of the source population. The mean values, however, showed increases of 4.6% and 2.8%, respectively for B1SC₁ and B1RFSC₁.

For selection on Manis Madu at Field 2 the number of ears per hectare in both the improved populations, MMSC₁ and MMRFSC₁ were reduced by 0.8% and 1.9%, respectively, when compared to that of the source population, MMC₀. At Field 10B, however, the number of ears per hectare was 18.1% higher in MMSC₁, but was 2.0% lower in MMRFSC₁, compared to that of the source population. The mean values were 8.7% higher in MMSC₁, but 2.0% lower in MMRFSC₁, when compared to the source population.

DISCUSSION

The moderate to high heritability estimates obtained from the B1S₁ and MMS₁ progeny evaluations indicated the presence of a substantial amount of genetic variability in the populations; and selection carried out on the populations should be able to isolate favourable genes to be recombined in the new genetic background. Similar estimates of heritability were also obtained in similar studies on other corn populations (Obilana and Hallauer 1974; Silva 1974; Bartual and Hallauer 1976). The generally higher heritability estimates obtained in the B1S₁ population compared to those of the MMS₁ population, might have led to the generally higher response to the simple recurrent selection revealed by the Bakti-1 as compared to Manis Madu.

In this study, comparisons of selection response were only made between the improved populations and their respective source populations, and not between the crosses of the improved populations and the respective source populations. This was because the main intention was to observe the direct effect of the selection, and to make inferences on the superiority of one selection method over the other in accumulating additive genes in the populations.

The significant increase in fresh ear yield in B1SC₁ and B1RFSC₁ also indirectly increased fresh dehusked ear yield and the number of ears per hectare, indicating the presence of positive correlations among these characters. From the selection response, simple recurrent selection based on fresh largest ear weight per plant was

found to be more effective in increasing population yield than in the full-sib reciprocal recurrent selection, and the response was higher on Bakti-1 than in Manis Madu, although differences were significant only in one environment (Field 2). Previous researchers have also reported a higher response of selection based on S_1 progeny evaluation in bulked inbred or random-mated populations compared to full-sib reciprocal recurrent selection to increase yield in corn. (West *et al.* 1980; Odhiambo and Compton 1989). Genter (1971), Jinahyon and Moore (1973) and Hable (1985) also reported that simple recurrent selection showed significant effects in improving genetic composition of the traits used as the criteria of selection.

The Bakti-1 population showed a higher response to both selection procedures compared to Manis Madu in improving fresh ear yield, fresh dehusked ear yield and number of ears per hectare.

Further selection using both procedures in the succeeding cycles should produce higher responses in the population improvement.

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