Quantitative inheritance of total soluble solids and flour color in sweet-field corn crosses

Wahba, B. K., Zaki, H. E. M., Moustafa, Y. M. M., Abdel Ati, Y.Y. and Gadelhak, S.H.

Horticulture Department, Faculty of Agriculture, Minia University, El-Minia 61517, Egypt
haitham.zaki@mu.edu.eg

Abstract: In Egypt, field corn is growing well and fully adapted with the Egyptian environment however, it lacks sweetness which could be found in sweet corn. The main objective of this study is to evaluate the genetic parameters in two different sweet-field corn crosses using the generation mean analysis for total soluble solids (TSS) and kernels color. The F_1, F_2, BC_1P_1 and BC_1P_2 were produced from cross1 (Country Gentleman "P_1" X yellow field corn inbred 2605-1288Y"P_2") and cross2 (white field corn inbred 82 "P_1" X Golden Bantam "P_2"). Sweet corn cultivars had the highest TSS compared with field corn inbreds. However, the F_1 means in both crosses were higher than mid parent's values, but did not exceed those of their high parent suggesting partial dominance. Values of A, B and C of the scaling test were significant confirming the existence of non-allelic gene interaction. Broad and narrow sense heritability values were higher in cross 1than cross 2 and this increased the possibility of selection for high TSS contents in the studied materials. Additive and dominance gene effects of TSS values were significant and their values had similar or opposite signs. Kernel color was evaluated by Hunter L*, a* and b* parameters. The two parents of each cross were differed significantly for Hunter L*, a*, b* readings. The estimated genetic parameters of both three and six models on the studied populations indicated that additive and non-additive genetic effects were involved in the causes of the existing genetic variations of the L*, a* and b* color scale. Positive b* is an index of yellow color, the higher the values, the greater pigments content. In the studied crosses, F_1 values were between the midparent and lower parent in both crosses indicated the recessiveness. The estimated C values of the scaling model were significant when the A values were insignificant in both crosses. B values were insignificant in the cross1 and significant cross 2.The arithmetic and geometric F_2 means which suggest non-additive and additive genetic effects are contributed to the observed b* variations in both crosses. Furthermore, the estimated heritabilitieswere relatively high in broad sense, whereas those values in narrow sense were low in both crosses. The relative high heritability of b*values suggested that improving yellow color in sweet-field corn populations could be done.

Keywords: Quantitative inheritance, Total soluble solids, Kernel color, Hunter L*, a*, b* readings, Sweet-field corn crosses

1. Introduction

Maize or corn (*Zea mays*) has long been one of the most important food crops in the world being grown for both human and animal consumption (Farham *et al*., 2003.). Because of the importance of this crop, corn breeders have focused a great deal of attention on improvement of a number of generally valuable characteristics, such as yield, tolerance of environmental stress, and disease and insect resistance (Tracy, 1997.). For human consumption, particular efforts have been devoted to the development of a genotype with an improved taste, especially with respect to increasing the sweetness of the kernels. The most active area of research has been centered on manipulation of the endosperm genes which, to a large extent, controls the level of sugar in the kernel. Mature kernel as a whole is composed of 70–75% starch, 8–10% protein and 4–5% oil (Boyer and Hannah 1994). The amount of sugar in sweet corn depends on the type of corn, the variety, the maturity at the time of harvest and the post-harvest handling (Tracy and Hallaner, 1994). Three general types of sweet corn are recognized. Normal sugary (*su*) corn contains the *sugary1* gene mutation. Sugar enhanced (*se*) corn contains the *sugary enhancer1* gene mutation, in addition to *sugary1* (La Bonte and Juvik, 1990). *Super sweet* (*sh2*) corn has the *shrunken2* gene variation. Newer varieties may have a combination of all three genes. Brix readings range from 10–15% for *su* corn, 13–28% for *se* corn, and 25–35% for *sh2* corn. Sugars are converted to starch when the corn reaches maturation and after harvest. In *sh2* corn, this conversion is much reduced, leading to greater retention of sugar content after harvest(Maynard, 2010 a and b). Some of these genes are involved in altering carbohydrate synthesis (Creech, 1965 and Simla, 2009).

Generally, the kernel colors of sweet corn include a wide range of whites, yellows, and oranges, (Bonte and Jufik, 1990). Sweet corn had primarily white kernels until the year 1902 when Golden Bantam cv., a yellow variety, was developed. Then,

crosses were made and resulted in bi-color varieties. While the color of sweet corn kernels is important with regard to consumer preference, it does not have anything to do with flavor. The yellow color is based on particular carotenoids types and concentrations that are influenced by both genetic and environmental factors (Esiyok *et al*., 2004 and Esiyok and Bozokalfa, 2005). Major detected carotenoids were lutein and zeaxanthin, and to a lesser extent, *α*-, *β*-cryptoxanthin, *α*-, and *β*-carotene (Hallauer, 2001). Color characteristic`s values were reported by McGuire, 1992. The narrowness of present genetic variability of sweet corn was the result of the fact that most of today's sweet corn germplasm originates from only few open-pollinated varieties (Gerdes and Tracy, 1994). In general, inducing genetic variability of quantitative agronomic and yield traits is a key component of broadening the gene pool of crops (Allard, 2000).Field and sweet corn crosses were initiated in several sweet corn breeding programs (Kaukis and Davis, 1989). Some studies have pointed to the existence of differences among the types and inbreds of field corn and their ability to improve the quality of sweet corn (Tracy, 1994, Carta *et al*., 1996, Malvar *et al*., 1997 and Malvar *et al*., 2001). The difference between sweet and common or field corn is that in the genome of the former at least one of the eight genes which influence carbohydrate biosynthesis in the endosperm is mutant, preventing the conversion of carbohydrate to starch (Tracy *et al*. 2006 and Qi *et al*. 2009). These genes comprise;*shrunken-2* (*sh2*), *brittle* (*bt*), *amylose extender*(*ac*), *sugary enhancer* (*se*), *sugary* (*su*), and *brittle-2* (*bt2*), *dull*(du), and *waxy* (*wx*), all is monogenic and recessive. Among the corn cultivars with high sugar contents, the super-sweet corn cultivars stand out with even higher levels of carbohydrates than the sweet corn varieties (Oliveira *et al*. 2006).

To understand the gene action, the knowledge of genetic variances, levels of dominance and the importance of genetic effects are necessary (Wolf and Hallauer, 1977). Generation mean analysis is one of the genetic models which developed for the estimation of different gene effects (Kearsey and Pooni, 1996).It is a simple but useful technique toestimate gene effects for a polygenic trait and its greatest merit lying in the ability to estimate epistatic gene effects such as additive × additive, dominance × dominance and additive × dominance effects (Singh and Singh, 1992). Besides gene effects, breeders would also like to know how much of the variation in a crop is genetic and to what extent this variation is heritable, because efficiency of selection mainly depends on additive genetic variance, influence of the environment and interaction between genotype and environment. Very little work has been done in this area of joint scaling

test and sequential best fit model of generation mean analysis in sweet corn in Egypt. Moreover, as far as we know from the available literature, no report was conducted to quantitatively study Hunter colors readings in sweet-field corn populations. Meanwhile, the aim of this study is to estimate the genetic parameters in two different sweet-field corn crosses using generation mean analysis. In order to design an appropriate breeding strategy for improving sweetness and kernels color of sweet-field corn populations. Also, broad sense heritability, narrow sense heritability and number of effective factors for color subjective "L*, a* and b*" readings as well as total soluble solids (TSS) contents were measured.

2. Materials and Methods
Plant materials
Two USA sweet corn commercial cultivars (Country Gentleman cv. and Golden Bantam cv.) and two Egyptian field corn inbreds (yellow field corn "Inbred 2605-1 288Y" and white field corn "Inbred 82") were used in this study. A single plant from these initial materials was used as the parental parent in the summer season of 2013 to produce F_1 plants as shown in Figure 1. Also, F_1 plants from each mating were crossed in the Fall season of 2013 to produce BC_1P_1 ($P_1 \times F_1$) and BC_1P_2 ($P_2 \times F_1$) progeny, and it was also self-pollinated to generate F_2 progeny. All tested populations were formed by manual pollination using bulk pollen technique (as mentioned by Whaba, 2009).

Seeds from each of the six generations P_1, P_2, F_1, F_2, BC_1P_1 and BC_1P_2 were sown during the summer season of 2014 at the private farm of Wahba`s family, Taha Village, Minia Governorate, Egypt. The plants were spaced at 25 cm within rows, 70 cm apart and standard cultivation practices were followed according to The Egyptian Ministry of Agriculture recommendations for field corn production under valley soil conditions.

Total soluble solids measurement
In both crosses, total soluble solids "TSS" were determined according to the official methods of analysis "AOAC", 1995 using handheld refractometer model "FG103/113 measuring range 0~ 32%. Several drops of hand pressing immature kernels were carefully removed from each ear after 20–21 days from siliking. Three to four sites of the right side of first ear per plant were collected and placed on the prism surface of the instrument. The TSS contents were measured as ^{o}Brix in 0.1 % graduations.

Kernel colorestimation
This experiment was done at the Food Technology Dept., Faculty of Agriculture, Minia University, El-Minia, Egypt. At the maturity growth stage of each cross, the estimation of the kernel flour

color was detected using 25, 100 and 76 random plants from the parents and their F_1 plants, backcrosses and F_2 populations, respectively. To measure Hunter L*, a* and b* readings, the kernels from each plant were collected and air dried. Dry grain samples were powdered using electrical mill for

obtaining whole corn flour. Each grain sample was evaluated objectively by scoring their flour Hunter L*, a* and b* parameters using a colormet instrument "Color Tec PCM Color Meter Tec. NJ.USA" reflectance spectra model.
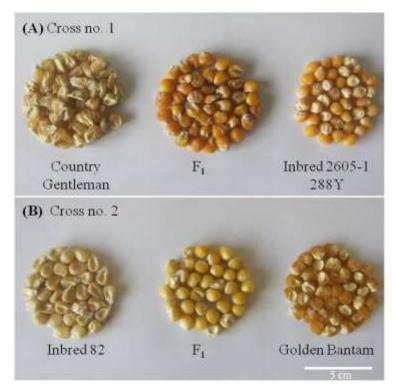

Figure 1. Grain color of two sweet-field corn crosses. (A) Cross no. 1 (Country Gentleman "P_1" X yellow field corn Inbred 2605-1 288Y "P_2") and (B) cross no. 2 (white field corn Inbred 82 "P_1" X Golden Bantam "P_2").

Statistical analysis

The recorded data were subjected to various statistical methods to shed light upon the dominance, the component of generation means, gene action, heritability and minimum number of operating genes. Also, the scaling test for A, B and C scales were calculated to examine the adequacy of simple additive-dominance model according to the method suggested by Mather (1949). Joint scaling test of Cavalli (1952) was applied to estimate mid-parental value (m), dominance (h) and additive (d) gene effects following the method proposed by Mather and Jinks, (1971). Hayman's equations (1958) were used to estimate the six-parameter model to explain the observed variation as suggested by Mather and Jinks (1977):

m= average effect = F_2.
d= additive effect = BC_1P_1- BC_1P_2.
h= dominance effect.
i= additive $\times$ additive interaction effect.
j= additive $\times$ dominance interaction effect.

L= dominance $\times$ dominance interaction effect.

These parameters were tested for significance using t-test with the tabular t values at n-1 degrees of freedom, where n is the number of plants used in estimating the variances of all generation involved. Phenotypic variances of the six generations were used to estimate the heritabilites based on the procedure proposed by Mather and Jinks (1971). Heritability was characterized as low ($<$30%), moderate (31-60 %) and high ($>$61%) as described by Robinson et $al.$ (1949). Number of effective factors controlling inheritance of each trait was estimated using the following equation (Burton, 1951 and Wright, 1968):

$F_2 = 0.25 (0.75 - h+h^2)D^2/(V_{F2} - V_{F1})$
Where h= $(F_1-P_2)/(P_1-P_2)$.
D= P_1-P_2.
P_1= mean of the female parent.
P_2= mean of the male parent.
F_1= mean of F_1 population.
F_2= mean of the F_2 population
V_{F1}= variance of the F_1 population.
V_{F2}= variance of the F_2 population.

3. Results and Discussion
Total Soluble Solids (TSS)

TSS contents showed different readings in each corn cross used; field and sweet corn genotypes with high significant differences (Table 1). Sweet corn cultivars had the highest TSS contents (21.23% and 19.41%) and white and yellow field in breds had the lowest TSS contents (9.02% and 8.02%). However, the F_1 means in both crosses were higher than mid parent's values, but did not exceed those of their high parent suggesting partial dominance. Also, the estimated potency values of both crosses confirmed the existence of partial dominance towards the high parent.

Differences between observed and calculated arithmetic F_2 means as well as close agreements between geometric and observed means suggested that non-additive gene effects influenced TSS contents in the first cross. In the second cross, observed F_2 mean was in good agreement with calculated arithmetic mean, indicating that additive effects contributed to the variation of this trait. A, B and C values of the scaling test were significant confirming the existence of non-allelic gene interaction and suggesting significant contribution of epistasis in controlling the inheritance of TSS contents in both crosses(Table 2). To exploit the gene effects for this trait, three and six parameters models were applied. The obtained results showed that the three parameters did not explain the whole variations of TSS in the tested materials whereas additive and dominance gene effects were significant and their values had similar or opposite signs (Table 3).

The first cross between Country Gentleman cv. and yellow field corn Inbred 2605-1288Y exhibited the presence of positive additive gene effects when the three and six parameters models were applied suggesting that selection in early generations was effective. On the other hand, negative additive genetic effects were observed in the second cross, which indicated that, no scope of improvement in early generations. In waxy corn, Simla *et al.* (2009) found that dominance and epistatic gene effects explained most of sucrose and total sugar contents in two crosses, however, attempts to improve waxy corn sweetness had not been succeeded (Creech, 1965). In the present study, duplicate epistasis was noticed in the first cross which had opposite signs of dominance (d) and dominance X dominance (l) interactions. These results suggested that recurrent selection or bi-parental mating in early segregating generations might prove to be effective to improve this trait as suggested by Shekhawat *et al.* (2006).

Broad sense heritability values for TSS were 63.61% in the first cross and 58.43% in the second one, suggesting the possibility of selection for high TSS values in the studied materials (Table 2). The obtained narrow sense values (60.04% and 54.39% for the first and the second crosses, respectively) implied that selection in early generations could be fruitful in both crosses whereas additive genetic effects contributed to a large extend of the behavior of this trait (Table 3). Cardosa *et al.* (2002) reported medium heritability values for TSS contents in Brazilian sweet corn.

Numbers of effective factors influencing TSS contents in sweet-field corn crosses were estimating using Wright (1969) formula. The estimated values were 18.88 and 16.41 loci in the first and second crosses, respectively (Table 2). These estimates relied on several assumptions as reported by Wright (1968). One of them might be quite improbable which pointed out that all factors had equal contribution to the observed value. Cardoso *et al.* (2002) pointed out that several genes were involved in the genetics of soluble solids content in Brazilian sweet corn.

Kernel colorestimation
Hunter L* reading

The two parents of each cross were differed significantly for this trait and the differences were greater in cross 2 (Table 1). The mean of the F_1 was greater than the high parent, suggesting the presence of over-dominance of genes with dark color. The potency values were 2.021 and 1.36 in the first and second crosses, respectively, which was also a proof of over-dominance of the high parent (Table 3). Transgressive segregation was observed in the F_2 and backcross population and F_2 individuals ranged from 65.2 to 81.5 scale in the first cross and from 75.1 to 88.2 in the second one. The performance of a backcross population was related to its recurrent parent. The A, B and C values deviated significantly from zero, indicating the presence of non-allelic interaction represented in high epistatic genetic effects in both crosses (Table 2).

Using F_2 means to explain the type of gene effects were varied in both crosses. There were good agreements among observed, arithmetic and geometric F_2 means in the second cross suggesting the contribution of additive and non-additive gene effects. But significant differences among them were detected in the first cross confirming the existence of additive genetic effects (Table 3).

The three and six parameter models revealed that the magnitude of additive component was lower than the dominance component, indicating the relative importance of dominance effect. The significant estimate of dominance gene effects was positive in both models. The results of the six parameters indicated that m, h, i, and l components played a significant role in both crosses. But the dominant (h) and dominant×dominant (l) type of genes action were

possessing opposite signs indicating the prevalence of duplicate type of epitasis(Table 3). Such type of gene effects would not enhance the isolation of superior recombination from the segregating generation. Hence, selection in early segregation generation could break some undesirable linkage producing few useful recombinations as mentioned before by Gamble (1962) and Jatothu *et al*. (2013).

For L* Hunter readings, the heritability values in the broad sense were 54.8% in the first cross and 10.93% in the second one. On the other side, in narrow sense, these values were 3.13% and 7.69% indicating the strong influence of environment on the behavior of this trait and suggesting that selection for higher L* values may be difficult in the early generation and it may be necessary to use another approach in order to obtain genetic progress in the evaluated population (Table 2).

The minimum number of genes controlling this trait was 4.15 in the first cross and 29.68 in the second one (Table 2). The results confirmed that genetic parameters could be vary from cross to another and from region to another and the materials should be tested under the prevailing conditions.

Hunter a* reading

According to McGuire (1992) positive a* indicates of red-purple and negative of bluish-green and when a*=0, the color is gray. Means for a* trait differed significantly among populations. Thea* values of P_1 ranged from 2.9 to 11.8 with a mean of 7.52 in cross 1 and from 3.8 to 9.5 and a mean of 5.91 in cross 2. While P_2 ranged from 6.33 to 14.72 and from 7.55 to 16.17 with means of 11.07 and 12.45 in cross1 and cross2, respectively (Table 1). The F_1 means in the two studied crosses tended towards the lower parent. The F_2 population exhibited transgressive segregation in both directions in the first cross and only in lower direction in the second cross. Mid parent values were 9.30 and 9.18 with F_1 means (7.17 and 7.26) in the first and the second cross, respectively. The potency values were -1.2 and -0.59, indicating nearly complete and partial dominance for lower parent in the first and second crosses, respectively over the higher parent (Table 2).

In F_2 populations, agreement between observed and arithmetic means as well as existing significant differences between observed and geometric means suggested additive gene action for this trait in the first cross was. The opposite trend was detected in the second cross, whereas significant differences were found between observed and both arithmetic and geometric means suggested that non-additive effects influenced the a* scale. For the joint scaling test, the probability was insignificant and less than 0.05 in the first cross and less than 0.01 in the second cross (Table 2). Therefore, the model is inadequate

indicating presence of non-allelic interaction in addition to both additive and non-additive genetic effects. The A, B and C scaling values were significant in both crosses indicating inadequacy of additive/dominance model; hence, six parameters model was applied to shed some lights on the causes of the existing genetic variations in these populations. In the mean time, the results of the individual scaling test suggested the major role of epistatic effect. In the application of six parameter model, additive X dominance and dominance X dominance interactions had positive insignificant values in the first cross. On the other hand, dominance, additive X additive and additive X dominance types of gene actions had significant effects in the second cross (Table 3). These results suggested that the observed variations in these populations depended on the investigated cross and opposite sign of dominance X dominance to dominance effects confirming the exiting of duplicate type of epistasis (Gamble, 1962 and Mbogo *et al*., 2015). The estimations of dominance X dominance in the first cross and dominance effects in the second cross were higher than additive values, indicating the importance of dominance gene effects.

Estimates of broad-sense heritability for this trait was medium (55.15%) in the first cross and was very low (15.15%) in the second cross. This low to moderate heritability values indicated that a large proportion of the phenotypic variance of a* reading was due to non-genetic effects. However, narrow-sense heritability values were 54.76% in the first cross and 14.49% in the second one (Table 1). These results suggested, in the first cross, that selection for higher a* value could be achieved in large population at later generation. The estimated number of factors which might be controlling the expression of this trait according to Burton formula (Wright, 1968) was 2.7 and 6.27 in the first and the second cross, respectively.

Hunter b* reading

Values of b*-reading referred to the concentration of color. Thompson, 1954 stated that b* is chroma factor and as the b* scale increases the concentration of appearance increases. Positive b* indicated of yellow color (McGuire, 1992), the higher the values, the greater pigments content. In the studied sweet-field corn populations, F_1 values were between the mid parent and lower parent in both crosses indicated the recessiveness of this trait. The potency ratio values of both crosses confirming the partially dominant of lower parent (Table 3).

Regarding the gene effects, the estimated C values of the Mather and Jinks, 1971 model were significant when the A values were insignificant in both crosses. On the other hand, B values were insignificant in the first cross and significant in the second one. According to Mother and Jinks, 1979, if

one or more of the A, B, and C values deviated significantly from zero, existence of epistasis was indicated for expression of the trait concerned. Meanwhile, the obtained results indicated that digenic epistasis involved in the expression of the b* trait in both crosses. Also, the results of the observed, arithmetic and geometric F_2 means suggesting that non-additive and additive genetic effects are contributed to the observed b* reading variation in both crosses (Table 3). The estimates of the three parameters model; (m), (d), and (h) are shown in Table (3). Values of (d) and (h) had negative signs in both crosses. This indicated that this simple model was inadequate to explain the inheritance of b* trait in cross 1 and cross 2. The results of six-parameter model are presented in Table (3). Values of additive (d), dominance (h), additive X additive (i), and dominance X dominance (l) were significant in the first cross while, in the second cross, additive X dominance (j) value was significant. Presence of significant interaction parameters along with existence of additive and dominance components indicated complex nature of the inheritance of b* trait in these populations. Also, the opposite sign of (h) and (l) in both crosses indicated that duplicate type of genetic effects controlled the expression of yellow color concentration trait in the studied sweet-field corn populations. Gamble (1962) showed that population means of parents, F_1, F_2 and backcrosses generations could be used to estimate the relative importance of the different types of gene effects and the resulting information is important for choosing appropriate strategy for improvement of target trait(s).

Estimation of heritability was relatively high in broad sense (73.21% in the first cross and 60.03% in the second cross), whereas those values in narrow sense were 35.28% and 56.17% in the first and second crosses, respectively. These results suggested that most of the total genetic variances were associated with dominance effect in the first cross for this trait. But the relative high heritability values in the second cross suggested that improving yellow color in sweet-field corn could be done. Number of effective factors controlling segregating for b* trait were 17.4 and 31.2 in the first and second crosses, respectively.

Table1. Total soluble solid (TSS) and kernels flour color values (mean $\pm$ SE) and range (-) for two sweet X field corn crosses in parental, F_1, F_2, and backcrosses generations.

Generation	No. of tested plants	Mean of TSS$\pm$SE	No. of tested plants	Means of Hunter readings $\pm$ SE		
				L*	a*	B*
Cross No. 1 (Country Gentleman "P_1" X Yellow field corn Inbred2605-1 288Y "P_2")						
P_1	39	21.23$\pm$0.17 (19-23)	25	71.50 $\pm$ 0.51 (66.1-75.6)	7.52 $\pm$ 0.49 (2.9-11.8)	14.05$\pm$0.40 (11.7-20.1)
P_2	41	9.02$\pm$0.15 (8 – 11)	25	74.80 $\pm$ 0.33 (70.7-77.7)	11.07 $\pm$ 0.41 (6.3-14.7)	25.62$\pm$0.48 (21.5-31.3)
F_1	44	16.13$\pm$0.19 (15 – 20)	25	76.49 $\pm$ 0.61 (69.9-81.1)	7.17 $\pm$ 0.37 (4.1-11.7)	18.17$\pm$0.48 (12.2-23.0)
F_2	249	14.69$\pm$0.12 (8 – 21)	100	74.75 $\pm$ 0.35 (65.2-81.5)	8.07 $\pm$ 0.31 (2.2-16.6)	19.98$\pm$0.44 (9.3-33.6)
BC_1P_1	100	16.52$\pm$0.15 (12 – 21)	76	75.21 $\pm$ 0.37 (67.9-81.4)	7.23 $\pm$ 0.30 (1.0-13.7)	16.46$\pm$0.54 (8.9-31.2)
BC_1P_2	92	12.83$\pm$0.18 (10 – 16)	76	77.16 $\pm$ 0.43 (68.7-83.1)	8.71 $\pm$ 0.31 (3.2-21.6)	20.93$\pm$0.36 (14.8-29.8)
Cross No. 2 (White field corn Inbred 82 "P_1" X Golden Bantam "P_2")						
P_1	43	8.02$\pm$0.14 (7-10)	25	78.53$\pm$0.35 (74.9-81.0)	6.67$\pm$0.28 (3.8-9.5)	11.87$\pm$0.22 (9.49-14.24)
P_2	42	19.41$\pm$0.17 (18 – 21)	25	67.44$\pm$0.44 (64.1-70.5)	11.86 $\pm$0.52 (7.6-16.2)	26.93$\pm$0.36 (22.98-30.88)
F_1	41	14.63$\pm$0.13 (13 – 16)	25	80.55$\pm$0.34 (77.3-84.0)	7.68 $\pm$0.38 (4.2-11.1)	15.55$\pm$0.50 (10.30-20.80)
F_2	151	14.48$\pm$0.12 (9 – 19)	100	80.54$\pm$0.22 (75.1-88.2)	8.91$\pm$0.21 (2.6-15.2)	13.78 $\pm$0.35 (5.52-22.03)
BC_1P_1	104	9.913$\pm$0.14 (7 – 13)	76	79.79$\pm$0.20 (74.1-83.0)	8.77$\pm$ 0.23 (3.9-13.6)	14.87$\pm$0.31 (8.6-21.13)
BC_1P_2	108	15.88$\pm$0.096 (14 – 19)	76	77.00$\pm$0.24 (70.98-80.2)	8.63$\pm$0.23 (4.4-12.9)	18.25$\pm$0.21 (13.36-23.14)

Table 2. Estimates of broad and narrow sense heritabilities, potency ratio, arithmetic, geometric and observed means F$_2$, minimum number of factors and A, B and C scaling test values for cross1 (Country Gentleman "P$_1$" X Yellow Field Corn Inbred 2605-128Y "P$_2$") and cross 2 (White Field Corn Inbred 82 "P$_1$" X Golden Bantam "P$_2$").

Genetic Parameters	TSS	L*	a*	b*
Cross No. 1 (Country Gentleman "P$_1$" X Yellow field corn Inbred2605-1 288Y "P$_2$")				
Broad sense heritability (H)	63.61	54.80	55.15	73.21
Narrow sense heritability (h^2)	60.04	3.13	54.76	35.28
Mid-parent	15.13	73.15	9.30	19.84
Potence ratio	-0.17	2.02	-1.20	-0.29
Arithmetic mean F$_2$	15.63**	74.82^{ns}	8.23^{ns}	19.00^{ns}
Geometric F$_2$	14.95^{ns}	74.79^{ns}	8.09^{ns}	18.57^{ns}
Observed mean F$_2$	14.69	74.75	8.07	19.98
Minimum no. of genetic Factor (n)	18.88	4.15	2.70	17.43
Scaling test A	-4.33**	2.43*	-0.23^{ns}	0.70^{ns}
Scaling test B	0.49^{ns}	3.03*	-0.82^{ns}	-1.93^{ns}
Scaling test C	-3.78^{ns}	-0.28^{ns}	-0.65^{ns}	3.9*
Cross No. 2 (White field corn Inbred 82 "P$_1$" X Golden Bantam "P$_2$")				
Broad sense heritability (H)	58.43	10.93	15.60	60.03
narrow sense heritability (h^2)	54.39	7.69	14.49	56.17
Mid-parent	13.71	70.43	9.18	18.48
Potence ratio	0.16	-1.36	-0.59	-0.55
Arithmetic means F$_2$	14.17*	76.77**	8.22**	16.46**
Geometric F$_2$	13.51**	76.56**	7.89**	15.64**
Observed means F$_2$	14.48	80.37	6.66	14.41
Minimum no. of genetic Factor (n)	16.41	29.68	6.27	31.19
Scaling test A	-2.83^{ns}	0.502^{ns}	1.61	0.81^{ns}
Scaling test B	-2.83^{ns}	6.01*	-3.01	-6.16**
Scaling test C	1.21^{ns}	14.41**	-6.24	-8.17**

ns non-significant, * significant and ** highly significant at P≤ 0.05 and P≤ 0.01, respectively.

Table 3. Generation mean analysis for TSS values andL*, a* and b* color Hunter scaling in two sweet-field corn crosses.

Parameters	Country Gentleman "White" × Yellow Field Corn Inbred 2605-128Y (Cross 1)				"White" Field Corn Inbred 82 × Golden Bantam "Yellow" (Cross 2)			
	TSS	L*	a*	b*	TSS	L*	a*	b*
Gene effect estimated from three parameter model								
Mid-parent (m)	15.18**	67.41**	9.70**	24.98**	20.04**	80.89**	4.34**	15.65**
Additive (d)	6.10**	-1.65^{ns}	-1.78^{ns}	-5.79**	-5.69**	5.55**	-3.27*	-7.37**
Dominance(h)	-2.49*	20.28**	-3.98**	-13.18**	-16.83**	-1.73^{ns}	3.36**	-3.74**
Epistatic effects estimated from six parameter model								
Mid-parent (m)	14.69**	74.75**	8.07**	19.98**	14.48**	80.37**	6.66**	14.41**
Additive (d)	3.69*	-1.95^{ns}	-1.48^{ns}	-4.47*	-5.97**	2.79*	-0.96^{ns}	3.88*
Dominance (d)	0.95^{ns}	9.08**	-2.53^{ns}	-6.81**	-5.40*	-0.335^{ns}	2.92**	-1.21^{ns}
Additive x additive (i)	-0.06^{ns}	5.74*	-0.40*	-5.14**	-6.32**	-7.90**	4.84**	2.82*
Additive x dominance (j)	-2.41*	-0.30^{ns}	0.30^{ns}	1.32^{ns}	-0.28^{ns}	-2.76*	2.31*	3.49**
Dominance xdominance (l)	3.89**	-11.20**	1.45^{ns}	6.37**	11.43**	1.39^{ns}	-3.44**	2.53*

Conclusion

F$_1$ means of TSS did not exceed those of their high parent suggesting the existence of the partial dominance. Differences between observed and calculated arithmetic F$_2$ means suggested that non-additive gene effects influenced TSS contents in cross1

and additive effects in cross 2. The A, B and C values were significant confirming the existence of non-allelic gene interaction and indicating significant contribution of epistasis in controlling the inheritance of TSS trait in both crosses. The two parents of each cross were differed significantly for Hunter L*, a*, b* readings. Values of b* in F_1 means were between the midparent and lower parent in both crosses. The potency ratio values confirmed the partially dominant of lower parent. The A, B, and C values deviated significantly from zero. Meanwhile, the obtained results indicated that digenic epistasis involved in the expression of the b* trait in both crosses. Presence of significant interaction parameters along with existence of additive and dominance components indicated complex nature of the inheritance of b* trait. The results of broad and narrow sense heritability suggested that most of the total genetic variances were associated with dominance effect in the first cross. But the relative high heritability values in the second cross suggested that improving yellow color in sweet-field corn could be done.

Corresponding author
Zaki, H. E. M.
Horticulture Department, Faculty of Agriculture, Minia University, El-Minia 61517, Egypt
Email: haitham.zaki@mu.edu.eg
h_alhame@yahoo.com

References
1. Allard R.W., 2000. Principles of plant breeding 2nd Ed. John Wiley & Sons, New York. 254 P.
2. Boyer, C. D. and L. C. Hannah. 1994. Kernel mutants of corn. pp. 1-28. In: A.R. Hallauer (Ed.), Specialty Corns. CRC Press, Boca Raton, FL.
3. Cardoso, E. T., Sereno, M. D. M., and J. F. Barbosa Neto. 2002. Heritability estimates for quality and ear traits in sweet corn. Crop Breeding and Applied Biotechnology, 2(4), 493-498.
4. Cavalli, L., 1952. An analysis of linkage in quantitative inheritance. p. 135-144. Quantitative Inheritance. H.M.S.O. London.
5. Creech, R. G. 1965. Genetic control of carbohydrate synthesis in maize endosperm. *Genetics*, *52*(6), 1175.
6. Esiyok, D. and M.K. Bozokalfa, 2005. The effects of sowing and planting dates on yield and some agronomic properties of sweet corn (*Zea mays* var. saccharate). Ege Univ. Ziraat Fak. Derg., 42: 35-46.
7. Esiyok, D., M.K. Bozokalfa and A. Ugur. 2004. Determination of yield quality and some plant characteristics of some sweet corn (*Zea mays* var. saccharate) varieties in different locations. Ege Univ. Ziraat Fak. Derg., 41: 1-1
8. Farnham, D. E., G. O.Benson and R. B.Pearc.
9. Gamble, E. E., 1962. Gene effects in corn (*Zea mays* L.). I. Separation and relative importance of gene effects for yield. Can. J. Plant Sci. 42: 339–348.
10. Gerdes, J. T., W. F. and Tracy. 1994. Diversity of historically important sweet corn inbreds as estimated by RFLPs, morphology, isozymes, and pedigree. Crop science, 34(1): 26-33.
11. Hayman, B. I. 1958. The separation of epistatic from additive and dominance in gene ratio means. Heredity, 12: 371-390.
12. Jatothu, J. L., K. S. Dangi andS. S. Kumar. 2013. Evaluation of sesame crosses forheterosis of yield and yield attributing traits. Journal of Tropical Agriculture, 51(1/2), 84-91.
13. Kaukis, K., and D. W. Davis. 1986. Sweet corn breeding. Breeding Vegetable Crops. Westport, CN: AVI, 477-512.
14. Kearsey, M.J., and H.S. Pooni. 1996. The genetical analysis of quantitavarious models. Chapman and Hall, London.
15. La Bonte, D. R., and J. A.Juvik. 1990. Characterization of *sugary-1* (*su-1*) and *sugary enhancer* (*se*) kernels in segregating sweet corn populations. Journal of the American Society for Horticultural Science, 115(1): 153-157.
16. Malvar, R. A., M. E. Cartea, P. Revilla and A. Ordás. 1997. Identification of field corn inbreds adapted to Europe to improve agronomic performance of sweet corn hybrids. Crop science, 37(4): 1134-1141.
17. Malvar, R. A., P.Revilla, M. E. Cartea, A. M. Butrón and A. Ordás. 2001. Checking performance of field corn inbreds as donors of favorable alleles to improve early vigor and adaptation of sweet corn hybrids to European conditions. Maydica, 46: 187-193.
18. Mather, K. 1949. The genetical theory of continuous Variation. Proc 8th Int, Cong Genetics. Hereditas, 35(S1), 376-401.
19. Malvar, R.A., P. Revilla, M.E. Cartea, and A. Ordás. 1997. Field corn inbreds to improve sweet corn hybrids for early vigor and adaptation to European conditions. Maydica 42:247.
20. Mather, K, and J. L. Jinks. 1971. Biometrical Genetics, 2nd edition. Chapman and Hall, London.
21. Mather, K. and Jinks, J. L. 1977. Introduction to Biometrical Genetics, Chapman and Hall, London.
22. Maynard, E. T. 2010a. Sugar-enhanced sweet corn cultivar evaluation for northern Indiana, 2010. Midwest Vegetable Trial Report for 2010,
8. 2003. Corn perspective and culture Chapter1. In: PJ. White, LA Johnon, eds. Corn: chemistry and technology, 2nd Edition. American Association of Cerial Chemicals, Inc. St. Panl, Minesota, USA. 1-33.

176-180. Retrieved from http://www.hort.purdue.edu/fruitveg/rep_pres/201011/maynard10_secorn_final.pdf.

23. Maynard, E. T. 2010b. Super-sweet sweet corn cultivar evaluation for northern Indiana. Midwest Vegetable Trial Report for 2010, 181-186. Retrieved from http://www.hort.purdue.edu/fruitveg/rep_pres/201011/maynard10_sh2corn_final.pdf.

24. Mbogo, P. O., M. M. Dida and B. Owuor. 2015. Generation means analysis for estimation of genetic parameters for *striga hermonthica* resistance in Maize (*Zea mays* L.). Journal of Agricultural Science, 7(8), p143.

25. McGuire, R. G. 1992. Reporting of objective color measurements. Hort Science, 27(12): 1254-1255.

26. Oliver, J. R., A. B. Blakeney and H. M. Allen, 1992. Measurement of flour color in color space paramenters. Cereal chem. 69: 546- 550.

27. Qi, J., A. J. Wijeratne, L. P. Tomsho, Y. Hu, S. C. Schuster and H. Ma. 2009. Characterization of meiotic crossovers and gene conversion by whole-genome sequencing in *Saccharomyces cerevisiae*. BMC genomics, 10(1): 475.

28. Robinson, H. F., R. E. Comstock, and P. H. Harvey. 1949. Estimates of heritability and the degree of dominance in corn. Agron. J, 41(8): 353-359.

29. Shekhawat U. S., V. Prakash and Bhardwaj R. P. 2006. Inheritance of grain yield and tillers per plant in wheat (*Triticum aestivum* L.). Ind J Genet 66(1):16-18.

30. Simla, S., K.Lertrat and B. Suriharn. 2009. Gene effects of sugar compositions in waxy corn. *Asian Journal of Plant Sciences*, *8*(6): 417.

31. Singh R. P. and S. Singh. 1992. Estimation of genetic parameters through generation mean analysis in bread `wheat. Indian Journal of Genetics 52: 369-375.

32. Thompson, W. H. 1954. Objective methods of determining maturity in sweet corn for processing. Retrieved from http://hdl.handle.net/1957/26320.

33. Thompson J. N.1977. Analysis of gene number. Stadler Genet. Symp. 9, 63–82.

34. Thompson, S. A. 1983. Mass selection for prolificacy in corn at high and low plant densities: cycle means and genotypic variances. Diss Abstr Int 43:2414B.

35. Tracy, W. and A. Hallauer. 1994. "Sweet corn" Specialty corns: 147-187. ISBN 0-8493-4612-6.

36. Tracy, W. F., S. R. Whitt and E. S. Buckler. 2006. Recurrent mutation and genome evolution: example of the origin of sweet Maize. Crop Science, 46 (Supplement_1), S-49.

37. Wahba, B. K. 2009. Genetic studies on *Zea mays* var. *Saccharata*. M. Sc. Thesis in Agric. Sci. Vegetable Crops Fac. of Agric., Minia Univ., El-Minai, Egypt.

38. Wolf, D. P. and A. R. Hallauer. 1977. Triple test cross analysis to detect epistasis in maize. Crop Sciences 37, 763-770.

39. Wright, S. 1968. The genetics of quantitative variability In. Wright, S (Ed.), Evolution and genetics of population, Vol. 1. Genetics and biometric foundation. University of Chicago, Press, Chicago ш.

12/20/2015