

## Genetic Diversity in Sweet Corn (*Zea mays* L. *saccharata*) Cultivars Evaluated by Agronomic Traits

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### ABSTRACT

Parental cultivars selection and essential broadening of crops based on the genetic diversity need to be interpreted. That is why custodians of gene banks characterized their resources, noting the selected traits. In this investigation 11 sweet corn cultivars were studied in Erzurum, Turkey during 2017 season to characterize the cultivars based on agronomic capacity. Twenty two traits were analyzed using correlation and regression, principal component analysis (PCA) and cluster analysis. The results showed a positive and significant correlation of the yield of marketable ear (YME) with ear diameter (ED) and number of marketable ear (NME), whereas, it was negatively correlated with 1000 kernel weight (TKW). Fresh kernel yield (FKY) indicated positive and highly significant correlated with ear yield (EY), ear length (EL), number of kernels per row (NK/R) and number of kernels per ear (NK/E). Total soluble sugar content showed negative and significant correlation with green yield (GY) and NK/R. Stepwise regression showed that an increase of FKY, TKW traits leads to the reduction of the YME and FKY. Cluster analysis based on traits classified the genotypes into two groups. The highest genetic distance was shown between Argos and Kompozit Seker cultivars. The results revealed a remarkable variation in morphological and agronomical ability in genetic materials in different genotypes.

*Keywords:* Cluster analysis, Genetic diversity, PCA, Regression, Sweetcorn

SWEET Corn (*Zea mays* L. var. *saccharata*), is a special type of corn with particular properties, such as sweet taste, thin pericarp and endosperm with a soft texture, and a high nutritional value. In Turkey, there is no data about sweet corn yield and production, but the estimated production area is of 1-2 per cent of the total production area of the corn crop (Arslan and Williams, 2015).

The kernel yield of fresh corn is a quantitative character and dependent on its own component parts. Crop breeders commonly prefer yield components that indirectly increase yield. Indirect selection of yield components can increase grain yield. Therefore, it is important to know the relationships among yield traits in sweet corn to create higher yields (Kashiani and Saleh, 2010). With respect to the increasing demand and utilization of sweet corn, there is a need to improve productivity. Approximation of the genetic distance is

one of the appropriate tools for parental selection of sweet corn hybridization programs. The logical orientation of genotypes under the influence of agronomic traits can be applied as an effective tool for rapid selection of high and early maturing varieties through counting at the significant adaptation with the common method and providing a clear view of the strength of the genotype (Mohammed *et al.*, 2015). Theoretically, a characteristic is a desirable criterion for selection of yield breeding programs which has a high correlation with yield and heritability. Correlation of specific feature with other features leading to grain yield is crucial for indirect selection of genotypes for higher grain yield (Kumar *et al.*, 2010). Several investigations have been carried out to determine the phenotypic and genotypic correlation between important agronomic traits and corn production. However, choices based on simple correlation only without the interactions among yield components may

mislead the breeders to reach their primary goals (Kaya *et al.* 2009). The relationships between morphological and agronomic traits have been set up in some crops in which the genotypes were evaluated using stepwise regression to know which parameter (s) delivers the optimal values for each genotype or group of genotypes (Al-Naggar *et al.*, 2015). The study of genetic diversity with suitable measurements such as genetic coefficient of variance evaluations is essential to have an applicable training program (Al-Tabbal and Al-Fraihat, 2012). The primary aim of study was to screen the sweet corn based on agronomical traits and capture the potential genetic diversity among the cultivars.

#### MATERIAL AND METHODS

##### Plant material and experimental design

Seeds of eleven sweet corn cultivars (Argos, Baron F<sub>1</sub>, BATEM Tatly, Challenger, Febris, Khan F<sub>1</sub>, Kompozit, Overland, SHY1036, Signet and Tanem F<sub>1</sub>) were sown in a randomized complete block design (RCBD) with three replications under Erzurum/Turkey conditions. The experimentation was directed at the Experimental Farm of Atatürk University, Faculty of Agriculture, Erzurum/Turkey during 2017 cropping season. Agricultural techniques were done according to the recommendations for corn production.

##### Measure of parameters

Different agronomic traits were evaluated such as: silking period (SP), harvesting period (HP) Asabe (2008), moisture content (MC %), number of tillers/plant (NT/P), number of plants/ha (NP/ha), plant height (PH, cm), first ear height (FEH, cm), number of leaves/plant (NL/P), number of ears/plant (NE/P), green yield (GY, kg/ha), ear yield (EY, kg/ha), Ear weight (EW, g), ear length (EL, cm), ear diameter (ED, mm), number of marketable ear/ha (NME/ha), number of kernel rows per ear (NKR/E), number of kernel per row (NK/R), number of kernels per ear (NK/E), fresh kernel yield (FKY, kg/ha), 1000 kernels weight (TKW, g) and total soluble sugar (TSS) content (%) during harvest time.

##### Statistical analysis

Evaluations of the cluster analysis were based on the world's method using squared Euclidian distance and identify the cutting point using discriminate analysis. Correlation, PCA, and stepwise regression analysis were performed using SPSS version 20.0 computer program. Based on mathematical expectation genotypic and phenotypic variance mean squares was estimated and by using the below equations their coefficient variations were calculated:

$$1. V_E = MS_e$$

$$2. V_G = \frac{MS_g - MS_e}{r}$$

$$3. V_P = V_G + V_E$$

$$4. \% PCV = \frac{\sqrt{V_P}}{\bar{X}} \times 100$$

$$5. \% GCV = \frac{\sqrt{V_G}}{\bar{X}} \times 100$$

In which  $V_E$  is environmental variation,  $MS_e$  and  $MS_g$  are the mean squares of the error and genotypes respectively,  $V_p$  is phenotypic variance,  $V_G$  is genotypic variable, PCV and GCV are phenotypic and genotypic coefficient variation respectively, and  $\bar{X}$  is mean of the parameter in the experiment (Bhagasara, 2017).

Correlation analysis was also done as an important measurement between two or more traits to determine the effect of morphological traits on kernel yield which should be given importance to increase yield (Dewey and Lu, 1959).

#### RESULTS AND DISCUSSION

##### Correlation

In the study, the correlation analysis was done based on the yield of the marketable ear (YME), fresh kernel yield (FKY) and total soluble sugar content (TSS). The results showed that YME was positive and significantly correlated with ED ( $r=0.579^*$ ) and NME ( $r=0.882^{**}$ ) whereas, it was negatively and significantly correlated with TKW ( $r=0.690^*$ ). Fresh kernel yield was positively and highly significantly correlated with EY ( $r=0.882^{**}$ ), EL ( $r=0.981^{**}$ ), NK/

TABLE 1  
Correlation coefficients among different morphological and agronomic traits of sweet corn under Erzurum conditions

	SP	HP	MC	NT	NP	PH	FEH	LN	NE	GY	EY	EW	EL	ED	YME	NME	NKR/E	NK/R	NK/E	FKY	TKW	
HP	.949**																					
MC	0.23	0.40																				
NT	-.694*	-.679*	-0.05																			
NP	-0.01	-0.04	-0.41	-0.07																		
PH	0.47	0.31	-0.19	-0.37	0.33																	
FEH	.738**	.597*	0.14	-0.48	0.20	.789**																
LN	.646*	.661*	0.26	-.716**	-0.09	0.40	.652*															
NE	-.723**	-.733**	-0.14	0.40	-0.12	-0.27	-0.50	-.633*														
GY	-0.32	-0.31	-0.16	-0.11	-0.45	-0.52	-.597*	-0.35	.605*													
EY	-0.29	-0.14	0.18	0.19	-0.39	-.709**	-.584*	-0.21	0.26	0.44												
EW	.799**	.678*	0.06	-0.57	0.27	.871**	.959**	.643*	-0.54	-.580*	-.587*											
EL	-0.34	-0.15	0.24	0.29	-0.39	-.888**	-.766**	-0.35	0.21	0.48	.916**	-.761**										
ED	0.25	0.34	0.04	-0.52	-0.47	-0.34	-0.21	0.36	-0.08	.583*	0.23	-0.17	0.32									
YME	0.26	0.29	0.48	-0.24	-0.21	-0.25	0.12	0.22	-0.04	0.08	.579*	0.06	0.41	-0.01								
NME	0.35	0.45	0.25	-0.57	-0.50	-0.42	-0.12	0.42	-0.09	0.55	0.48	-0.11	0.47	.882**	0.46							
NKR/E	.723**	.659*	-0.11	-.845**	0.28	.631*	.629*	.604*	-0.55	-0.17	-.585*	.738**	-.611*	0.26	-0.18	0.15						
NK/R	-0.47	-0.33	0.03	0.15	-0.40	-.767**	-.840**	-0.45	0.55	.815**	.814**	-.795**	.864**	0.43	0.27	0.50	-0.50					
NK/E	-0.40	-0.23	0.20	0.25	-0.45	-.891**	-.797**	-0.39	0.35	.632*	.911**	-.801**	.980**	0.36	0.41	0.51	-.605*	.933**				
FKY	-0.45	-0.27	0.20	0.35	-0.40	-.930**	-.818**	-0.42	0.35	0.55	.882**	-.838**	.981**	0.33	0.37	0.46	-.692*	.891**	.980**			
TKW	-0.54	-.595*	-0.13	.710**	0.41	0.13	-0.05	-0.52	0.45	-0.35	-0.35	-0.13	-0.30	-.690*	-0.37	-.778**	-0.46	-0.29	-0.32	-0.18		
TSS	0.15	0.01	-0.24	-0.24	0.21	0.50	0.17	0.32	-0.04	-0.52	-0.41	0.24	-0.34	-0.56	-0.08	-0.54	0.08	-.609*	-0.42	-0.37	0.29	

Note: \* : significant at 5 per cent; \*\* : significant at 1 Per cent; SP: silking period; HP: harvesting period; MC: moisture content; NT: number of tillers per plant; NP: number of plants/ha; PH: plant height; FEH: first ear height; LN: leaf number per plant; NE: number of ears per plant; GY: green yield kg/ha; EY: ear yield kg/ha; EW: ear weight; EL: ear length; ED: ear diameter; YME: yield of marketable ear kg/ha; NME: number of marketable ear/ha; NKR/E: number of kernel rows per ear; NK/R: number of kernel per row; NK/E: number of kernels per ear; FKY: fresh kernel yield kg/ha; TKW: 1000 kernels weight and TSS: total soluble sugar content.

R ( $r=0.891^{**}$ ) and NK/E ( $r=0.980$ ) while it was negative and highly significantly correlated with PH ( $r=0.930^{**}$ ), FEH ( $r=0.818^{**}$ ), EW ( $r=0.838^{**}$ ) and NKR/E ( $r=0.692^*$ ). In case of total soluble sugar content the result showed negative and significant correlation with GY ( $r=0.617^*$ ) and NK/R ( $r=0.609^*$ ). The number of kernel rows per ear were positively correlated with a number of kernels per ear ( $r=0.77^{**}$ ), which agree with (Alaei, 2012) and (Hefny, 2011) observed a negative correlation between TKW ( $r=0.69^*$ ). The same result was observed on a number of kernels per row with the number of kernels per ear ( $r=0.78^{**}$ ) which was negatively correlated with 1000 kernel weight ( $r=0.67^*$ ) (Table 1). The number of marketable ears, number of kernels per row and number of kernels per ear have a positive correlation with the yield of marketable ears. The results are in conformity with the findings of (Kashiani *et al.*, 2010 and Xie *et al.*, 2010). The positive significant correlation between plant height and yield/plant has been recorded by Salami *et al.* (2007) and Rafiq *et al.* (2010). This positive and significant association between the traits suggested an additive genetic model, thereby less affected by the environmental fluctuation.

Besides, most of the associations were recorded as positive but non-significant. This type of association referred to as inherent relationships between the pairs of the combination. The positive and non-significant association between plant height, ear height, and grain yield was observed by Olakojo and Olaoye (2011). Munawar *et al.* (2013) also reported the non-significant association between plant height, ear height, and ear length. Similarly, the positive and non-significant association for ear height with ear length and yield/plant was recorded by Rafiq *et al.* (2010). The negative insignificant association for a number of kernels/ear and 1000-kernel weight referred to a complex linked of relation among the pair of combinations.

**Regression**

The result of the stepwise regression showed that with the input of FKY, TKW, EY and NKR/E, the model resulted in 96.1, 1.8, 1.0 and 0.8 respectively with the total of 99.7 variances (Table 2). From the same result, NKR/E and TKW referred to the YME negatively, which means that an increase of these two traits may lead to the decrease of the EY and FKY. Khazaei *et al.* (2010) in his study of correlation, regression,

TABLE 2  
Regression

Model	Level	Independent variable	Width of Origin	Coefficients	F	Explanation factor minor	Explanation factor Model (cumulative)
Y1	Y1	FKY	673.11	1.44	219.16 **	96.1	96.1
	Y1	FKY	673.11	1.4	219.16 **	96.1	96.1
Y2	Y2	TKW	10987.6	-31.43	189.24 **	1.8	97.9
	Y1	FKY	673.11	1.11	219.16 **	96.1	96.1
Y3	Y2	TKW	10987.6	-24.83	189.24 **	1.8	97.9
	Y3	EY	4577.78	0.43	209.20 **	1.0	98.9
Y4	Y1	FKY	673.11	1.1	219.16 **	96.1	96.1
	Y2	TKW	10987.6	-42.69	189.24 **	1.8	97.9
	Y3	EY	4577.78	0.5	209.20 **	1.0	98.9
	Y3	NKR/E	16762.4	-443.66	458.13 **	0.8	99.7

$$Y1 = 673.11 + 1.44 (X1)$$

$$Y2 = 10987.56 + 1.40 (X1) - 31.436 (X2)$$

$$Y3 = 4577.78 + 1.11 (X1) - 24.83 (X2) - 0.43 (X3)$$

$$Y4 = 16762.37 + 1.10 (X1) - 42.69 (X2) - 0.50 (X3) - 443.66 (X4)$$

Note: F: significance.

and path coefficient analysis on sweet corn (*Zea mays* var. *saccharata*) reported that the results of regression analysis for grain yield presented that grain number and 1000 grain weight ended 98 per cent of the grain yield difference. Based on the study inference can be drawn that higher fresh kernel yield improvement may be achieved by the selection of ear weight, ear length, yield of marketable ears and a number of marketable ears (Kumar *et al.*, 2015).

### Principal component analysis

In this work, the four common components have been taken out, since four components had eigen values greater than or equal to one. The first principal component solely account for 44.31 per cent of the total variation, while the second principal components accounted for 26.17 per cent of the total variation, the third principal component alone contributed for 10.10 per cent of the total variation and the fourth principal component alone contributed 6.19 per cent of the total variation. The first four principal components explained 86.76 per cent of the total variation across the 11 sweet corn accessions for the twenty-two traits studied (Table 3). To obtain better knowledge about the relationship among all genotypes principal component analysis (PCA) was executed to discover diverse genotypes for successful hybridization program (Tarighaleslami *et al.*, 2012). Mohammed *et al.*, (2015) in their study found sweet potato accessions (116) were grown under rain fed conditions and Mushtaq *et al.*, (2016) in their study on maize, reported that PCA abridged the total variation into four principal components.

Table 4 shows the weight of each traits component. The trait that contributed most positively to PC<sub>1</sub> was EL (0.96), FKY (0.95), NK/E (0.94) and EY (0.84), whereas PH (-0.93), FEH and EW (-0.82) were negatively contributed with PC<sub>1</sub>. Similarly, Disasa *et al.* (2017) demonstrated that fresh kernel yield and total soluble solid content respectively was positively and negatively contributed in the PC<sub>1</sub> in sorghum (*Sorghum bicolor* L.). The PC<sub>2</sub> had 26.17 per cent of the total variance. The HP (0.82), SP (0.79), LN/P (0.71) and NKR/E (0.72) have positive contribution,

TABLE 3  
Principal Components Analysis of sweet corn  
(*Zea mays* L. *saccharata sturt*) genotypes

Component Name	Eigen value	Percentage of Variance	Cumulative Percentage
SP (day)	9.75	44.31	44.31
HP (day)	5.76	26.17	70.47
MC (%)	2.22	10.10	80.58
NT/P	1.36	6.19	86.76
NP/ha	0.99	4.53	91.29
PH (cm)	0.58	2.63	93.92
FEH (cm)	0.51	2.31	96.23
LN/P	0.44	1.98	98.21
NE/P	0.33	1.48	99.69
GY/ha	0.07	0.31	100.00
EY/ha	0.00	0.00	100.00
EW (g)	0.00	0.00	100.00
EL (cm)	0.00	0.00	100.00
ED (mm)	0.00	0.00	100.00
YME/ha	0.00	0.00	100.00
NME/ha	0.00	0.00	100.00
NKR/E	0.00	0.00	100.00
NK/R	0.00	0.00	100.00
NK/E	0.00	0.00	100.00
FKY/ha	0.00	0.00	100.00
TKW (g)	0.00	0.00	100.00
TSSC (%)	0.00	0.00	100.00

whereas TKW (-0.88), NE/P traits were negative with the PC<sub>2</sub>. This was reinforced by the study of Latif *et al.* (2015) and Disasa *et al.* (2017) on sixty cotton (*Gossypium hirsutum* L.) genotypes and sweet sorghum (*Sorghum bicolor* L.) who found positive contribution of ear diameter and PH in the first component, while the rest the traits was having negative contribution positive significant correlation between plant height and yield per plant same was also recorded in their study conducted by Mushtaq *et al.* (2016) and Disasa *et al.* (2017). The PC<sub>3</sub> having

TABLE 4  
Component Weights

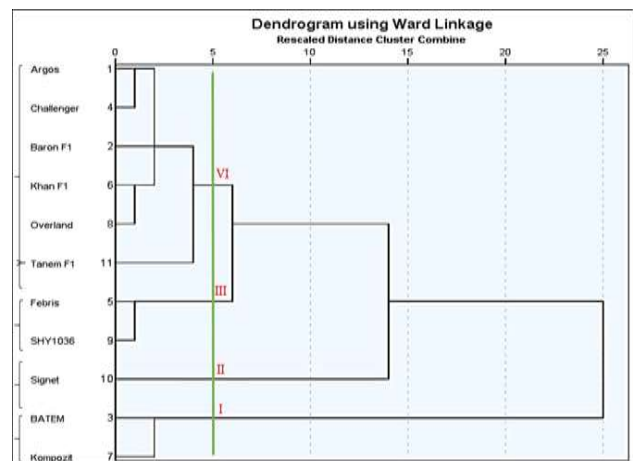
Weights	Ear length	Harvesting period	Green yield	Moisture content
SP (day)	-0.39	0.79	-0.21	0.26
HP (day)	-0.24	0.82	-0.18	0.35
MC (%)	0.04	0.08	0.08	0.85
NT/P	0.30	-0.86	-0.21	0.04
NP/ha	-0.27	-0.11	-0.55	-0.43
PH(cm)	-0.93	0.11	-0.09	-0.06
FEH(cm)	-0.82	0.35	-0.25	0.29
LN/P	-0.40	0.71	-0.03	0.28
NE/P	0.17	-0.66	0.65	-0.10
GY/ha	0.50	0.07	0.75	-0.27
EY/ha	0.84	0.01	0.18	0.33
EW (g)	-0.82	0.43	-0.23	0.19
EL(cm)	0.96	-0.01	0.12	0.22
ED(mm)	0.32	0.67	0.53	-0.15
YME/ha	0.31	0.24	-0.04	0.71
NME/ha	0.42	0.71	0.45	0.20
NKR/E	-0.58	0.72	-0.03	-0.26
NK/R	0.83	-0.06	0.51	-0.03
NK/E	0.94	-0.03	0.27	0.17
FKY/ha	0.95	-0.11	0.20	0.17
TKW (g)	-0.28	-0.88	-0.19	-0.08
TSSC (%)	-0.16	-0.09	-0.89	-0.16

positive correlations with ED (0.87), NE/P (0.77), NKR/E (0.63), ED (0.58), NK/E (0.43), EY (0.42), FKY (0.22), YME (0.20), MC (0.13), NME (0.10), EL (0.09) and NK/R (0.04), Mushtaq *et al.* (2016) reported a positive contribution of PC3 with ear diameter, whereas the other traits were negatively correlated. In case of PC4 positive contribution was proved with MC (0.86), NK/R (0.68), NK/E (0.34), HP and LN/P (0.31), FEH and NE/P (0.25), EL (0.24), SP (0.22), NME (0.19), FKY (0.11), YME (0.09), NT/P (0.08) and TKW (0.01). The positive contribution of PC4 was observed with the first ear height while

the negative contribution was obtained with 1000 kernels. The result conquered the work of Mushtaq *et al.* (2016) and Disasa *et al.* (2017) on maize and sweet sorghum (*Sorghum bicolor*) respectively.

**Cluster analysis**

The phenotypic characterization was used in the cluster analysis to determine whether homogenous groups are formed by relatedness and to what extent, and whether gained results were in accordance with the pedigree of observed sweet maize inbreds. Therefore, the results of the cluster analysis can be beneficial for the selection of genotypes for further crosses (Babic *et al.*, 2010). Eventually, the genotypes are grouped in four major clusters I (18.18%), II (9.09%), III (18.18%) and IV (54.55%). The result was reinforced by Rahman *et al.* (2015) and Subramanian and Subbaraman (2010) on diversity maize genotypes made dendrogram of 9 and 38 genotypes, respectively which results in four clusters. Cluster I has two genotypes (Kompozit and BATEM), cluster II consist of Signet genotype; cluster III consist of SHY1036 and Febris genotypes. Cluster IV was divided into two sub-clusters; cluster IV<sub>1</sub> which contains Tanem F1 genotype whereas sub-cluster IV<sub>2</sub> consists of five genotypes; Overland, Khan F1, Baron F1, Challenger, and Argos. By incising the dendrogram, the genotypes were categorized into four groups. Discriminant analysis revealed that 100 per cent of the members constituted four groups (Mhoswa *et al.*, 2016). The highest genetic distance was shown between Argos and Kompozit genotypes.



In the present study, both cluster analysis and PCA could effectively discriminate the accessions from different agronomical traits of sweet corn cultivars. Thus, it can be inferred that phenotypic attributes do have an important role in genetics and breeding studies. Grouping large number of germplasm accessions into few numbers of homogeneous clusters, facilitates the selection of diverse parents for crossing programs. The present study revealed the existence of adequate genetic variability in the material studied. This knowledge could be crucial in enhancing the efficiency of maize breeding programs in Turkey. This genetic diversity and the strong genetic association between grain yield and the agronomic traits would aid in indirect selection thus helping the breeders in the development of composites and synthetics for the resource constraint farmers with limited access to hybrid seeds. In addition, the correlation of the highly heritable traits with complex ones could help determine whether selection for one trait has any effect on another. Ear diameter and ear yield traits which showed the highest genotypic coefficient variability and had a strong positive association with a yield of the marketable ear can be used as effective selection indices for kernel yield improvement.

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