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Evaluation of genetic variation and relationships among tropical sweet corn inbred lines using agronomic traits

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Abstract

Genetic variability and relationship of 13 tropical sweet corn inbred lines derived from different source populations were investigated using agronomic traits during three consecutive years. Non-significant effects of years and years-by-lines indicated the stability of performance of the inbred lines per se over years. Contrastively, the effects of inbred lines were significant for all traits measured, indicating great genetic variability in their performance. Among the inbred lines, TSN-S8, TSK-S8, BAK-S8, MAN-S8, MMIN-S8 and TSG-S8 were found to be high yielding, with high husked fresh ear yield, dehusked fresh ear yield and number of ears per hectare, while DFS-S8 and TFZ-S8 were found to be superior for ear characteristics including husked ear length, dehusked ear length, number of kernel rows per ear and TSS. The high heritability estimates obtained from husked and dehusked fresh ear yields in this study indicate that the inbred lines have become homozygous at almost all the loci after eight generations of selfing. Husked fresh ear yield was phenotypically and genetically correlated with dehusked fresh ear yield, number of ears per hectare, husked and dehusked ear weights, dehusked ear length, husked and dehusked ear diameter, number of kernels per row and number of kernel rows per ear, indicating direct positive contribution of these traits to husked fresh ear yield. Visualizing the relationship among the inbred lines using singular value decomposition biplot analysis revealed that the inbred lines could be assigned into three distinct groups. This indicates a strong indication of the potential of the inbred lines for their utilisation towards production of new hybrid varieties by crossing the inbred lines from different groups. It can be concluded that the inbred lines studied varied substantially in many aspects, and these differences could be exploited for specific purposes in breeding programs.

Keywords: sweet corn (*Zea mays* L *saccharata*), inbred line, genetic variation, agronomic traits

Introduction

Sweet corn inbred lines and hybrids developed in temperate environment routinely fail when planted in the tropics. This emphasizes the importance of inbred line development for hybrid production in the tropical environment. Inbred lines are genotypes characterized by the homozygosity of their genes. Utilization of inbred lines for hybrid variety production began in 1908, when Gorge H Shull (1908) proposed a method for producing corn hybrid cultivars. Inbred line development is the main prerequisite for production of hybrid varieties (Basra, 2002). This process is achieved through successive generations of inbreeding followed by repeated testing and selection. Inbreeding is the process of mating between genetically related individuals. The fundamental genetic change that inbreeding produces, the loss of heterozygosity, was well understood early in the development of the field of genetics (Wright, 1921; Marquez-Sanchez, 1998; Marquez-Sanchez, 2001). Selfing, the most extreme form of inbreeding, reduces heterozygosity by 50% each generation. The decrease in heterozygosity typically results in phenotypic changes that we call inbreeding depression, the genetic basis of which has been debated for almost a century. As a consequence of selfing, recessive genes, which were 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 sweet corn, inbred lines for hybrid varieties are developed through selfing. The source populations used for inbred line extraction should be superior. The common sources are open-pollinated varieties, single crosses, double crosses, synthetic varieties, composite varieties and other improved varieties (Hallauer and Miranda, 1988; Stoskopf et al, 1993; Poehlman and Sleper, 1995). Extensive studies on inbreeding depression in sweet corn (*Zea mays* L *saccharata*) have indicated that selfing is important in inbred line development because it leads to rapid gene homozygosity, whereby desirable dominant genes can be accumulated while the undesirable ones are eliminated (Saleh et al, 1993; Gallais, 2009). Selected plants are usually self-pollinated for several generations until homozygosity is reached. Hallauer and Miranda (1988) reported that many undesirable recessive genes are eliminated from families as a result of the inbreeding process, then selection is applied within and between lines for

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the best individual plants (Acquaah, 2007). Hallauer (1990) added that corn inbred lines developed from improved source populations would have greater vigor and grain yield as compared to those developed from unimproved sources. Stoskopf et al (1993) also cited that inbred lines are developed after five to seven generations of selfing, during which selection for characters of interest is also conducted. Since not all inbred lines produce superior hybrids, they should be selected appropriately on the basis of their performance in hybrid combinations.

In this experiment, a number of selected tropical inbred lines developed from various source populations were evaluated for their performance. The results were used to reveal heritability and phenotypic and genetic correlations of the traits measured, and to investigate the relationships among the inbred lines based on their agronomic performance.

Materials and Methods

Location of Experiment

The Study was conducted at Field 10, Faculty of Agriculture, Universiti Putra Malaysia, Serdang, Selangor, located at 2°59'28.66"N; 101°42'48.78"E, and 49 meters above sea level. The inbred lines were planted and evaluated three times from 2010 to 2012.

Plant materials

A series of 13 selected tropical near-homozygous inbred lines previously developed from various source populations of tropical origin through a long-term breeding program conducted at Faculty of Agriculture, Universiti Putra Malaysia were used as plant materials in this experiment. A commercial hybrid variety (Hybrid 968) was used as a control (Table 1).

Experimental design and cultivation practices

The evaluation was carried out in a Randomized Complete Block Design (RCBD) with three replications. Each replicate consisted of 14 plots, each represented by an inbred line. The planting density used was 0.75 m x 0.25 m. Each plot consisted of seven 12 m long plant rows, where the three middle rows measuring four meters in length were used as the harvest area. All experimental plots were subjected to the standard uniform agronomic practices over the three years.

Data collection

Data were collected from both pre- and post-harvest characters including days to tasselling, days to silking, plant height (cm), ear height (cm), number of ears per hectare, fresh ear yield (kg ha^{-1}), ear length (cm), ear diameter (mm), number of kernels per row, number of kernel rows per ear and total soluble solids concentration (TSS) (%).

Statistical analyses

The analysis of variance (ANOVA) was conducted using the General Linear Model (PROC GLM) of the Statistical Analysis System computer software (SAS Institute Inc, 2005) to determine the significance of variation among inbred lines. Subsequently, the Duncan's New Multiple Range Test (DNMRT) was applied for comparison of mean performance of the inbred lines and the control variety (Hybrid 968).

Simple phenotypic correlations among the traits were determined based on the formula suggested by Gomez and Gomez (1984) and calculated using PROC CORR procedure of SAS. PROC MIXED of the SAS software was used to estimate genetic correlation coefficients among the traits based on the method described by Kashiani and Saleh (2010a).

Broad-sense heritability (h^2_B) for each trait was estimated using the variance components based on the method suggested by Becker (1992). Heritability estimates were classified as low if values were lower than 20%, moderate if the estimates ranged from 20 to 50%, and high if they were greater than 50% (McWhirter, 1979).

A biplot analysis was run to visualize the relationship between lines and traits. Data matrix with columns representing the traits and rows representing the inbred lines was first standardized, then subjected to Principal Component Analysis (PCA) to obtain

Table 1 - List of inbred lines selected and the control variety, their source populations, countries of origin and population structures.

Inbred Line / Variety	Source Population	Country of Origin	Source Population Structure
BAK-S8	Bakti-1	Malaysia	Composite
TSG-S8	Thai Super Sweet	Thailand	Composite
TSK-S8	Thai Super Sweet	Thailand	Composite
TSN-S8	Thai Super Sweet	Thailand	Composite
TFZ-S8	Hybrid 240	USA	Single cross hybrid
DFS-S8	Hybrid D56	Taiwan	Single cross hybrid
IND-S8	Indo	Indonesia	Composite
MAS-S8	Mas Madu	Malaysia	Composite
MAN-S8	Manis Madu	Malaysia	Composite
MMIN-S8	Manis Madu x Indo	Malaysia	Cross between Manis Madu and Indo
THI-S8	Thailand	Thailand	Composite
SBY-S8	Surabaya	Indonesia	Composite
HAW-S8	Hawaiian	USA	Single cross hybrid
Hybrid 968 (control)	Commercial Variety	Thailand	Single cross hybrid

information on the traits most effective in discriminating the corn lines using SAS PROC PRINCOMP. The standardized table was then decomposed into principal components (PC) via singular value decomposition (SVD) using SAS PROC GPLOT.

Results

Performance of inbred lines

Results of the analysis of variance revealed that the effects of year and its interaction with inbred lines were not significant for all the traits measured. This shows the stability of the performance of the inbred lines over the years. The effects of blocks within years were significant only for husked fresh ear yield, number of ears per hectare, TSS and husked ear diameter, while effects of inbred lines were significant for all traits measured. The significant effects of lines indicate that the lines evaluated varied greatly in their performance. Average performance of the inbred lines and the control variety (Hybrid 968) over three years are presented in Table 2.

All the inbred lines evaluated had values significantly lower than those obtained from the control variety, Hybrid 968 for all the traits measured except plant and ear heights and number of days to tasseling and silking. The lower performance of the inbred lines is due to the effect of inbreeding depression after eight generations of self-pollination.

Among the inbred lines, the highest husked fresh ear yield was obtained from TSN-S8, with value of 6,549 kg ha^{-1}. However, this was not significantly higher than those of from TSK-S8, BAK-S8 and MAN-S8 (6,483, 6,402, and 5,798 kg ha^{-1}, respectively). The second group of inbred lines with highest husked fresh ear yield was MMIN-S8, DFS-S8, TFZ-S8 and TSG-S8, with mean values of 5,456, 5,334, 5,138, and 5,088 kg ha^{-1}, respectively. The lowest husked fresh ear yield was obtained from THI-S8 (3,453 kg ha^{-1}), followed by MAS-S8 (3,678 kg ha^{-1}), IND-S8 (3,722 kg ha^{-1}) and HAW-S8 (3,767 kg ha^{-1}). As expected, the variations revealed by the inbred lines for dehusked fresh ear yield were almost similar to those

Table 2 - Mean values for 16 agronomic traits measured on 13 sweet corn inbred lines and the control variety, Hybrid 968.

Line	Mean Value							
	Husked Fresh Yield (kg ha^{-1})	Dehusked Fresh Yield (kg ha^{-1})	No. of Ears per Hectare	Husked Ear Weight (g)	Dehusked Ear Weight (g)	TSS (%)	Husked Ear Length (cm)	Dehusked Ear Length (cm)
BAK-S8	6,402 b	4,630 cd	42,778ab	132.3 ef	94.5 f	9.7 h	19.3 bc	14.0 bcd
TSG-S8	5,088 cd	3,890 de	38,377 cd	142.6 cde	99.6 ef	9.9 h	18.6 bcd	13.9 bcd
TSK-S8	6,483 b	5,190 bc	40,815 bc	146.0 cde	102.9 ef	10.4 gh	15.9 def	12.3 cde
TSN-S8	6,549 b	5,731 b	44,218 ab	159.3 bcd	124.1 bcd	12.2 ef	15.7 def	12.6 cde
TFZ-S8	5,138 cd	4,256 de	35,550 defg	161.9 bc	134.1 bc	16.3 ab	20.3 bc	16.6 b
DFS-S8	5,334 c	4,433 cd	32,355 efgh	173.7 b	144.2 b	16.8 a	20.7 b	16.7 b
IND-S8	3,722 ef	2,407 f	34,802 defgh	91.1 i	58.4 g	12.6 ef	17.6 bcde	12.2 cde
MAS-S8	3,678 ef	2,470 f	31,696 fgh	101.7 hi	68.0 g	12.0 ef	18.0 bcde	13.9 bcd
MAN-S8	5,798 bc	4,495 cd	36,374 de	154.4 bcd	110.1 def	13.5 de	18.6 bcd	15.0 bc
MMIN-S8	5,456 c	4,289 de	45,926 a	155.2 bcd	119.0 cde	14.3 cd	20.0 bc	14.4 bcd
THI-S8	3,453 f	1,823 f	30,897 h	112.9 gh	60.5 g	15.3 bc	17.1 cde	13.0 cde
SBY-S8	4,432 de	3,584 e	35,984 def	140.4 edf	92.3 f	11.0 fgh	15.0 ef	11.6 ed
HAW-S8	3,767 ef	1,988 f	31,470 gh	121.4 gf	65.1 g	11.6 fg	13.7 f	10.3 e
Control	10,569 a	7,751 a	46,605 a	195.5 a	166.7 a	17.3 a	25.6 a	22.6 a

Line	Mean Value							
	Husked Ear Diameter (mm)	Dehusked Ear Diameter (mm)	No. of Kernels per Row	No. of Kernel Rows per Ear	Plant Height (cm)	Ear Height (cm)	Days to Tasseling (number)	Days to Silking (number)
BAK-S8	30.2 gh	26.9 gh	21.2 defgh	12.6 bc	145.7 a	69.1 bcd	54.8 bcde	57.5 bcd
TSG-S8	36.4 cde	33.3 cde	23.6 cdef	11.4 c	130.3 abcd	73.7 abc	54.0 cdef	56.0 de
TSK-S8	40.7 b	37.6 b	29.2 bcd	11.8 c	116.3 bcde	65.8 cde	59.3 a	63.0 a
TSN-S8	37.6 bcd	33.2 cde	27.8 bcde	11.4 c	109.9 bcde	77.0 ab	57.0 abcde	58.3 bcd
TFZ-S8	39.6 bc	36.1 bc	29.0 bcde	15.3 a	108.2 cde	68.5 bcde	53.0 f	56.3 cde
DFS-S8	40.7 b	38.9 ab	34.2 ab	14.5 ab	132.3 abc	70.5 bc	53.7 def	56.0 de
IND-S8	27.7 h	24.8 h	20.3 efgh	10.8 c	106.2 de	74.7 abc	55.0 bcde	56.3 cde
MAS-S8	30.8 fgh	26.0 gh	14.6 gh	11.8 c	123.5 abcde	60.3 def	58.0 abc	63.3 a
MAN-S8	35.3 de	31.9 def	23.2 cdefg	12.4 bc	126.4 abcd	65.9 cde	57.3 abcd	60.0 abcd
MMIN-S8	38.8 bcd	35.1 bcd	30.6 bc	12.7 bc	146.8 a	81.3 a	58.0 abc	60.3 abc
THI-S8	33.8 ef	28.7 fgh	15.6 fgh	11.9 c	132.8 ab	67.8 bcde	59.0 ab	60.7 ab
SBY-S8	33.2 efg	29.9 efg	18.4 fgh	10.5 c	101.6 f	58.6 ef	59.7 a	63.7 a
HAW-S8	29.6 h	27.4 gh	12.8 h	10.5 c	83.8 f	53.5 f	55.7 abcde	58.0 bcd
Control	46.1 a	41.9 a	39.8 a	15.7 a	133.3 ab	66.9 bcde	50.1 f	53.0 e

Means followed by the same letter in the same column are not significantly different at $p \leq 0.05$ based on DNMRT.

Table 3 - Genotypic variances (σ^2_G), phenotypic variances (σ^2_P) and broad-sense heritability estimates (h^2_B) for traits measured on 13 sweet corn inbred lines.

Trait	σ^2_G	σ^2_P	h^2_B (%)
Husked Fresh Yield	1,206,840	1,375,301	87.8
Dehusked Fresh Yield	1,479,981	1,698,262	87.2
No. of Ears per Hectare	28,505,941	3,4260,111	83.2
Husked Ear Weight	575.55	701.93	82.0
Dehusked Ear Weight	765.84	901.03	85.0
Total Soluble Solids	5.26	6.09	86.5
Husked Ear Length	3.68	6.77	54.4
Dehusked Ear Length	2.64	5.01	52.7
Husked Ear Diameter	18.43	22.31	82.6
Dehusked Ear Diameter	19.72	24.89	79.2
No. of Kernels per Row	37.54	60.27	62.3
No. of Kernel Rows per Ear	1.56	3.05	51.2
Plant Height	291.94	405.29	72.0
Ear Height	49.34	78.98	62.5
Days to Tasseling	3.77	7.96	47.4
Days to Silking	6.85	10.69	64.1

of husked fresh ear yield, where TSN-S8 and TSK-S8 produced the highest dehusked fresh ear yield (5,731 and 5,190 kg ha^{-1}, respectively) among the inbred lines evaluated.

Among the inbred lines, the highest husked and dehusked ear weights were obtained from DFS-S8 (173.7 and 144.2 g), followed by TFZ-S8 (161.9 and 134.1 g), TSN-S8 (159.3 and 124.1 g), MMIN-S8 (155.2 and 119.0 g) and MAN-S8 (154.4 and 110.1 g). BKT-S8 was found to have produced small ears with the weight of 132.3 g with husk and 94.5 g without husk, although it was found to be one of the high-yielding inbred lines. DFS-S8 and TFZ-S8 had also the highest percentage of TSS among the inbred lines (16.8% and 16.3%, respectively) which was not significantly lower than that of the hybrid variety (17.3%). BKT-S8 and TSG-S8, which were derived from local open-pollinated varieties, were found to have the lowest TSS with values of 9.7% and 9.9%, respectively. Among the inbred lines, the highest husked and dehusked ear diameters, and number of kernels per row were obtained from DFS-S8 (40.7 and 38.9 cm, and 34.2, respectively). Among the inbred lines, TFZ-S8, DFS-S8 and TSG-S8 were found to be the earliest in tasseling and silking. These variations indicate the superiority of DFS-S8 and TFZ-S8 as parental lines for production of new hybrid varieties.

Broad-sense heritability estimates

Genotypic and phenotypic variances and broad-sense heritability (h^2_B) estimates for yield and yield components measured on the inbred lines are shown in Table 3. All traits measured on the inbred lines showed high broad-sense heritability except for days to tasseling. Husked and dehusked fresh ear yield were found to be the most heritable traits in the inbred lines, with heritability estimates of 87.8% and 86.5% (Table 3).

Correlations among traits

Results on phenotypic correlations among characters measured on the inbred lines are presented in Table 4. Based on phenotypic correlation estimates, Husked fresh ear yield was found to be highly positively correlated with dehusked fresh ear yield, number of ears per hectare, husked ear weight, dehusked ear weight, husked ear length, dehusked ear length, husked ear diameter, dehusked ear diameter, number of kernels per row and number of kernel rows per ear, with correlation coefficients of 0.95, 0.61 0.79, 0.77, 0.58, 0.70, 0.69, 0.66, 0.70, and 0.56, respectively, but negatively correlated with days to tasseling and days to silking (r = -0.48 and -0.44, respectively).

Results on genetic correlations among characters measured on the inbred lines are presented in Table 4. Husked fresh ear yield was found to be highly genetically correlated (at $p \leq 0.01$) with dehusked fresh ear yield, number of ears per hectare, number of kernels per row, husked ear weight, dehusked ear weight, dehusked ear diameter, husked ear diameter and ear height, with correlation coefficients of 0.97, 0.84, 0.79, 0.77, 0.77, 0.63, 0.62, and 0.47, respectively, and correlated (at $p \leq 0.05$) with plant height, number of kernel rows per ear and dehusked ear length (r = 0.39, 0.34, and 0.33, respectively).

Association of traits with inbred lines

Biplot analysis was used to visualize and depict the relationships between inbred lines and the traits measured. It was generated by singular value decomposition on two-way data table for lines and traits. The importance of various variables in distance computation was balanced by standardizing the variables. The singular value decomposition biplot presented in Figure 1 confirms results of the correlation analysis, and also gives more details to enhance the interpretation of the data.

Husked fresh ear yield was found to be highly positively correlated with dehusked fresh ear yield and number of ears per hectare. TSS, days to tasseling and days to silking were not positively correlated with husked fresh ear yield as depicted by the

Table 4 - Simple phenotypic correlation coefficients (below diagonal) and genetic correlation coefficients (above diagonal) among traits measured on 13 sweet corn inbred lines.

Trait	Correlation Coefficient															
	HY	DHY	NE	HEW	DEW	TSS	HEL	DEL	HED	DED	NKR	NKRE	PH	EH	DT	DS
HY		0.97**	0.84**	0.77**	0.77**	-0.19	0.28	0.33*	0.62**	0.63**	0.79**	0.34*	0.39*	0.47**	-0.07	-0.08
DHY	0.95**		0.79**	0.82**	0.85**	-0.08	0.34*	0.43**	0.72**	0.62**	0.89**	0.42**	0.31*	0.51**	-0.05	-0.04
NE	0.61**	0.63**		0.51**	0.52**	-0.41*	0.18	-0.01	0.29	0.27	0.55**	0.08	0.48**	0.72**	0.10	-0.00
HEW	0.79**	0.85**	0.38*		0.99**	0.38*	0.47**	0.66**	0.87**	0.90**	0.89**	0.73**	0.28	0.33*	-0.23	-0.19
DEW	0.77**	0.85**	0.35*	0.93**		0.47**	0.64**	0.81**	0.88**	0.89**	0.94**	0.87**	0.31*	0.49**	-0.35*	-0.26
TSS	0.28	0.26	-0.03	0.42*	0.45**		0.63**	0.77**	0.45**	0.44**	0.48**	0.83**	0.12	0.25	-0.28	-0.27
HEL	0.58**	0.51**	0.33*	0.47**	0.58**	0.52**		0.99**	0.46**	0.48**	0.73**	0.98**	0.90**	0.73**	-0.61**	-0.46**
DEL	0.70**	0.63**	0.26	0.61**	0.69**	0.60**	0.91**		0.65**	0.68**	0.71**	0.99**	0.73**	0.53**	-0.58**	-0.41*
HED	0.69**	0.74**	0.34*	0.77**	0.80**	0.54**	0.50**	0.63**		0.98**	0.97**	0.77**	0.29	0.45**	-0.04	0.00
DED	0.66**	0.72**	0.30*	0.78**	0.81**	0.50**	0.45**	0.56**	0.97**		0.99**	0.77**	0.22	0.40*	-0.17	-0.10
NKR	0.70**	0.75**	0.41*	0.74**	0.79**	0.42*	0.57**	0.68**	0.76**	0.74**		0.89**	0.47**	0.85**	-0.41*	-0.40*
NKRE	0.56**	0.54**	0.17	0.63**	0.67**	0.63**	0.66**	0.71**	0.56**	0.55**	0.52**		0.54**	0.40*	-0.63**	-0.39*
PH	0.29	0.29	0.40*	0.23	0.30*	0.26	0.49**	0.34*	0.33*	0.28	0.25	0.24		0.53**	0.02	0.01
EH	0.17	0.27	0.46**	0.14	0.24	0.23	0.29	0.13	0.25	0.22	0.30*	0.12	0.55**		-0.29	-0.50**
DT	-0.48**	-0.42*	-0.14	-0.39*	-0.49**	-0.37*	-0.54**	-0.61**	-0.30*	-0.32*	-0.36*	-0.55**	-0.14	-0.11		0.96**
DS	-0.44**	-0.39*	-0.19	-0.36*	-0.45**	-0.39*	-0.48**	-0.50**	-0.30*	-0.33*	-0.33*	-0.48**	-0.18	-0.23	0.92**	

n = 39

** and * = significant at $p \leq 0.01$ and $p \leq 0.05$, respectively

HY = husked fresh ear yield, DHY = dehusked fresh ear yield, NE = number of ears per hectare, HEW = husked ear weight, DEW = dehusked ear weight, TSS = total soluble solids concentration, HEL = husked ear length, DEL = dehusked ear length, HED = husked ear diameter, DED = dehusked ear diameter, NKR = number of kernels per row, NKRE = number of kernel rows per ear, PH = plant height, EH = ear height, DT = days to tasseling, and DS = days to silking

angle between the vectors of these traits larger than 90°. In general, days to tasseling and days to silking were found to have negative relationship with all traits measured.

Figure 1 clearly shows that the inbred lines evaluated could be categorized into three main groups, i.e. as inbred lines with high yield but low quality (Group I), inbred lines with high quality and moderate yield (Group II), and inbred lines with low yield and quality (Group III). Among the inbred lines, TSN-S8, TSK-S8, BAT-S8, MAN-S8, MMIN-S8, and TSG-S8 were found to be the high yielding inbred lines (Group I), while THI-S8, MAS-S8, IND-S8, HAW-S8, and SBY-S8 were the low yielding ones (Group III). DFS-S8 and TFZ-S8 were found to be the lines with better quality for ear characteristics, which include husked and dehusked ear lengths, number of kernel rows per ear and TSS (Group II). In Group III, SBY-S8 was found to be slightly deviated from THI-S8, MAS-S8, IND-S8, and HAW-S8 as it was the inbred line latest in tasseling and silking. The control variety (Hybrid 968) was separated from the inbred lines evaluated since it possessed high yield and high quality simultaneously.

Discussion

The significant differences in yield and yield components between the inbred lines evaluated and the control variety (Hybrid 968) indicate drastic decrease in the performance of inbred lines which after undergoing eight generations of selfing, as expected. Other investigators also reported that performance of lines obtained from selfing decreased, resulting in yield reduction, reduction in plant resistance to pests and diseases, reduction in growth rate, and increase in the number of stunted plants and days to tasseling and silking (Genter, 1971; Harris et al, 1972; Hallauer and Sears, 1973; Cornelius and Dudley, 1974; Saleh et al, 1993; Kashiani et al, 2010). Hybrid 968 was found to have husked fresh ear yield, dehusked fresh ear yield, husked ear weight and dehusked ear weight significantly higher than all the inbred lines evaluated. This indicates that yield characters experienced a higher rate of inbreeding in the inbred lines as they were controlled by a higher number of genes (Genter, 1970, 1971; Harris et al, 1972; Marsum, 1972; Hallauer and Sears, 1973; Cornelius and Dudley, 1974; Saleh et al, 1993; Kashiani et al, 2010)

The inbred lines evaluated showed a wide range of performance for husked fresh ear yield and its components. This indicates that these inbred lines varied substantially in many aspects, and these differences could be exploited for specific purposes in breeding programs. Among the inbred lines, TSN-S8, TSK-S8, BAK-S8, MAN-S8, MMIN-S8, and TSG-S8 were found to be high yielding, with high husked fresh ear yield, dehusked fresh ear yield and number of ears per hectare. The superiority of these inbred lines for fresh ear yield and number of productive ears per hectare was also revealed through biplot analysis, in which the relationship between the inbred lines evaluated and the traits measured was visualized. Kashiani et al (2010) reported that inbred lines extracted from the source populations Bakti-1, Thai Super Sweet, Manis Madu and MM x Indonesia performed better than the rests for fresh ear yield and number of productive ears per hectare.

Inbred lines DFS-S8 and TFZ-S8 which were derived from single-cross hybrid source populations were found to be superior for ear characteristics including husked ear length, dehusked ear length, number of kernel rows per ear and TSS, compared to the other inbred lines evaluated. Result of the biplot analysis indicates that these inbred lines are placed

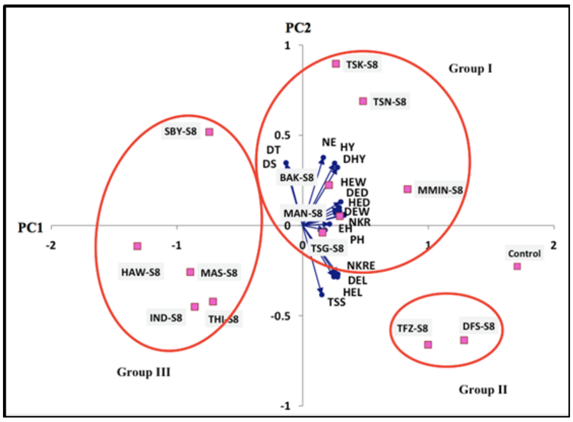

Figure 1 - Singular value decomposition biplot showing the relationships among traits measured and sweet corn inbred lines and one control variety grown under optimum condition at Field 10, UPM.

in a separate group far from the other inbred lines studied. Poehlman and Sleper (1995) reported that the inbred lines developed from single-cross hybrid source populations passed down better characteristics to their progenies compared to those derived from other kinds of population sources. Similarly, Hallauer (1990) emphasized that corn inbred lines developed from improved source populations would have greater vigor and grain yield as compared to those developed from unimproved sources. There is therefore a strong indication of the potential of these inbred lines for their utilisation towards production of new hybrid varieties and they could be short listed for further testing for general and specific combining abilities towards development of hybrid varieties.

Among the inbred lines, THI-S8, IND-S8, MAS-S8, HAW-S8, and SBY-S8 were found to be low yielding, late in maturity and tall. The result of singular value decomposition biplot revealed that these inbred lines were separated from the other inbred lines studied. Although HAW-S8 and SBY-S8 were developed from single-cross hybrid populations with high performance, they were found to be among the worst performing inbred lines in the study. This could be mainly due to the fixation of undesirable recessive alleles that in the hybrid source populations were preserved in large amounts by heterozygosity. Similar results where single-cross hybrids showing high inbreeding depression were not preferred as germplasm owing to their genetic backgrounds were also reported by Fasoulas (1988) and Kashiani and Saleh (2009, 2010b). Basra (2002) reported that single-cross hybrids with low inbreeding depression revealed a desirable load of genes that correspond to an F_2 capable of developing elite inbred lines.

All traits measured in the study were found to have high to moderate broad-sense heritability (h^2_B), with estimates ranging from 87.8% (for husked fresh ear yield) to 47.4% (for days to tasseling). Similar results on broad-sense heritability were reported by Sujiprihati et al (2003) and Kashiani et al (2010) showing high estimates for number of days to silking, plant height, number of days to tasseling and ear height, while moderate for husked ear yield, total soluble solids concentration, number of kernel rows per ear, ear diameter, dehusked ear yield, number of kernels per row and number of ears per hectare. Saleh et al (2002) also reported high broad-sense heritability estimates for plant height and number of days to tasseling on selected sweet corn synthetic populations. This indicates that selection for these traits with high broad-sense heritability estimates in these inbred lines would be most effective for the expression of these traits.

Corn yield is a quantitative trait controlled by multiple loci located on different parts of the corn chromosomes and is highly influenced by environmental factors. Many investigators reported that segregation of heterozygous loci during meiosis led to low to moderate heritability for yield (Klein, 1974; Fernandez and Miller, 1985; Umakanth et al, 2000; Gusmini et al, 2007; Akbar et al, 2008; Kashiani et al, 2012b). However, advance inbred lines which are homozygous at almost all loci are able to pass almost the same characteristics to their progenies obtained from self-pollination, providing high estimates of heritability. Hence, the high heritability estimates obtained from husked and dehusked fresh ear yields in this study prove that the inbred lines have become homozygous at almost all the loci after eight generations of selfing. In addition, total genetic variation among the advanced inbred lines with homozygous loci is mainly due to additive gene effects. Therefore, the heritability estimates obtained from those inbred lines tend to be narrow-sense rather than broad-sense.

With regards to phenotypic relationships among the traits, fresh ear yield was positively correlated with yield components and agronomic traits, but negatively correlated with tasseling and silking traits. However, the result of genetic correlations revealed that there was no significant relationship between fresh ear yield and the flowering traits. This indicates that late flowering did not have any genetic relationship with yield reduction per se, but the yield of the inbred lines with late flowering was decreased by environmental factors such as different kinds of diseases, pests and biotic and abiotic stresses. Beebe (2009) reported up to 20% reduction of potential yield by biotic and abiotic stresses in any given environments. Generally, it was reported that higher corn yield was associated with early maturity more often than with late maturity (Espinoza and Ross, 2007).

Genetic correlation coefficients reveal stronger relationship between fresh ear yield and number of ears per hectare and number of kernels per row compared to phenotypic correlations. In contrast, husked ear length was highly correlated with fresh ear yield when based on phenotypic coefficient, but not correlated when based on genetic coefficient. Fresh ear yield was genetically correlated with plant and ear heights, but there was no relationship between these traits based on phenotypic values. This might be attributed to the high dry matter accumulation function carried out by the high number of leaves possessed by tall plants. Generally, husked fresh ear yield was found to be phenotypically and genetically correlated with dehusked fresh ear yield, number of ears per hectare, husked and dehusked ear weights, dehusked ear length, husked and dehusked ear diameter, number of kernels per row and number of kernel rows per ear. This indicates that high measurements of these traits had direct positive contribution to husked fresh ear yield. Therefore, for selection purposes to improve the inbred lines, it is suggested that emphasis should be given on these traits. The results on simple correlation coefficients from the present study were found to be similar to those reported by Martin and Russell (1984), Burak and Magoja (1991), Akanvou et al (1997), Wang et al (1999), Yousuf and Saleem (2001), Liu (2009), Kashiani and Saleh (2010a), Kashiani et al (2010), and Xie (2010).

In conclusion, significant differences in performance indicate that the inbred lines varied substantially among themselves for the traits measured in many aspects, and these differences could be exploited for specific purposes in breeding programs. Based on agronomic traits, the inbred lines could be divided into three main groups: those with high yield but low ear quality, those with moderate yield and high ear quality and those with low yield and low ear quality. This indicates that the inbred lines belong to different heterotic groups and could be used as promising parents for potential hybrid production. Since phenotypic values obtained from the inbred lines were influenced by environmental factors, analysis of molecular variation can be performed on the inbred lines as an additional tool to help in the selection process for superior parental lines toward hybrid variety development, before further analysis on general and specific combining abilities could be executed (Kashiani et al, 2012a).

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