

Assessment of some Agronomic Traits for some Different Genotypes of *Zea mays*

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ABSTRACT

This work was carried out to evaluate some agronomic traits in eleven different genotypes. In order to achieve such a purpose 11 different genotypes were kindly obtained from Field Crops Research Institute and cultivated at two different successive seasons and some agronomic traits were evaluated. These agronomic traits are Plant height, Ear height, Days to mid silking, Grain yield/plant, Ear diameter, Kernel depth, No. of rows/ear, No. of kernels/row, Shelling% and 100-kernel weight. The obtained result showed that differential gene expression was obtained and such a result might be used in breeding program and selection.

INTRODUCTION

Corn is one of the most common planted crops in the world. To increase corn grain yield, technological improvements to cultures are necessary (Golbashy et al. 2010). The correct choice of genotypes for a given region is a very important practice to obtain a good yield. Annually, new genotypes are made available by companies and submitted to an evaluation network of corn genotypes (Ashofteh Beiragi et al. 2010). There are two major sources of variation in field experiments: the first and most important is soil heterogeneity and the second, is the genetic variability of the experimental material (Le Clerg 1967). Familiarity with these error sources is one of the main problems faced by researchers (Miranda Filho 1987, Guzman et al. 1992). Improvement in grain yield and related traits and grain quality for different end uses is essential for the development of corn hybrids. Multivariate data analysis facilitates a graphic display of the underlying latent factors and an interface between individual samples and variables (Nielsen and Munck, 2003). Principal component analysis (PCA) has been widely used in plant sciences) Kamara et al.(2003) used PCA to identify traits of maize (*Zea mays* L.) that accounted for most of the variance in the data. Granati et al. (2003) used PCA to investigate the relationship among *Lathyrus* accessions. Žáková and Benková (2006) identified traits that were the main sources of variation of genetic diversity among 106 Slovakian barley accessions. Salihu et al. (2006) used PCA and cluster analysis to group

kale populations and winter wheat genotypes, respectively. When dissimilarity between a pair of a variety is defined on a multivariate criterion, it is useful to be able to determine the specific plant characters which cause the dissimilarity and the relative contributions that the various characters make to the total variability in the germplasm (Ariyo 1993). Factor analysis and principal component analysis identified some similar characters as the most important for classifying the variation among corn hybrids. While PCA does not rely on any statistical model or assumptions, factor analysis does. It is also imperative to note that factor analysis suffers from other drawbacks, such as the absence of an 'error' structure and the dependence upon scale used to measure the variables (Bartual et al. 1985). The categorization of diversity among the genotypes into groups with similar characteristics can be used to design a collection strategy (Ariyo 1993). Furthermore, the high level of variability exhibited by this population indicates that heterosis could be utilized to produce a superior hybrid which can be used to enhance crop production. Development of such a genotype however, involves the understanding of the variance components in the population (Lukhele 1981, Makinde 1988). In the current study, a set of data comprising agronomic traits of 34 new corn hybrids were subjected to multivariate data analysis, namely, PCA, FA and cluster analysis. The main objectives of the study were to (1) characterize and classify diverse corn hybrids based on their overall similarity in agronomic data and (2) identify the genotypes that best combine agronomic characters for future use in corn breeding.

MATERIALS AND METHODS

The present study has been conducted to characterize different genotypes of maize using multivariate traits; in El-Nubaria station during 2012/2013, the following agronomic characters were estimated they are:

Plant height (cm): the distance from the soil surface up to collar of the uppermost node.

Ear height(cm): the distance from the soil surface up to the internode bearing the uppermost ear.

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Days to mid silking(days): measured as the number of days from planting to 50% plants with visible silk.

Grain yield/plant(g): weight of the harvested grains per plant.

Ear diameter(cm): average diameter of ears taken from each plant

Ear length(cm): average length of ears taken from each plant

Kernel depth(mm): as the average difference between ear diameter and cob diameter for each plant's ears.

No. of rows/ear: as an average of the ears of each plant.

No.of kernels/row: as an average for each plantears(s).

Shelling %: the percentage of the grain weight to the harvested ears of plant

100-kernel weight(g): average weight of two samples from each plant.

The experiment was laid out in randomized complete block design (RCBD) with three replications at normal irrigation conditions. Data were statistically analyzed using ANOVA appropriate for RCBD with SAS ver. Estimated:

$$\sigma^2_e = \frac{MSE}{r}, \sigma^2_g = \frac{MSG}{r}, \sigma^2_{phenotypic} = \sigma^2_e + \sigma^2_g$$

$$H^2_b = \frac{\sigma^2_g}{\sigma^2_{phenotypic}}, \Delta g = KH^2\sigma_{phenotypic}$$

$$\Delta g \% = \frac{\Delta g}{\bar{x}} \times 100$$

The predicted genetic advance under selection (Δg) was computed.

Where: K is the selection differential and equals to 2.06 upon selection the highest 5% of the population, h^2 heritability is narrow sense and σ_{Ph} = phenotypic standard deviation.

RESULTS AND DISCUSSION

First season

The data obtained from the analysis of measurements are shown in (Table 1): the studied characters might be illustrated as follows:

1- Plant height: it might be arranged in the following rank (Table 1) genotype No.6 was found to be the lower one while No.4 was proven to be the height one .

2- Ear height(cm): As show in tabel (Table 1) genotype No9 was proven to be the highest one; whie No.11 proved to be the lowest genotype .

3- Days to mid silking(days): genotype No.3 proved to be the highest; No.4 was proven to be the lowest genotype .

4- Grain yield/plant(g):genotype No.10 proved to be the highest; No.11 was proven to be the lowest genotype.

5- Ear diameter(cm): genotype No.3 proved to be the highest; No.9 was proven to be the lowest genotype.

6- Ear length(cm): genotype No.8 proved to be the highest; No.5 was proven to be the lowest genotype.

7- Kernel depth(mm): genotype No.4 proved to be the highest; No.5 was proven to be the lowest genotype.

8- No. of rows/ear: genotype No.3 proved to be the highest; No.9 was proven to be the lowest genotype.

9- No.ofkarnels/row:genotype No.10 proved to be the highest; No.9 was proven to be the lowest genotype.

10-Shelling%: genotype No.10 proved to be the highest; No.11 was proven to be the lowest genotype.

11-100-korneal weight(g): genotype No.8 proved to be the highest; No.11 was proven to be the lowest genotype.

Table 1. Season 1

Traits	Genotypes Rank
1	4>9>8>2>7>10>5>1>3>11>6
2	9>7>8>2>1>10>4>3>5>6>11
3	3>5>7>1>11>10>8>9>2>6>4
4	10>8>4>3>6>1>7>5>2>9>11
5	3>10>7>8>11>6>4>2>1>5>9
6	8>10>11>4>9>6>7>1>2>3>5
7	4>8>3>11>7>6>10>1>2>9>5
8	3>10>2>6>7>4>1>8>11>5>9
9	10>8>4>5>7>11>6>1>2>3>9
10	10>4>8>6>3>1>5>2>9>7>11
11	8>6>7>4>3>2>9>10>5>1>11

Secondseason

The data obtained from the analysis of measurement are given are show in (Table 2): the studied characters might be illustrated as follows:

1- Plant height: it might be arranged in the following rank (Table 2) genotype No.4 was found to be the highest one while No.6 was proven to be the lowest one.

2- Ear height(cm): As show in table (Table 2) genotype No 9 was proven to be the highest one; whie No.11 proved to be the lowest genotype.

- 3- Days to mid silking(days): genotype No.3 proved to be the highest; No. 4 was proven to be the lowest genotype.
- 4- Grain yield/plant(g): genotype No.10 proved to be the highest; No. 9 was proven to be the lowest genotype.
- 5- Ear diameter (cm): genotype No. 3 proved to be the highest; No. 1 was proven to be the lowest genotype.
- 6- Ear length(cm): genotype No. 10 proved to be the highest; No.5 was proven to be the lowest genotype.
- 7- Kernel depth(mm): genotype No.8 proved to be the highest; No.5 was proven to be the lowest genotype.
- 8- No. of rows/ear: genotype No.3 proved to be the highest; No.9 was proven to be the lowest genotype.
- 9- No. of kernels/row: genotype No.10 proved to be the highest; No.9 was proven to be the lowest genotype.
- 10- Shelling%: genotype No.10 proved to be the highest; No.7 was proven to be the lowest genotype.
- 11- 100-kernel weight(g): genotype No.7 proved to be the highest; No.11 was proven to be the lowest genotype.

12- One can conclude that there are highly significant difference between some of these characters. In addition some characters showed negative correlation. Such result might be useful in selection and breeding program.

Table 2. Season 2

Traits	Genotype Rank
1	4>9>8>10>5>2 >7>3>11>1>6
2	9>7>8>2>1>4>3> 10>5> 6>11
3	3>5>7>1>10>11>9>8>2>6>4
4	10>8>4>3>6>1>7>5>2>11>9
5	3>7>11>6>8>4>10>9>5>2>1
6	10>8>11>4>6>9>1>2>7>3>5
7	8>4>3>11>7>6>10>2>1>9>5
8	3>10>6>2>7>4>1>8>11>5>9
9	10>8>4>5>7>11>6>1>2>3>9
10	10>4>8>6>3>1>5>2>9>11>7
11	7>6>4>8>3>9>10>2>5>1>11

Table (3-a) Season 1. Means(\bar{X}) and Standard deviation of 11 genotypes maize

Level of var	x1		x2		x3		x4		x5		x6	
	\bar{x}	S. d	\bar{x}	S. d	\bar{x}	S. d	\bar{x}	S. d	\bar{x}	S. d	\bar{x}	S. d
1	C	3.72	DE	1.46	AB	2.08	E	2.80	D	0.30	D	0.42
	161.27		59.87		62.67		56.28		3.40		13.83	
2	C	5.09	CD	1.61	CDE	1.53	HG	2.15	CD	0.10	D	0.64
	162.73		61.90		58.33		35.73		3.50		13.83	
3	C	3.32	G	2.09	A	1.15	C	1.23	A	0.10	E	0.79
	160.10		53.70		63.67		72.27		5.00		12.80	
4	A	3.86	FG	1.49	E	1.15	B	4.11	BC	0.20	BC	0.44
	189.50		55.00		55.67		76.43		3.80		15.30	
5	C	1.80	H	1.61	A	2.08	G	2.12	D	0.23	E	0.32
	161.33		50.70		63.33		39.47		3.23		12.73	
6	D	2.31	H	2.59	DE	2.89	D	2.85	B	0.25	C	0.55
	153.03		50.23		56.67		64.13		3.87		15.07	
7	C	3.79	B	1.51	A	2.08	F	1.39	B	0.20	D	0.32
	162.43		68.73		63.33		46.13		3.90		13.97	
8	B	3.50	C	2.49	ABC	1.53	A	1.94	B	0.21	A	0.46
	172.60		62.90		60.67		83.97		3.87		16.30	
9	A	3.61	A	2.28	BCD	1.53	H	1.15	D	0.25	BC	0.35
	185.57		72.73		59.67		35.07		3.23		15.13	
10	C	3.08	EF	1.75	ABC	2.65	A	1.71	B	0.10	AB	0.38
	161.90		57.40		61.00		87.37		3.90		15.93	
11	CD	2.74	H	1.16	AB	1.53	H	1.87	B	0.21	BC	0.15
	157.10		49.97		61.33		34.70		3.87		15.33	

Table(3-b) Season 1. Means(\bar{X})and Standard deviation of 11 genotypes maize

Level of var	x7		x8		x9		x10		x11	
	\bar{x}	S. d	\bar{x}	S. d	\bar{x}	S. d	\bar{x}	S. d	\bar{x}	S. d
1	DE 5.97	0.15	C 10.53	0.67	FG 24.40	0.82	EF 78.60	0.56	I 31.65	0.38
2	DE 5.90	0.53	B 12.07	0.25	GH 23.07	0.45	G 69.97	0.42	F 34.22	0.60
3	B 7.93	0.15	A 14.40	0.26	H 21.50	0.87	DE 80.40	0.62	E 35.04	0.86
4	A 8.93	0.49	B 11.63	0.67	C 32.27	0.80	AB 84.47	0.67	D 37.36	0.51
5	F 5.27	0.21	C 10.07	0.25	D 30.40	1.08	F 76.93	2.08	HI 32.00	0.50
6	C 6.97	0.42	B 11.97	0.32	F 24.80	1.57	CD 81.50	0.60	B 39.72	0.74
7	C 7.03	0.21	B 11.80	0.30	DE 29.83	0.55	GH 68.60	2.34	C 38.24	0.66
8	A 8.93	0.15	C 10.47	0.55	B 35.07	1.11	BC 82.90	0.72	A 87.67	0.53
9	EF 5.60	0.10	C 10.07	0.45	I 19.67	0.38	HG 69.43	0.61	G 33.30	0.33
10	D 6.20	0.10	B 12.17	0.31	A 37.10	1.20	A 85.33	1.27	GH 32.71	0.89
11	B 7.83	0.25	C 10.43	0.21	E 28.77	0.72	H 67.77	1.03	I 29.90	0.41

Table(4-a) Season 2.Means(\bar{X})and Standard deviation of 11 genotypes maize

Level of var	x1		x2		x3		x4		x5		x6	
	\bar{x}	S. d	\bar{x}	S. d	\bar{x}	S. d	\bar{x}	S. d	\bar{x}	S. d	\bar{x}	S. d
1	F 158.67	2.80	C 61.50	1.44	ABC 62.00	1.00	F 56.37	3.26	E 3.43	0.21	D 13.93	0.15
2	DE 161.47	2.49	C 62.97	1.70	EF 57.33	1.53	H 38.70	1.74	E 3.47	0.15	D 13.90	0.30
3	DEF 160.77	3.65	D 57.17	3.43	A 64.67	1.53	D 74.05	2.12	A 4.90	0.30	E 13.20	0.36
4	A 191.43	4.15	D 57.63	2.12	G 54.33	1.53	C 77.73	1.72	BCD 3.80	0.10	BC 15.30	0.26
5	DE 162.30	3.41	E 51.67	1.56	AB 64.00	2.65	H 40.00	1.21	E 3.47	0.23	E 12.97	0.32
6	F 155.53	3.40	E 51.03	1.83	FG 56.00	1.00	E 64.60	1.10	B 3.87	0.15	C 15.20	0.30
7	DE 161.40	1.65	B 70.00	1.47	ABC 63.33	2.08	G 47.10	1.91	B 3.93	0.15	D 13.73	0.12
8	C 174.80	3.56	C 64.53	1.46	DE 59.00	1.00	B 83.97	2.12	BC 3.83	0.15	AB 15.73	0.47
9	B 185.13	4.36	A 73.80	3.11	CD 60.67	3.215	I 33.87	1.86	DE 3.50	0.10	C 15.13	0.45
10	D 164.83	2.19	D 55.33	3.48	BCD 61.33	1.53	A 87.27	1.69	CDE 3.53	0.21	A 16.03	0.21
11	DEF 159.37	2.47	E 50.70	1.40	BCD 61.33	0.58	I 35.17	1.70	B 3.90	0.10	BC 15.37	0.21

Table(4-b) Season 2.Means(X)and Standard deviation of 11 genotypes maize

Level of var	x7		x8		x9		x10		x11	
	x̄	S. d	x̄	S. d	x̄	S. d	x̄	S. d	x̄	S. d
1	D 5.93	0.15	DE 10.73	0.51	EF 24.60	0.56	D 78.50	0.60	EF 31.53	0.38
2	D 6.17	0.38	B 11.93	0.49	FG 23.40	0.82	E 70.27	0.76	CD 33.21	0.21
3	B 8.03	0.21	A 14.30	0.26	G 22.80	0.61	C 80.10	0.26	B 35.87	0.75
4	A 8.77	0.31	CD 11.20	0.46	B 31.70	0.85	A 84.63	0.84	A 38.41	0.90
5	E 5.37	0.21	EF 10.17	0.45	C 30.07	0.75	D 78.00	0.36	DE 32.30	0.71
6	C 6.90	0.40	B 11.93	0.38	E 25.37	0.67	B 81.97	0.42	A 38.70	1.48
7	C 7.07	0.25	BC 11.77	0.64	C 30.03	0.76	F 68.63	1.02	A 38.83	0.91
8	A 9.07	0.15	DE 10.57	0.06	A 36.77	0.93	B 82.50	1.44	A 38.12	0.10
9	E 5.37	0.25	F 9.60	0.46	H 20.17	1.14	EF 69.23	1.25	C 34.13	0.07
10	D 6.30	0.20	B 12.33	0.38	A 38.03	0.67	A 85.80	0.44	CD 33.27	0.39
11	B 7.90	0.10	EF 10.23	0.12	D 28.43	1.10	EF 69.03	1.01	F 30.91	0.94

Table 5. Heritability % in broad and expected genetic advance for the different Traits of 11 genotype of maize during the two seasons

Traits	Season 1		Season 2	
	H ² .broed %	Δg.broed%	H ² .broed%	Δg.broed%
1	85	29.4	80	21.03
2	78	25.1	81	34.44
3	83	7.73	79	20.5
4	56	23.1	49	35.36
5	83	21.97	79	31.42
6	85	14.4	68	10.44
7	68	26.1	53	18.32
8	76	17.7	69	16.43
9	62	25	53	21.9
10	61	14.1	67	12.05
11	53	31.2	61	35.6

Table 6. Correlation between the studied agronomical traits data obtained from the analysis of the studied agronomic traits are given in tables 6-7

	V1	V2	V3	V4	V5	V6	V7	V8	V9	V10	V11
V1	1	.404*	-.359*	.114	-.248-	.292	.243	-.267-	.055	.089	.194
V2	.404*	1	.138	-.171-	-.281-	.164	-.188-	-.201-	-.193-	-.371*	.203
V3	-.359*	.138	1	-.114-	.135	.473**	-.217-	.040	-.005-	-.194-	-.067-
V4	.180	-.192-	-.218-	1	.473**	.407*	.533**	.387*	.543**	.265	.105
V5	-.248-	-.281-	.135	.473**	1	-.067-	.561**	.770**	.006	.265	.105
V6	.292	.164	.473**	.407*	-.067-	1	.385*	-.289-	.477**	.244	.454**
V7	.243	-.188-	-.217-	.533**	.561**	.385*	1	.262.	.341	.343	.543**
V8	-.267-	-.201-	.040	.387*	.770**	-.289-	.262	1	-.163-	.281	-.156-
V9	.055	-.193-	-.005-	.543**	.006	.477**	.341	-.163-	1	.464**	.402*
V10	.089	-.371*	-.194-	.896**	.265	.244	.343	.281	.464**	1	.330
V11	.194	.203	-.067-	.478**	.105	.454**	.543**	-.156-	.402*	.330	1

**. Correlation is significant at the 0.01 level (2-tailed).

*. Correlation is significant at the 0.05 level (2-tailed).

Table 7. Correlation between the studied agronomical traits data obtained from the analysis of the studied agronomic traits are given in tables

	V1	V2	V3	V4	V5	V6	V7	V8	V9	V10	V11
V1	1	.404*	-.359	.180	-.111-	.398*	.249	-.351*	.136	.152	.291
V2	.404*	1	.138	-.192-	-.129-	-.015-	-.141-	-.196-	-.226-	-.426*	.231
V3	-.359*	.138	1	-.218-	.234	.450**	-.308-	.080	-.054-	-.227-	-.353*
V4	.180	-.192-	-.218-	1	.291	.402*	.555**	.469**	.602**	.878**	.462**
V5	-.111-	-.129-	.234	.291	1	-.206-	.526**	.643**	-.143-	.112	.367*
V6	.398*	-.015-	.450**	.402*	-.206-	1	.334	-.246-	.460**	.307	.168
V7	.249	-.141-	-.308-	.555**	.526**	.334	1	.249	.387*	.323	.520**
V8	-.351*	-.196-	.080	.469**	.643**	-.246-	.249	1	-.050-	.307	.277
V9	.136	-.226-	-.054-	.602**	-.143-	.460**	.387*	-.050-	1	.530**	.199
V10	.152	-.426*	-.227-	.878**	.112	.307	.323	.307	.530**	1	.288
V11	.291	.231	-.353*	.462**	.367*	.168	.520**	.277	.199	.288	1

* correlation is significant at the 0.05 level (2-tailed).

** correlation is significant at the 0.01 level (2-tailed).

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الملخص العربي

تقييم بعد الصفات المحصوليه في ١١ تركيب وراثي من الذره الشاميه

محمد عبد العزيز محمد عامر، رجب محمد فهمي

- تم الحصول علي ١١ تركيب وراثي من الذره الشاميه وذلك من قسم بحوث الاصول الوراثيه التابع لمعهد بحوث المحاصيل الحقلية وهذه الاحدي عشر تركيب وراثي هي:
- وارد معهد المحاصيل ٢٤٩- و ارد معهد ٢٣٧- و ارد معهد ٢٣٥- و ارد معهد ٢٢٢- و ارد معهد ١٦٥- و ارد معهد ٩١- و ارد معهد ٨٩- و ارد معهد ٨٦- و ارد معهد ٨٥- و ارد معهد ٨٢- تراوة
- وقد اوضحت النتائج المتحصل عليها ان هناك فروق جوهريه في الصفات المدروسه وهي:
- ٤- محصول الحبوب/ للنبات(جرام)
٥- قطر الكوز(سم)
٦- طول الكوز(سم)
٧- عمق الحب(مم)
٨- عدد السطور / كوز
٩- عدد الحبوب/ كوز
١٠- نسبه التفريط %
١١- وزن ١٠٠ حبه(جم)

وقد اوضحت النتائج المتحصل عليها ان هناك فروق جوهريه بين التراكيب الوراثيه قيد الاختبار واوصي البحث باستخدام تلك النتائج في برامج الانتخاب والتربيه.

- ١- ارتفاع النبات(سم)
٢- ارتفاع الكوز(سم)
٣- عدد الايام اللازمه للتزهير(يوم)