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Inbreeding Depression and Heterosis in Sweet Corn Varieties Manis Madu and Bakti-1

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ABSTRAK

Famili-famili progeni S_1 dan penuh-sib yang dibentuk dari penyendirian dan kacukan antara varieti jagung manis Manis Madu dan Bakti-1 telah dinilai untuk menganggarkan kemelesetan penginbredan dan heterosis dalam populasi. Penyendirian telah menyebabkan berlakunya pengurangan yang bererti di dalam nilai ukuran untuk semua ciri yang diukur dalam kedua-dua populasi penyendirian, kecuali untuk ciri masa pentaselan yang menunjukkan pertambahan pada nilainya. Anggaran heterosis berdasarkan nilai pertengahan induk untuk ciri-ciri yang dinilai ialah di antara -2.83% dan 22.34% bagi populasi progeni kacukan Manis Madu X Bakti-1 (MMB1), dan di antara -2.65% dan 16.57% bagi populasi progeni kacukan Bakti-1 X Manis Madu (B1MM). Kedua-dua varieti menunjukkan potensi baik untuk digunakan sebagai induk dalam kacukan antara populasi-populasi maju atau warisan-warisan inbred yang terbentuk darinya.

ABSTRACT

S_1 and full-sib progeny families developed from selfing and crossing between Manis Madu and Bakti-1 sweet corn varieties were evaluated to estimate inbreeding depression and heterosis in the populations. Selfing has caused a significant decrease in the measurements of all characters taken in both selfed populations, except for days to tasseling which has shown an increase. Midparent heterosis estimates for the characters evaluated ranged from -2.83% to 22.34% for the Manis Madu X Bakti-1 cross progeny population (MMB1), and from -2.65% to 16.57% in the Bakti-1 X Manis Madu cross progeny population (B1MM). The two varieties revealed good potential to be used as parents for crosses between improved populations or inbred lines developed from them.

Keywords: ***Zea mays*****, sweet corn, inbreeding depression, heterosis**

INTRODUCTION

Inbreeding is the process of mating between genetically related individuals. Selfing is the strongest form of inbreeding. As a consequence of selfing, recessive genes, earlier masked in the heterozygous forms, become homozygous. These genes, if conferring to undesirable phenotypes, will result in the deterioration of the succeeding generations. In cross-pollinated crops which do not have self-incompatibility problems, like corn, however, inbred lines for hybrid varieties are developed through selfing.

Extensive studies on inbreeding depression in corn have indicated that selfing is important in inbred development because it leads to rapid gene homozygosity, and desirable dominant genes can be accumulated while the undesirable ones are eliminated. The performance of inbred lines or lines produced from selfing decreased drastically, resulting in yield reduction, increase in the number of stunted plants, reduced plant resistance to pests and diseases and reduced growth rate (Genter 1971; Harris *et al.* 1972; Hallauer and Sears 1973; Cornelius and Dudley 1974; Good and Hallauer 1977; Saleh *et al.* 1990).

Heterosis or hybrid vigour is the effect which is opposite to inbreeding depression. From the aspect of quantitative genetics, heterosis is the value or measurement of a hybrid beyond the average value of the two parents. However, in plant breeding a hybrid that performs better than the better parent is desired. Heterosis estimates for corn yield based on the mid-parental values in crosses between populations have been reported, including 19.2% from the variety cross of 'Jarvis' X 'Indian Chief' (Moll and Stuber 1971), 14.4% from the cross of 'Iowa Stiff Stalk Synthetic' X 'Iowa Corn Borer Synthetic No. 1'

(Eberhart *et al.* 1973), 6.0% from the cross of 'Teko Yellow' X 'Natal Yellow Horse Tooth' (Gevers 1975), 39.3% from the cross of 'KII' X 'EC573' (Darrah *et al.* 1978) and 14.9% from the cross of 'BSSS' X 'BSCB1' (Martin and Hallauer 1980).

The objectives of this study were to determine inbreeding depression in the S_1 families, and to estimate heterosis revealed by the full-sib progenies developed from the crosses, in the first cycle of a recurrent selection programme involving the sweet corn varieties Manis Madu and Bakti-1.

MATERIALS AND METHODS

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

This study was part of the simple and reciprocal recurrent selection programmes undertaken on the two varieties. In the first planting season, self-pollinations and full-sib crosses were carried out to develop selfed and full-sib progeny families. The selfed-progeny families were MMS_1 for Manis Madu and $B1S_1$ for Bakti-1, while the full-sib families were MMB1 from the Manis Madu X Bakti-1 cross, and B1MM from its reciprocal cross. For this purpose, the source populations, Manis Madu and Bakti-1 were planted at the density of 100 cm x 50 cm, and female inflorescences of 250 plants of each population were hand-pollinated to form each of the progeny families. The total number of uncontaminated families formed were 195 MMS_1 families, 197 $B1S_1$ families, 176 MMB1 families and 189 B1MM families.

In the second planting season, evaluations of the S_1 and full-sib families were conducted in a randomised complete block design, with two replications. The planting density used was 75cm x 25 cm. The original source populations were used for comparison, where one row of the respective source population was planted for every six progeny rows in the S_1 family evaluation, while one row of each of the source populations was planted for every six progeny rows in the full-sib progeny evaluation. Every progeny-row in a replication comprised twelve plants. Six plants from each family were taken at random as samples for the analysis of data. Seven plant characters and yield components were studied.

Estimates of inbreeding depression in the selfed populations were determined as follows:

$$\text{Inbreeding depression} = \frac{\bar{S}_1 - \bar{S}_0}{\bar{S}_0};$$

where $\bar{S}_0$ = S_0 population mean, and
$\bar{S}_1$ = S_1 population mean.

Estimates of heterosis in the cross-progeny populations were determined as follows:

$$\text{Mid-parent heterosis} = \frac{\bar{F}_1 - \overline{MP}}{\overline{MP}};$$

$$\text{Better-parent heterosis} = \frac{\bar{F}_1 - \overline{HP}}{\overline{HP}};$$

where $\bar{F}_1$ = performance of full-sib crossed-progeny,
$\overline{MP}$ = mean of the performance of the two parental populations, and
$\overline{HP}$ = performance of the better parental population.

RESULTS AND DISCUSSION

Inbreeding Depression

The estimates of inbreeding depression for the selfed populations are shown in Table 1. In both selfed populations, the estimate of inbreeding depression was highest for fresh largest-ear weight per plant, followed by ear length, ear height, plant height, ear diameter and days to tasselling. Contrary to the other characters, inbreeding depression for days to tasselling was shown by the increase in the magnitude of the measurement.

There were substantial differences in the inbreeding depression estimates between MMS_1 and $B1S_1$ populations. For all characters evaluated, except days to tasselling, estimates of inbreeding depression in MMS_1 were higher than those in $B1S_1$. The estimates in population MMS_1 and $B1S_1$ respectively, were -33.58% and -21.17% for fresh largest-ear weight per plant, -20.48% and -11.10% for ear length, -16.75% and -10.18% for ear height, -14.77% and -8.43% for plant height, and -8.73% and -6.57% for ear diameter. Selfing caused lateness in tasselling in both populations. There was no obvious difference in inbreeding depression for days to tasselling between the two selfed populations, i.e. +3.35% in MMS_1 and +3.24% in $B1S_1$.

One generation of selfing in the two populations reduced plant and ear size and yield. This was due to the unmasking of the recessive alleles of the genes responsible for the control of these characters as the result of selfing. The accumulation of recessive alleles in the homozygous form due to selfing, thus, resulted in plant and ear size, and yield reductions. Similar results were reported by Cornelius and Dudley (1974)

TABLE 1
Estimates of inbreeding depression in MMS_1 and $B1S_1$ populations

Character	Population	Mean ± SE		Inbreeding depression (%)
		S_0	S_1	
Fresh largest-ear weight per plant (g)	MM	198.84 ± 3.10	132.07 ± 2.79	- 33.58**
	B1	226.48 ± 2.91	175.90 ± 2.72	- 22.23**
Fresh dehusked largest-ear weight per plant (g)	MM	133.72 ± 2.15	84.95 ± 1.96	- 36.47**
	B1	na	na	na
Days to tasselling (days)	MM	53.15 ± 0.12	54.93 ± 0.13	+ 3.35**
	B1	49.10 ± 0.10	50.69 ± 0.13	+ 3.24**
Ear diameter (mm)	MM	40.54 ± 0.27	37.00 ± 0.21	- 8.73**
	B1	40.56 ± 0.30	37.85 ± 0.20	- 6.68**
Ear length (cm)	MM	13.87 ± 0.18	11.03 ± 0.16	- 20.48**
	B1	14.19 ± 0.20	12.58 ± 0.17	- 11.35**
Plant height (cm)	MM	146.15 ± 1.16	124.57 ± 1.14	- 14.77**
	B1	183.41 ± 1.20	167.94 ± 1.14	- 8.43**
Ear height (cm)	MM	70.50 ± 0.85	58.61 ± 0.83	- 16.75**
	B1	90.86 ± 0.96	81.61 ± 0.86	- 10.18**

na Data not available
** Significantly different from zero at $p < 0.01$

and Good and Hallauer (1977), who found reduction in yield and other characters, except for tasselling date. Lateness in tasselling as a consequence of selfing showed that the alleles responsible for earliness are dominant to those responsible for lateness. Lateness in tasselling due to inbreeding was also reported by Marsum (1972), Sears and Hallauer (1973), Cornelius and Dudley (1974).

The highest estimates of inbreeding depression were obtained from yield characters, i.e. fresh largest-ear weight per plant and fresh dehusked largest-ear weight per plant. Similar results were reported by Genter (1970), who found that yield characters experienced a higher rate of inbreeding because they were controlled by a higher number of genes. High rates of inbreeding depression were also reported by Genter (1971), Harris *et al.* (1972), Marsum (1972), Hallauer and Sears (1973), Cornelius and Dudley (1974).

The difference in the estimates obtained between populations MMS_1 and $B1S_1$ could be due to the difference in the nature and number of genes involved in the control of the characters in the two source populations. It could also be due to the interactions between the genotype and the environment, because the two populations were evaluated separately at different times. Genter (1971) also reported that different corn populations gave different inbreeding depression estimates. Harris *et al.* (1972) also indicated that differences in inbreeding depression estimates were caused by genetic and environmental factors.

Heterosis

Estimates of heterosis obtained from mean performance of all families in each of the populations, MMB1 and B1MM are shown in Table 2. In general, the MMB1 population showed higher heterosis compared to the B1MM population.

Based on mid-parental value in the MMB1 population, fresh largest-ear weight per plant showed the highest heterosis estimate (22.34%), followed by fresh dehusked largest-ear weight per plant (19.13%), ear height (18.97%), plant height (13.11%), ear length (9.63%) and ear diameter (3.95%). In the B1MM population however, the highest estimate of heterosis, based on the mid-parental value was shown by fresh dehusked largest-ear weight per plant (16.57%),

TABLE 2
Estimates of heterosis in MMB1 and B1MM populations

Character	Cross Pop.	Mean ± SE			Heterosis (%)	
		B1	MM	F_1	Mid-Parent	Better-Parent
Fresh largest-ear weight per plant (g)	MMB1	152.25 ± 3.01	138.95 ± 2.80	178.12 ± 3.05	22.34 **	16.99 **
	B1MM	175.60 ± 3.25	198.79 ± 3.82	195.40 ± 3.61	4.38 *	- 1.71
Fresh dehusked largest-ear weight per plant (g)	MMB1	109.43 ± 2.06	97.48 ± 1.98	123.25 ± 2.19	19.13 **	12.63 **
	B1MM	105.22 ± 2.03	115.68 ± 2.13	128.75 ± 2.43	16.57 **	11.30 **
Days to tasselling (days)	MMB1	54.16 ± 0.14	54.27 ± 0.15	52.68 ± 0.13	- 2.83 *	- 2.73 **
	B1MM	56.18 ± 0.19	55.40 ± 0.17	54.31 ± 0.17	- 2.65 *	- 1.97
Ear diameter (mm)	MMB1	36.29 ± 0.17	36.05 ± 0.15	37.60 ± 0.20	3.95 *	3.61 *
	B1MM	38.92 ± 0.19	41.01 ± 0.22	40.07 ± 0.21	0.26	- 2.29 *
Ear length (cm)	MMB1	11.10 ± 0.11	10.92 ± 0.10	12.07 ± 0.13	9.63 **	8.74 **
	B1MM	12.05 ± 0.13	12.60 ± 0.14	12.72 ± 0.15	3.20 *	0.95
Plant height (cm)	MMB1	135.23 ± 1.35	126.47 ± 1.20	148.01 ± 1.29	13.11 **	9.45 **
	B1MM	145.96 ± 1.40	141.83 ± 1.36	147.88 ± 1.47	2.77 *	1.32
Ear height (cm)	MMB1	56.73 ± 0.73	56.04 ± 0.76	67.08 ± 0.89	18.97 **	18.24 **
	B1MM	60.96 ± 0.80	63.13 ± 0.86	67.96 ± 1.00	9.53 **	7.65 **

**,* Significantly different from zero at $p < 0.01$ and 0.05, respectively.

followed by ear height (9.57%), fresh largest-ear weight per plant (4.38%), ear length (3.20%), plant height (2.77%) and ear diameter (0.26%). Heterosis for days to tasselling did not show a large difference between populations (-2.83% for MMB1, and -2.65% for B1MM).

Based on better-parent value in the population MMB1, highest heterosis estimate was shown by ear height (18.24%), followed by fresh largest-ear weight per plant (16.99%), fresh dehusked largest-ear weight per plant (12.63%), plant height (9.45%), ear length (8.75%) and ear diameter (3.61%). In the B1MM population, the highest estimate of heterosis was obtained for fresh dehusked largest-ear weight per plant (11.30%), followed by ear height (7.65%), plant height (1.32%) and ear length (0.95%). For fresh largest-ear weight per plant and ear diameter, heterosis estimates were negative (-1.71% and -2.29%, respectively), indicating that the crossed population did not perform better than the better parent for these characters. Better-parent heterosis estimates for days to tasselling were -2.73% for MMB1 and -1.97% for B1MM.

In both populations, many families showed very high heterosis estimates. In population MMB1, mid-parent heterosis and better-parent heterosis in individual families were as high as 99.18% and 90.48% respectively, for fresh largest-ear weight per plant. Similarly, in population B1MM, the highest values shown by a family for this character were 68.86% for mid-parent heterosis, and 59.01% for the better-parent heterosis. For fresh dehusked largest-ear weight per plant, the estimates for the individual families were as high as 86.84 and 76.64% for mid-parent heterosis and better-parent heterosis, respectively in population MMB1; the two estimates were 93.53 and 84.78%, respectively for the population B1MM. Heterosis estimates for ear diameter and ear length for families were as high as 21.37% (mid-parent) and 24.23% (better-parent), in MMB1, and as high as 24.23% (mid-parent) and 21.07% (better-parent), in B1MM. A similar trend was found for the other characters measured.

Positive estimates of heterosis obtained for yield components including fresh dehusked largest-ear weight per plant and ear length, as shown in this study were also reported by Peterniani and Lonnquist (1963), Moll and

Stuber (1971), Eberhart *et al.* (1973), Gevers (1975), Darrah *et al.* (1978), Martin and Hallauer (1980). The differences in the estimates of heterosis were due to the different populations used.

Both progeny populations produced tassels earlier than their respective parents, as evidence of heterosis. This showed that the alleles which determine earliness in tasselling are dominant to those responsible for lateness, as reported by Robinson *et al.* (1949). Positive heterosis for plant and ear heights were also reported by Pasev and Trifunovic (1968).

The presence of some degree of reciprocal effects was also detected, where Manis Madu variety gave a higher heterotic effect in the progenies, if used as the female parent (MMB1), compared to when it was used as the male (B1MM).

The presence of substantial heterosis in the progenies of crosses between Manis Madu and Bakti-1 indicates that the two varieties have good potential as parents for population crosses or inbred development for hybrid variety production. A very high heterosis revealed by many families indicates that recombination of the promising lines selected from these populations in the later phase of the recurrent selection programme, should help develop new populations with higher combining ability with the reciprocal populations.

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