



UNIVERSITI PUTRA MALAYSIA

**GENETICS AND GENETIC RESPONSE IN
POPULATIONS GENERATED FROM TWO
CYCLES OF PHENOTYPIC MASS SELECTION
IN SWEET CORN (ZEA MAYS L. SACCHARATA)**

ELTAHIR SIDDIG ALI

FP 2003 8

**GENETICS AND GENETIC RESPONSE IN POPULATIONS GENERATED
FROM TWO CYCLES OF PHENOTYPIC MASS SELECTION IN SWEET
CORN (*ZEAMAYS L. SACCHARATA*)**

By

ELTAHIR SIDDIG ALI

**Thesis Submitted to the School of Graduate Studies, Universiti Putra Malaysia,
in Fulfilment of the Requirements for the Degree of Doctor of Philosophy**

May 2003



DEDICATION

**TO MY BELOVED PARENTS, BROTHERS, SISTERS
AND MY SUPPORTING WIFE AWATIF**



Abstract of thesis presented to the Senate of Universiti Putra Malaysia in fulfilment of the requirements for the degree of Doctor of Philosophy.

GENETICS AND GENETIC RESPONSE IN POPULATIONS GENERATED FROM TWO CYCLES OF PHENOTYPIC MASS SELECTION IN SWEET CORN (*ZEA MAYS L. SACCHARATA*)

By

ELTAHIR SIDDIG ALI

May 2003

Chairman : Associate Professor Ghizan Saleh, Ph.D.

Faculty : Agriculture

Local composite varieties of sweet corn (*Zea mays L. saccharata*) offer moderate yields and eating quality, while imported hybrid varieties are less adaptable to the local environment, although having good eating quality. A breeding programme was therefore initiated at Universiti Putra Malaysia (UPM), utilising both genetic materials to produce new superior genotypes. The main objectives of this study were to investigate the genetics of populations, and to evaluate genetic response in two sweet corn populations generated from two cycles of phenotypic mass selection.

In Experiment 1, a local composite variety, Manis Madu and two imported hybrid varieties, Hybrid SSC 240 and Hybrid 368 were first evaluated, and found to show comparable performance. Consequently, Manis Madu and Hybrid SSC 240 were chosen as source populations for selection and were then crossed to generate the base population. In Experiment 2, the performance of the cross population was compared to its parents, and was found to show more resemblance to Hybrid SSC 240.



Separately and simultaneously, two cycles of phenotypic mass selection for ear length were employed on the two base populations, Manis Madu, designated as M C0, and the intermated crossed population, designated as MS C0, at Field 2, UPM. The two base populations and the populations generated from the two cycles of selection were then evaluated and compared for general performance at two locations, Field 2 and Share Farm, in UPM.

In Manis Madu populations (M), the predicted responses to individual cycles of selection were almost the same for both cycles, 19.3% in the first cycle and 19.6% in the second. The cumulative predicted response in M C2 population was 43.6%. In the cross populations (MS), the predicted response to individual cycles of selection was higher in the second cycle (26.5%) than it was in the first (16.8%). The cumulative predicted response in MS C2 population was 46.4%.

The two populations responded differently to the two cycles of selection, where, in Manis Madu populations, a positive realised response was only attained in first cycle (4.1%), while a negative one was observed in the second (-0.7%). In contrast, the cross populations showed negative realised response in the first cycle (-0.7%), while a reasonable positive one (2.08%) was observed in the second. The average cumulative realised response to selection was higher in M C2 (3.4%) than that in MS C2 (1.4%). As expected, the realized responses were lower than the predicted.

In the combined analysis, population generated from the second cycle of selection on Manis Madu (M C2), showed significant improvement in fresh husked ear yield

(10996 kg ha⁻¹) and dehusked ear length (15.2 cm). The population generated from the second cycle of selection on the cross (MS C2) showed significant improvement in fresh dehusked ear yield, giving 6887 and 6788 kg ha⁻¹ at Field 2 and Share Farm, respectively. In the combined analysis, MS C2 produced significantly longer dehusked ears (14.7 cm) than did the base population, MS C0 (14.5 cm).

Results of simple phenotypic correlations on traits measured on individual plant samples within the selected populations, showed positive phenotypic correlations between plant height and most of the other traits investigated, including ear height, ear length and number of kernel rows/ear. In addition, positive correlations were also observed among the ear traits, ear length, ear diameter, number of kernel rows/ear and number of kernels/row.

Ear length, which was taken as a criterion for selection in this study, showed moderate broad-sense heritability (h^2_B) estimates in the two populations investigated, indicating that selection for this trait in these populations would be effective for expression of this trait in the succeeding generations.

This study has revealed that both the local and imported germplasm materials were useful in the breeding of sweet corn populations. The two cycles of phenotypic mass selection for ear length were found to have shown some improvement in fresh ear yield of the populations. Introgression of foreign genes into the local germplasm might have enriched the available gene pool, although more cycles of selection are required for more pronounced genetic improvement to be realised.

Abstrak tesis yang dikemukakan kepada senat Universiti Putra Malaysia bagi memenuhi syarat untuk mendapatkan ijazah Doktor Falsafah.

**GENETIK DAN TINDAKBALAS GENETIK DALAM POPULASI
TERBENTUK DARI DUA PUSINGAN PEMILIHAN KASAR FENOTIP
PADA JAGUNG MANIS (*ZEAMAYS L. SACCHARATA*)**

Oleh

ELTAHIR SIDDIG ALI

Mei 2003

Pengerusi : Profesor Madya Ghizan Saleh, Ph.D.

Fakulti : Pertanian

Varieti-varieti komposit tempatan jagung manis (*Zea mays L. saccharata*) memberikan hasil dan kualiti pemakanan yang sederhana, manakala varieti-varieti hibrid yang diimport kurang kesesuaian pada persekitaran tempatan, walaupun mempunyai kualiti pemakanan yang baik. Oleh itu, satu program pembiakbakaan telah dimulakan di Universiti Putra Malaysia (UPM), menggunakan kedua-dua bahan genetik untuk menghasilkan genotip baru yang unggul. Objektif utama kajian ini ialah untuk mengkaji genetik populasi, dan tindakbalas genetik dalam dua populasi jagung manis yang dibentuk dari dua pusingan pemilihan kasar fenotip.

Dalam Eksperimen 1, varieti komposit tempatan, Manis Madu dan dua varieti hibrid yang diimport, Hibrid SSC 240 dan Hibrid 368 telah pada mulanya dinilai, dan didapati memberikan prestasi yang setara. Berikutan dengan itu, Manis Madu dan Hibrid SSC 240 telah dipilih sebagai populasi sumber untuk pemilihan dan kemudiannya dikacukkan bagi menghasilkan populasi bes. Dalam Eksperimen 2,

prestasi populasi kacukan telah dibandingkan dengan induknya, dan didapati lebih menyerupai Hibrid SSC 240.

Secara berasingan dan serentak, dua pusingan pemilihan kasar fenotip berdasarkan panjang tongkol telah dijalankan terhadap kedua-dua populasi bes, Manis Madu, dinamakan M C0, dan populasi kacukrawak dari kacukan tersebut, dinamakan sebagai MS C0, di Ladang 2, UPM. Dua populasi bes tersebut serta populasi yang dibentuk dari dua pusingan pemilihan kemudiannya dinilai dan dibandingkan untuk prestasi am di dua lokasi, Ladang 2 dan Ladang Kongs, UPM.

Dalam populasi Manis Madu (M), tindakbalas jangkaan dari pusingan individu adalah hampir sama bagi kedua-dua pusingan, 19.3% dalam pusingan pertama dan 19.6% dalam pusingan kedua. Tindakbalas jangkaan kumulatif dalam populasi M C2 adalah 43.6%. Dalam populasi kacukan (MS), tindakbalas jangkaan dari pusingan individu pemilihan adalah lebih tinggi dalam pusingan kedua (26.5%) berbanding pusingan pertama (16.8%). Tindakbalas jangkaan kumulatif dalam populasi MS C2 adalah 46.6%.

Kedua-dua populasi menunjukkan tindakbalas yang berbeza terhadap dua pusingan pemilihan, di mana, dalam populasi Manis Madu, tindakbalas sebenar yang positif hanya diperolehi dalam pusingan pertama (4.1%), manakala tindakbalas sebenar yang negatif diperolehi dalam pusingan kedua (-0.7%). Sebaliknya, populasi kacukan menunjukkan tindakbalas sebenar yang negatif dalam pusingan pertama (-0.7%), manakala tindakbalas sebenar positif yang memadai (2.08%) didapati dalam

pusingan kedua. Purata tindakbalas sebenar kumulatif terhadap pemilihan adalah lebih tinggi dalam M C2 (3.4%) berbanding dengan yang di tunjukkan dalam MS C2 (1.4%). Sebagaimana dijangka, tindakbalas sebenar adalah lebih rendah dari yang diramal.

Dalam analisis gabungan, populasi yang terbentuk selepas dua pusingan pemilihan terhadap Manis Madu (M C2), menunjukkan peningkatan yang ketara bagi hasil tongkol segar dengan kulit (10996 kg ha^{-1}) dan panjang tongkol tanpa kulit (15.2 cm). Populasi yang terbentuk selepas pusingan kedua pemilihan terhadap populasi kacukan (MS C2) menunjukkan peningkatan yang bererti bagi hasil tongkol segar tanpa kulit, memberikan 6887 dan 6788 kg ha^{-1} masing-masing di Ladang 2 dan Ladang Kongsi. Dalam analisis gabungan, MS C2 menghasilkan tongkol segar tanpa kulit yang lebih panjang (14.7 cm) berbanding populasi bes, MS C0 (14.5 cm).

Keputusan korelasi mudah fenotip di antara sifat-sifat yang diukur pada sampel individu pokok, di kalangan populasi terpilih, menunjukkan korelasi fenotip yang positif antara ketinggian pokok dengan kebanyakan sifat lain yang dikaji, termasuk ketinggian tongkol, panjang tongkol dan bilangan baris bijian/tongkol. Selain dari itu, korelasi positif juga didapati di antara sifat-sifat tongkol, iaitu panjang tongkol, diameter tongkol, bilangan baris bijian/tongkol dan bilangan bijian/baris.

Panjang tongkol, yang mana diambil sebagai kriteria untuk pemilihan dalam kajian ini, memberikan anggaran kebolehwarisan luas (h^2_B) yang sederhana dalam kedua-dua populasi yang dikaji, menunjukkan bahawa pemilihan untuk sifat ini dalam

populasi-populasi tersebut boleh memberikan kesan dalam meningkatkan ukuran sifat ini dalam generasi seterusnya.

Kajian ini telah menunjukkan bahawa kedua-dua germplasma tempatan dan juga yang diimport adalah berguna dalam pembiakbakaan populasi jagung manis. Dua pusingan pemilihan kasar fenotip berdasarkan panjang tongkol yang dijalankan telah menunjukkan sedikit peningkatan hasil tongkol segar dalam kedua-dua populasi. Introgresi gen dari luar ke dalam germplasma tempatan mungkin telah memperluaskan himpunan gen sediaada, walaupun lebih banyak pusingan pemilihan diperlukan untuk mencapai peningkatan genetic yang lebih besar.

ACKNOWLEDGEMENTS

My full praise to Allah S.W.T. for enabling me to complete my study. This is a real blessing from Him and thanks to Him in the way that suits His supreme greatness, will and power. Blessings and peace from Allah S.W.T. be upon our Prophet Muhammad and all his Family and Companions.

My sincere appreciation goes to my supervisory committee, who were a great source of inspiration and encouragement throughout the period of my study. I would like to express my deepest gratitude to my supervisor and chairman of the supervisory committee, Associate Professor Dr. Ghizan Saleh for his systematic guidance and advice during the study. All his contributions are truly appreciated.

I am also indebted to the supervisory committee members, Associate Professor Dr. Anuar Abdul Rahim and Dr. Zakaria Abdul Wahab for their valuable contributions and suggestions that added interesting new knowledge and validity to this study.

My thanks also go to the Sudanese Ministry of Higher Education and Scientific Research, University of Gezira (UG), National Oilseed Processing Research Institute (NOPRI), Agricultural Research Corporation (ARC), and the Malaysian Ministry of Science, Technology and Environment (through the Intensive Research in Priority Areas (IRPA) funds), for their financial support that made this study successful.

I would like to express my deepest thanks to the Graduate School and the Faculty of Agriculture, especially the Department of Crop Science, Universiti Putra Malaysia



for the extensive assistance offered throughout the duration of my study. I would like to thank the staff of Field 2 and Share Farm, especially Mr. Shahril Abdul Rahman and Mr. Yasin for their kind cooperation when conducting my field experiments.

Thanks to the technical staff of the plant breeding laboratory, Mrs. Maininah Tahir and Mr. Hanib Ali, and all my postgraduate colleagues Than Da Min, Khayamuddin Panjaitan, Panca Jarot Santoso and Mohammad Asraf Kamaluddin. Thanks also go to the students on the Bachelors programme, especially Hii Jung Mee and Tham Weng Seong for their assistance.

I am also much indebted to my Sudanese friends and colleagues for their pronounced assistance during the field experiments. My specific thanks go to Dr. Omer Hassan Arabi, Mr. Elsadig Mohamed Ali, Mr. Asaad Abdullah, Mr. Khalid Osman, Dr. Izzeldin Babiker and Dr. Ahmed Abdullah. My thanks also go to many others who were there for me but whose names remain unmentioned.

I would like to express my deepest appreciation and gratitude to my dear wife Awatif Mohamed Ibrahim for her wholehearted assistance throughout this study. Her patience and encouragement always remained as my inspiration to complete this degree. Finally, I owe a big thank you to my family members, father Siddig Ali, mother Arafa Elbasha, and my brothers and sisters for their spiritual, financial and moral support. All of you are respected, loved and cherished for being there for me.



TABLE OF CONTENTS

	Page
DEDICATION	ii
ABSTRACT	iii
ABSTRAK	vi
ACKNOWLEDGEMENTS	x
APPROVAL	xii
DECLARATION	xiv
LIST OF TABLES	xviii
LIST OF FIGURES	xxiii
LIST OF ABBREVIATIONS	xxv
CHAPTER	
1 INTRODUCTION	1
2 LITERATURE REVIEW	4
2.1 Classification of Sweet Corn	4
2.1.1 Botanical Classification	4
2.1.2 Classification Based on Endosperm Characters	4
2.2 Origin and Development of Sweet Corn	6
2.3 Production of Sweet Corn	7
2.4 Breeding Progress of Sweet Corn in Malaysia	8
2.5 Genetics and Breeding of Sweet Corn	9
2.5.1 General Aspects of Sweet Corn Breeding	9
2.5.2 Genes Controlling Sweetness in Sweet Corn	12
2.5.3 Use of Sweetness Genes in Sweet Corn Improvement	14
2.6 Heritability	16
2.7 Correlation among Plant Traits	18
2.8 Mass Selection in Maize	20
2.8.1 Background and Description	20
2.8.2 Phenotypic Mass Selection in Maize Breeding	21
2.8.2 Uses of Mass Selection	22
2.8.3 Modifications in Mass Selection	24
2.8.4 Comparison of Mass Selection with Other Selection Procedures	26
3 MATERIALS AND METHODS	28
3.1 Source Populations	28
3.2 Controlled Hand Pollination	28
3.2.1 Covering of Ear-shoot	28
3.2.2 Collection of Pollen Grains	29
3.2.3 Pollination	29
3.3 Crossing and Development of Base Populations	29
3.4 Selection Experiments	30
3.5 Evaluation Experiments	31



3.6 Cultural Practices	33
3.7 Preparation of Seed Lots	34
3.8 Data Collection	35
3.9 Data Analysis	38
4 EVALUATION OF PARENTS AND DEVELOPMENT OF BASE POPULATIONS FOR SELECTION	41
4.1 Introduction	41
4.2 Materials and Methods	42
4.3 Results	43
4.4 Discussion	58
4.5 Conclusion	61
5 EVALUATION OF PERFORMANCE OF INTERMATED CROSSED POPULATION	63
5.1 Introduction	63
5.2 Materials and Methods	64
5.3 Results and Discussion	67
5.4 Conclusion	75
6 PHENOTYPIC MASS SELECTION FOR EAR LENGTH AND EVALUATION OF POPULATIONS GENERATED	76
6.1 Introduction	76
6.2 Materials and Methods	77
6.3 Results	84
6.3.1 Response to Selection	84
6.3.2 General Performance of Populations Generated from Selection	88
6.3.3 Broad-sense Heritability	124
6.3.4 Simple Phenotypic Correlations within Populations Generated from Selection	126
6.3.6 Distribution of Individual Plants for Ear Length in the Population	141
6.4 Discussion	144
6.4.1 Response to Selection	144
6.4.2 General Performance of Populations Generated from Selection	147
6.4.3 Broad-sense Heritability	151
6.4.4 Simple Phenotypic Correlations within Populations Generated from Selection	153
6.4.6 Distribution of Individual Plants for Ear Length in the Population	156
6.5 Conclusion	157
7 GENERAL DISCUSSION AND CONCLUSION	158
REFERENCES	165
APPENDICES	177
Appendix A: Additional Tables	178
Appendix B: Soil Characteristics of Locations	205



Appendix C: Ear Length Values Measured in Grids Used in the Selection Experiments	209
Appendix D: Grades of Ears Produced by Populations	212
Appendix E: Meteorological Data (1998/2001)	215
BIODATA OF THE AUTHOR	220



LIST OF TABLES

Table		Page
3.1	Outline of the ANOVA table in the analysis at individual location	39
4.1	Outline of the ANOVA table for effects of blocks and varieties, where data entry was a single value of each variety in a block	44
4.2	Outline of the ANOVA table for effects of blocks and varieties, where data entries were from various samples taken from each variety in a block	44
4.3	Mean squares from ANOVA for plant traits measured on individual plot basis, on three sweet corn varieties	45
4.4	Mean squares from ANOVA for plant traits measured on individual plant samples, on three sweet corn varieties	47
4.5	Mean values for yield and other characters measured on three sweet corn varieties	49
4.6	Maximum, on individual plants in three sweet corn varieties	52
4.6	Genotypic and phenotypic variances and broad-sense heritability estimates for traits measured on three sweet corn varieties	55
4.7	Simple phenotypic correlations among plant traits measured on three sweet corn varieties	56
5.1	Mean squares from ANOVA for plant traits measured on the intermated population cross, and its parents, Manis Madu and Hybrid SSC 240	68
5.2	Mean values for plant traits measured on the intermated population cross and its parents, Manis Madu and Hybrid SSC 240	68
5.3	Phenotypic variance (variance within intermated population), environmental variance (variance within Hybrid SSC 240) and broad-sense heritability estimates for traits measured in the study	70
5.4	Simple phenotypic correlation coefficients among plant traits measured on the intermated population cross	70
6.1	Outline of the ANOVA table in the analysis at individual location	
6.2	Outline of the ANOVA table in the combined analysis over Locations	83
6.3	Estimates of predicted response to selection for ear length measured on sweet corn populations generated from two cycles of phenotypic mass selection on Manis Madu (M), and the cross Manis Madu x SSC 240 (MS)	85
6.4	Mean values and realized response to two cycles of phenotypic mass selection for ear length, measured on sweet corn populations of Manis Madu (M), and the cross Manis Madu x SSC 240, from evaluations at Field 2 and Share Farm	87



6.5	Comparison between predicted and realised responses to selection for ear length measured on sweet corn populations generated from two cycles of phenotypic mass selection on Manis Madu (M), and the cross Manis Madu x SSC 240 (MS)	89
6.6	Mean squares in ANOVA for traits measured on populations generated from selection and the base population of Manis Madu (M), evaluated at Field 2 and Share Farm	91
6.7	Mean squares in ANOVA for traits measured on populations generated from selection and the base population Manis Madu (M), evaluated at the two locations combined	93
6.8	Mean squares in ANOVA for traits measured on populations generated from selection and the base population of the cross Manis Madu x SSC 240 (MS), evaluated at Field 2 and Share Farm	95
6.9	Mean squares in ANOVA for traits measured on populations generated from selection and the base population of the cross Manis Madu x SSC 240 (MS), evaluated at the two locations combined	98
6.10	Mean values for traits measured on populations generated from selection and the base population of Manis Madu (M), evaluated at Field 2	100
6.11	Mean values for traits measured on populations generated from selection and the base population of Manis Madu (M), evaluated at Share Farm	102
6.12	Mean values for traits measured on populations generated from selection and the base population of Manis Madu (M), evaluated at the two locations combined	104
6.13	Mean values for traits measured on populations generated from selection and the base population of the cross Manis Madu x SSC 240 (MS), evaluated at Field 2	112
6.14	Mean values for traits measured on populations generated from selection and the base population of the cross Manis Madu x SSC 240 (MS), evaluated at Share Farm	114
6.15	Mean values for traits measured on populations generated from selection and the base population of the cross Manis Madu x SSC 240 (MS), evaluated at the two locations combined	116
6.16	Genetic variances (σ^2_G), phenotypic variances (σ^2_{ph}), and broad-sense heritability estimates (h^2_B) for traits measured on populations of Manis Madu and the cross Manis Madu x SSC 240	125
6.17	Simple phenotypic correlations among some traits measured on selected Manis Madu populations, M C1 (above diagonal) and M C2 (below diagonal), evaluated at Field 2	127
6.18	Simple phenotypic correlations among some traits measured on selected Manis Madu populations, M C1 (above diagonal) and M C2 (below diagonal), evaluated at Share Farm	129
6.19	Simple phenotypic correlations among some traits measured on selected Manis Madu populations, M C1 (above diagonal) and M C2 (below diagonal), evaluated at the two locations combined	132

6.20	Simple phenotypic correlations among some traits measured on selected populations of the cross Manis Madu x SSC 240, MS C1 (above diagonal) and MS C2 (below diagonal), evaluated at Field 2	134
6.21	Simple phenotypic correlations among some traits measured on selected populations of the cross Manis Madu x SSC 240, MS C1 (above diagonal) and MS C2 (below diagonal), evaluated at Share Farm	137
6.22	Simple phenotypic correlations among some traits measured on selected populations of the cross Manis Madu x SSC 240, MS C1 (above diagonal) and MS C2 (below diagonal), evaluated at the two locations combined	139
A.1	Results of test of homogeneity for errors variances from the ANOVA on performance of Manis Madu populations (M), evaluated at Field 2 and Share Farm	179
A.2	Results of test of homogeneity for errors variances from the ANOVA on performance of populations of the cross, Manis Madu x SSC 240 (MS), evaluated at Field 2 and Share Farm	180
A.3	Maximum, minimum and mean values for fresh husked ear yield measured on populations of Manis Madu (M), and the cross Manis Madu x SSC 240 (MS), evaluated at Field 2 and Share Farm, and the two locations combined	181
A.4	Maximum, minimum and mean values for fresh dehusked ear yield measured on populations of Manis Madu (M), and the cross Manis Madu x SSC 240 (MS), evaluated at Field 2 and Share Farm, and the two locations combined	182
A.5	Maximum, minimum and mean values for plant height measured on populations of Manis Madu (M), and the cross Manis Madu x SSC 240 (MS), evaluated at Field 2 and Share Farm, and the two locations combined	183
A.6	Maximum, minimum and mean values for ear height measured on populations of Manis Madu (M), and the cross Manis Madu x SSC 240 (MS), evaluated at Field 2 and Share Farm, and the two locations combined	184
A.7	Maximum, minimum and mean values for number of ears ha ⁻¹ counted on populations of Manis Madu (M), and the cross Manis Madu x SSC 240 (MS), evaluated at Field 2 and Share Farm, and the two locations combined	185
A.8	Maximum, minimum and mean values for tassel branch number counted on populations of Manis Madu (M), and the cross Manis Madu x SSC 240 (MS), evaluated at Field 2 and Share Farm, and the two locations combined	186
A.9	Maximum, minimum and mean values for days to tasseling counted on populations of Manis Madu (M), and the cross Manis Madu x SSC 240 (MS), evaluated at Field 2 and Share Farm, and the two locations combined	187

A.10	Maximum, minimum and mean values for days to silking counted on populations of Manis Madu (M), and the cross Manis Madu x SSC 240 (MS), evaluated at Field 2 and Share Farm, and the two locations combined	188
A.11	Maximum, minimum and mean values for days to maturity counted on populations of Manis Madu (M), and the cross Madu x SSC 240 (MS), evaluated at Field 2 and Share Farm, and the two locations combined	189
A.12	Maximum, minimum and mean values for fresh husked ear weight measured on populations of Manis Madu (M), and the cross Manis Madu x SSC 240 (MS), evaluated at Field 2 and Share Farm, and the two locations combined	190
A.13	Maximum, minimum and mean values for fresh dehusked ear weight measured on populations of Manis Madu (M), and the cross Manis Madu x SSC 240 (MS), evaluated at Field 2 and Share Farm, and the two locations combined	191
A.14	Maximum, minimum and mean values for husked ear length measured on populations of Manis Madu (M), and the cross Manis Madu x SSC 240 (MS), evaluated at Field 2 and Share Farm, and the two locations combined	192
A.15	Maximum, minimum and mean values for dehusked ear length measured on populations of Manis Madu (M), and the cross Manis Madu x SSC 240 (MS), evaluated at Field 2 and Share Farm, and the two locations combined	193
A.16	Maximum, minimum measured on populations of Manis Madu (M), and the cross Manis Madu x SSC 240 (MS), evaluated at Field 2 and Share Farm, and the two locations combined	194
A.17	Maximum, minimum and mean values for dehusked ear diameter measured on populations of Manis Madu (M), and the cross Manis Madu x SSC 240 (MS), evaluated at Field 2 and Share Farm, and the two locations combined	195
A.18	Maximum, minimum and mean values for number of kernel rows/ear counted on populations of Manis Madu (M), and the cross Manis Madu x SSC 240 (MS), evaluated at Field 2 and Share Farm, and the two locations combined	196
A.19	Maximum, minimum and mean values for number of kernels/row counted on populations of Manis Madu (M), and the cross Manis Madu x SSC 240 (MS), evaluated at Field 2 and Share Farm, and the two locations combined	197
A.20	Maximum, minimum and mean values for kernel total soluble solids recorded on populations of Manis Madu (M), and the cross Manis Madu x SSC 240 (MS), evaluated at Field 2 and Share Farm, and the two locations combined	198
A.21	Simple phenotypic correlations among traits measured on Manis Madu populations (M), evaluated at Field 2	199



A.22	Simple phenotypic correlations among traits measured on Manis Madu populations (M), evaluated at Share Farm	200
A.23	Simple phenotypic correlations among traits measured on Manis Madu populations (M), evaluated at the two locations combined	201
A.24	Simple phenotypic correlations among traits measured on populations of the cross Manis Madu x SSC 240 (MS), evaluated at Field 2	202
A.25	Simple phenotypic correlations among traits measured on populations of the cross Manis Madu x SSC 240 (MS), evaluated at Share Farm	203
A.26	Simple phenotypic correlations among traits measured on populations of the cross Manis Madu x SSC 240 (MS), evaluated at the two locations combined	204

LIST OF FIGURES

Figure		Page
3.1	Schematic illustration of the phenotypic mass selection and evaluation procedures undertaken on two sweet corn populations	32
5.1	Distribution of individual plant performance for plant height at 21 days after planting on the population cross and its parents, Manis Madu and Hybrid SSC 240	71
5.2	Distribution of individual plant performance for number of leaves at 21 days after planting on the population cross and its parents, Manis Madu and Hybrid SSC 240	72
5.3	Distribution of individual plant performance for ear height measured on the population cross and its parents, Manis Madu and Hybrid SSC 240	73
5.4	Distribution of individual plant performance for ear length measured on the population cross and its parents, Manis Madu and Hybrid SSC 240	74
6.1	Individual plants distribution for ear length in the base and selected populations of Manis Madu (M), evaluated at Field 2	142
6.2	Individual plants distribution for ear length in the base and selected populations of Manis Madu (M), evaluated at Share Farm	143
6.3	Individual plants distribution for ear length in the base and selected populations of the cross (MS), evaluated at Field 2	145
6.4	Individual plants distribution for ear length in the base and selected populations of the cross (MS), evaluated at Share Farm	146
A.B1	Sand, silt and clay percentage in the soil of Field 2, with sandy loam texture and Share Farm, with sandy clay loam texture	206
A.B2	Average pH values in the soils of Field 2 and Share Farm, taken before planting	206
A.B3	The amount of nitrogen (N) available in the soils of Field 2 and Share Farm, taken before planting	207
A.B4	The amount of phosphorus (P) available in the soils of Field 2 and Share Farm, taken before planting	207
A.B5	The amount of potassium (K) available in soils of Field 2 and Share Farm, taken before planting	208
A.C1	Ear length measured in experimental grids on Manis Madu populations (M) in Cycle 0	210
A.C2	Ear length measured in experimental grids on Manis Madu populations (M) in Cycle 1	210
A.C3	Ear length measured in experimental grids on the cross populations (MS) in Cycle 0	211
A.C4	Ear length measured in experimental grids on the cross populations (MS) in Cycle 1	211
A.D1	Grades of ears produced by Manis Madu populations (M), evaluated at Field 2	213
A.D2	Grades of ears produced by Manis Madu populations (M), evaluated at Share Farm	213



A.D3	Grades of ears produced by the cross Manis Madu x SSC 240 populations (MS), evaluated at Field 2	214
A.D4	Grades of ears produced by the cross Manis Madu x SSC 240 populations (MS), evaluated at Share Farm	214
A.E1a	Monthly mean temperature at Universiti Putra Malaysia, in 1998 (source: Malaysian Meteorological Service, 2002)	216
A.E1b	Monthly mean rainfall at Universiti Putra Malaysia, in 1998 (source: Malaysian Meteorological Service, 2002)	216
A.E2a	Monthly mean temperature at Universiti Putra Malaysia, in 1999 (source: Malaysian Meteorological Service, 2002)	217
A.E2b	Monthly mean rainfall at Universiti Putra Malaysia, in 1999 (source: Malaysian Meteorological Service, 2002)	217
A.E3a	Monthly mean temperature at Universiti Putra Malaysia, in 2000 (source: Malaysian Meteorological Service, 2002)	218
A.E3b	Monthly mean rainfall at Universiti Putra Malaysia, in 2000 (source: Malaysian Meteorological Service, 2002)	218
A.E4a	Monthly mean temperature at Universiti Putra Malaysia, in 2001 (source: Malaysian Meteorological Service, 2002)	219
A.E4b	Monthly mean rainfall at Universiti Putra Malaysia, in 2001 (source: Malaysian Meteorological Service, 2002)	219

