Evaluation of Some Promising Teosinte Genotypes for Morphological and Genetic Parameters under Egyptian Conditions

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ABSTRACT

This investigation was conducted at Gemmeiza, Agric. Res. Station, El –Gharbia Governorate, Agricultural Research Center (ARC), Egypt, during the period between 2014 and 2015 summer seasons to evaluate eight selected teosinte genotypes. The experimental design was a randomized complete block with three replicates. The data measured were fresh yield (fr) and dry yield (dy) over the consecutive cuts. Plant height (ph), stem dimeter (SD), number of leaves on the main stem (NL), leaf area per plant, dry matter (DM), fresh yield, dry yield, fresh leaves / stem (%) and dry leaves / stem (%) and were recorded at cutting time.

Heritability estimate, in the broad – sense (h^2b), on mean basis for traits, were carried out. Genotypes 3 and 4 were the superior to the other tested genotypes in morphological characters in both seasons. The heritability was high in fresh yield (fy) (99.9%) and dry matter (DM) (99.8%), followed by plant height (99.5%) and leaf area (99.5%).

(SDS – PAGE) official sodium dodecyl sulphate polyacrylamide gel electrophoresis was employed to detect variation in total soluble protein content technique among the eight genotypes of teosinte; namely, 1, 2, 3, 4, , 6, 7 and 8 genotypes. Different protein fragmentation was recorded for the teosinte genotypes, which ranged from 21 to 16 for 1, 2, 3 and 4 genotypes repectively, with molecular weight (MW) ranged from 154 to 7 kda. It was found that similarity and dissimilarity, for protein patterns of teosinte genotypes, showed that 3 and 4 genotypes showed the same protein patterns, with almost protein loci and molecular weights, with 18 and 16 protein bands. According to electrophoretic study. Phyllogenetic tree was constructed and indicated a clear genetic base from SDS – PAGE analysis, high similarity percentage i.e. (94.5%) for genotype 3, and the lowest similarity percentage (76.2%) for the fist genotype.

The genotypes were divided into three main groups; i.e., the genotypes (1, 8), were in one group, while genotype (2) was in the second group and (3, 4, 5, 6 and 7) genotypes were in third group.

Key words : Teosinte, genotypic, evaluation, SDS – PAGE and heritability in broad sense.

INTRODUCTION

Teosinte (Zea Mexicana (Schrad); 2n = 20, originated in Mexico) is grown in the summer season as a multi – cut forage crop (Fedoror, 1974). It is a promising forage summer crop in Egypt, which needs more research to introduce it to farmers and producers. Dewet et. al. (1971) assumed that Zea Mexicana (teosinte) originated from natural hybridization of Zea mays (Maize) with a species of Tripsacum. They showed that most modern races of maize resulted from introgression of primitive maize. With teosinte and tripsacum, or both. The assumption that teosinte originated as a hybrid between domesticated Zea mays and a species of Tripsacum by backcrossing remains an intriguing possibility (Aulicin and Magoja, 1991).

All species of teosinte, closely, resemble maize, with staminate flowers borne in tassels and pistillate flowers in axillary spikes. Teosinte has survived as a wild plant, because the pistillate spike breaks up at maturity to disperse the kernels, which, unlike maize kernels, are protected in heavy cellulose, lignin structures, called fruitcases.

Fruit cases are composed of hard segment of the rachis of the spike, and lignified outer glumes (Beadle, 1977).

Katiyar and Sachan (1992) found that the genetic distance (GD) was the least (0.309) between maize and teosient on Isozyme diversity in Zea maize and related genera.The early history of backcrossing was stated by Harian and Pope (1922) and Allard (1960). Backcross breeding is used as a conservative approach, and the goal is to improve the existing cultivars.

Srikumar and Bai (1995) evaluated nine fodder maize types and found high estimates of genotypic coefficient of variation, heritability and genetic advance, for plant height. Kumar (2000) put emphasis on maize plant height with greater ear weight, number of rows per ear and number of seeds/ear for better grain yield. A quantitative trait expresses itself in close association with many other traits-Alteration in the expression of one trait is usually associated with a change in the expression of other traits. Therefore, a plant breeder has to study the degree of characters association.

This field study was aimed to evaluate eight genotypes of teosinte obtained from the Forage Crops Research Department, FCRI, ARC, in addition to

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investigate the polyacrylamide gel electrophoresis (SDS- PAGE).

To define the best promising high yielding genotypes under this study, SDS – PAGE method was based on that of Laemmli (1970). For the determination of the protomer molecular weights, a mixture of the following marker proteins. The electrophoretic data were, statistically, analyzed by cluster and principal coordinate analysis of the matrix of similarity coefficients (Cs) to draw a relationship between the genotypes of teosinete (Sammour, 1994).

MATERIALS AND METHODS

Eight genotypes were obtained from the Forage Crops Research Department, FCRI, ARC, Giza, Egypt. The genotypes are indicated in Table (I) A field experiment was carried out at Gemmiza Experimental Research Station, El-Gharbia Governorate, ARC Egypt in 2014 and 2015 summer seasons Seeds were sown at 20kg/fed on May 10th 2014, and the May 18th 2015. A randomized complete block design in three replicates, was used. The experimental plot area was 12m^2. All other cultural practices were done on time. Three cuts were obtained under such conditions during the growing season Cuts were taken when plant height reached 90 to 120 cm according to USDA Plant Fact Sheet of Mexian Teosinte. Cuts were done about sixty days after planting for the 1st cut, the 2nd cut was taken after 32 days from the 1st one, and the last cut was taken after thirty days from the 2nd cut in both seasons. At cutting time, five plants from, each plot, were randomly taken to estimate plant height (cm), number of leaves on the main stem, main stem diameter (mm), measuring both the length and the maximum width of the third uppermost leaf blade on the main stem, to calculate leaf area (multiplied by 0.76cm^2), fresh fodder (fy) and dry (Dy) yields were estimated and then transformed to ton/fed., fresh leaves / stem (%) and dry leaves / stem (%). The broad – sense heritability was calculated, according to Eckebil et al. (1977) and Hamdi et al. (2003), Data were subjected to ANOVA statical analysis, using SAS and SPSS software to deduce the least significant differences (LSD) among genotypes at (5%) level.

Analysis of variance of treatments difference was performed according to Steel and *Torrie (1980)*. Statistical analysis was done by SAS software package (Version 9.1.3, 2007).

SDS – PAGE electrophoresis :

Total protein content was determined in grounded fine powder seeds of each sample by the method, described by Bradford (1976), using bovine serum albumin (96%, Sigma Chemical Co, St. Louis, MO, USA), as a standard. Then, the total souble proteins was extracted with an extraction buffer. Fifty ul of the extract were mixed with 50 ml of SDS-sample buffer (0.15 M TRIS-HC1, pH 6.8, (3%) w/v SDS, (5%) v/v β -mercaptoethanol, (7%) v/v glycerol and 0.03% Bromphenol Blue) and boiled for 7 min in a boiling water bath. 14ml of the sample was loaded onto each well. Electrophoresis (SDS-PAGE) was carried out according to the procedures of Laemmli (1970) in 1.5 mm thick gels with 14 % (w/v) separating gel and (4%) (w/v) stacking gel in a vertical electrophoreses unit (Cleaver Scientific, England). SDS-PAGE was carried out at 75 volts for three hours. After electrophoresis, the gels were overnight stained using 0.1% (w/v) Coomassie Brilliant Blue R-250. Then, distained using a (10%) (v/v) acetic acid solution until a clear background was achieved. A Page ruler pertained protein ladder (Thermo-Fisher Scientific) was used as protein molecular weight marker. Gel documentation system (GelDoc-It^e Imaging System, UVP, England), was applied for data scoring and documentation. Total lab analysis software (Total Lab TL120, v2008) was employed for constructing binary matrix for SDS PAGE data, according to presence or absence of a band of each sample, which remarked as one or zero.

Protein electrophoresis studies:

SDS polyacrylamide gel electrophoresis (SDS-PAGE) (12 % T) was performed to evaluate genetic variation among the eight **teosinte** genotypes, according to the methods of Lammli (1970).

Protein extraction and purification methods:

Protein precipitation :

The proteins ware precipitately from the ethanol/phenol supernatant with 1.5 ml isopropanol. The samples were stored at room temperature for ten minutes and was sediment the protein precipitate at 12,000 x g for ten minutes at 4 °C. 2. Protein Wash Remove supernatant and wash the protein pellet 3 times with a 2 ml solution of 0.3 M guanidinium hydrochloride in (95%) ethanol. The samples were kebt in washing solution for twenty minutes at room temperature before centrifuging at 7,500 x g for 5 minutes at 4 °C. Next vortex the protein pellet once with 2 ml of 100 % ethanol, stored for twenty minutes at room temperature and centrifuged at 7,500 x g for five minutes at 4 °C.

Protein solubilization :

Remove any ethanol and dry the protein pellet briefly for 5-10 minutes under vacuum and dissolve it in (1 %) SDS by pipetting it up and down. Incubation of the samples at higher temperatures (50-100 °C) might be necessary to yield complete solubilization. Unsoluble material could be removed by centrifugation at 10,000 x

g for ten minutes at 4 °C. The protein supernatant should be transferred to a fresh tube. It could either be used immediately or kept frozen at -20 °C for future use.

Protein fraction quantification:

The protein fraction concentration was determined, according to Bradford (1976) method, based on the interaction between protein and Coomassie Brillant Bleu G250 (CBBG-250) in acid conditions. An amount of 50 µl of distilled water and 200 µl Coomassie Bleu Reagent were added to 50 µl of protein extract. After color stabilization for 5 min, the absorbance at 595 nm was recorded. Protein sample concentrations were determined, in reference to a range of standards based on Bovin Serum Albumin (BSA). Standard's concentration varied from zero to 150 µg and prepared in the same operating conditions, as samples.

Stocks solutions used for electrophoresis were as follows:

1- Acrylamide bis - acrylamide solution (30:0.8) was prepared by dissolving 30 g of acrylamide and 0.8 bis- acrylamide in a total volume of 100 ml distilled water. The solution was filtered through Whatman filter paper No 1 and stored at 4 C in a dark bottle.

2- TEMED was used as undiluted solution and stored at 4 C in a dark bottled.

3- Ammonium per sulphate (1.5 % w/v) was prepared by dissolving 0.15 g in 10 ml water. This solution was unsuitable and was freshly prepared just before use.

4- SDS (10 %, w/v) was prepared by dissolving10 g of SDS in 100 ml distilled water.

5- 2- mercaptoethanol was used as undiluted solution.

6- Resolving gel buffer (3.0 M Tris- Hcl, pH 8.8) was prepared by resolving 36.39 g of Tris in 48.0 ml of 1 M Hcl and completed to 100 ml with distilled water. The solution was filtered through Whatman filter paper No. 1 and stored at 4℃ until used.

7- Staking gel buffer (0.5 M Tris-Hcl pH6.8) was prepared by dissolving 6.0g Tris in 40 ml distilled water. The pH was adjusted to 6.8, using 1 M Hcl and completed to 100 ml with distilled water. The solution was filtered through Whatman filter paper No.1 and stored at 4℃ until used.

8- Resolving buffer (10 X, pH 8.6) was prepared by dissolving 30.3 g Tris(0.25 M); 144.0 g glycine(1.92 M) and 10.0 g SDS (1%) in one litter of distilled water .The solution was stored at 4℃ until used.

Preparation of slab gel:

(13%) slab gel was applied,s according to Bamdad *et al*. (2009), prepared by mixing acrylamide- bisacrylamide, (10 ml), resolving gel buffer stock, (3.7 ml), (10%) SDS, (0.3 ml), freshly prepared, (1.5%) ammonium per sulphate, (1.5 ml), distilled water, (14.45ml) and TEMED (0.015). (4%) stacking gel was prepared, using acrylamide-bisacrylamide (2.5 ml), stacking gel buffer stock, (5.0 ml); SDS (10%) (0.2 ml); freshly prepared (1.5%) ammonium per sulphate, (1.0 ml), distilled water (11.3 ml) and TEMED (0.015 ml).

Loading of samples and electrophoresis:

For each sample, after gel polymerization, 30 µg proteins were loaded and electrophoresis was performed at 75 volt, through stacking gel, followed by 125v, during approximately 2 h.

Protein staining:

Gel was stained by (0.1%) comassie blue R- 250 for 2 h. Then, distained with a solution (1:3:6) of glacial acetic acid, methanol, and water, respectively.

Data analysis:

Gel documentation system (Geldoc-it, UVP, England) was applied for data analysis, using Totallab analysis software, ww.totallab.com, (Ver.1.0.1).

Table 1. The eight genotypes of teosinte

Number of genotypes	Genotypes	Origin
1	Teosinte Genotype	Egypt
2	Teosinte Genotype	Egypt
3	Teosinte Genotype	Egypt
4	Teosinte Genotype	Egypt
5	Teosinte Genotype	Egypt
6	Teosinte Genotype	Egypt
7	Teosinte Genotype	Egypt
8	Teosinte Genotype	Egypt

RERSULTS AND DISCUSSION

Plant height :

Plant height (ph) at cutting time is presented in Tables (2 and 11). As noticed in the previous characters, the second cut had the tallest plants. At the 2nd cut, the mean ph over all genotypes, was 121.6 cm, in 2014 and 122.3 cm, in 2015. Concerning genotypes differences in ph, the tallest plants were recorded by genotype 3, followed by genotype 4 in both seasons, where, the shortest genotypes were genotype 8, genotype 6 and genotype 5. These results are in agreement with those of Hong *et al*. (1987), Which supported the importance of plant height character, which affected different

morphological characters of plant, Amos *et al.* (2009) stated that, as moisture content increased, the plant height.

Stem diameter :

Main stem diamater (SD, mm), as one of the phenotypic characters to evaluate different genotypes of teosinte, was recorded in Tables (3 and 12). Data showed that genotype 3 and genotype 4 had the highest SD among the other genotypes, whereas, the lowest SD value was recorded for genotype 5 in both seasons. Similar results have been reported by Muhammad *et al*. (2006) and Hong *et al*. (1987), who reported that stem diameter of both maize and cowpea or soybean plants were, significantly, inflounced by seed combination.

Number of leaves (NL) :

The high yielding genotypes had more leaves (on the main stem) than the low yielding ones (Tables 4 and 13). The mean number of leaves (NL) of the second cut (in both seasons) was the best with 13.2 and 13.2 leaves in the two seasons, respectively, compared to the 1st and 3rd cuts. NL was slightly higher in the 1st cut over the 3rd one. The best genotypes, in NL, were genotype 3 and genotype 4 in the same order. Genotype 4 had the highest NL (13.1 and 14.8 leaves) in the two seasons of study. The lowest was G.8 (8.7 and 8.5 leaves) in the two seasons, respectively. These results are in agreement with those of Patrick *et al.* (2008).

Leaf area (LA, cm^2) :

Leaf area (LA, cm^2) of the fully expanded 3rd leaf (from top on the main stem) was shown in Tables (5 and 14). The mean LA, significantly increased from the 1st cut to the 2nd cut, and then, decreased at the 3rd cut in both seasons. Data revealed that genotype 3 and genotype 4 were the highest values for LA at the three cuts in both seasons. Similar results have been reported by Kim and Seo (1988) and Nawaz *et al.* (2004), Who stated that leaf area might be attributed to variation in genetic makeup and adaptability of the plants to different environmental conditions.

Dry matter (DM):

Dry matter (DM) of the tested genotypes, for three cuts, was presented in Tables (6 and 15). The mean DM of the second cut was significantly higher (19.6 and 20.2 in the 1st and 2nd seasons, respectively). compared to the other cuts. Genotype 3 and genotype 4 were the best producing (21.1, 20.9) and (21.7, 21.1) in 2014 and 2015, respectively. However, the lowest ones were 1, 2, 5, 6, 7 and 8 genotypes in dry matter recorded in the two seasons, Similar results have been reported by Frandsen (1986) and Kinght *et al.* (1996).

Fresh yield (Fy) :

Fresh yield (Fy) of the eight genotypes was shown in Tables (7 and 16). In general, Fy was slightly higher in the first season, in comparison with the second one, It was also noticed the FY, at the second cut, was significantly, higher than that of the first or third cuts in both seasons the total FY ranged from (38.4) t/fed, for genotype G3 to (47.9) t/fed for G4, in 2014 season, whereas it ranged from (36.3) t/fed for G3, to (37.3) T/Fed for G4 in 2015 season. G3 had the highest total fresh yield in both seasons, followed by G4, compared to the other tested genotypes. Similar results have been reported by Patrick et al. (2008) and Knight *et al.* (1996).

Fresh leaves/stem(%) :

Fresh leaves (FL/stem) of the tested genotypes for the three cuts, were presented in Tables (9 and 18) the mean (FL/stem) of the first and second cuts were significantly higher (204.4 and 75.5), in 2014 season, (168.2 and 71.7) in 2015 season, respectively compared to the third cut. Concerning the mean of the three cuts, genotype 3 and G4 were the best genotypes, producing (149.8 and 155.0) in 2014 season, (107.5 and 112.7) in 2015 season. The results are in agreement with those reported by Patrick *et al.* (2008).

Dry yield (DY) :

Dry yield (DY) of the tested genotypes for the three cuts, was presented in Tables (8 and 17). The mean DY, of the second cut, was significantly, higher (3.5 and 3.3 t/fed, in the 1st and 2nd seasons, respectively), compared to the other cuts. Concerning the total dry yield of the three cuts, genotype 3 was the best producing (8.2 and 7.8 t/fed) in 2014 and 2015, respectively. G3 and G4 were the best genotypes in this concern. The results are in agreement with those reported by Frandsen (1986), Knight et al. (1996) and Patricket *et al.* (2008).

Dry leaves / stem (%) :

Dry leaves / stem of the tested genotypes for the three cuts, were presented in Tables (10 and 19). The mean (Dry L / S) of the first and second cuts were, significantly higher (286.3 and 117.4) in 2014 season, and (273.4 and 136.4) in 2015 season, respectively, compared to the third cut. Concerning the mean of the three cuts, genotype 3 and genotype 4 were the best genotypes producing (230.9 and 218.3) in 2014 season, (223.8 and 247.3) in 2015 season. Similar results have been reported by Patrick *et al.* (2008).

Correlation coefficients :

Correlation coefficients, among the studied traits of teosinte genotypes were calculated and presented in Tables (22 and 23). Data revealed highly positive significant correlations among plant height, stem

dimeter, number of leaves / plant, dry matter, fresh yield and dry yield.

Less positive correlation coefficient values, for the fresh leaves / stem% and dry leaves / stem (%) with previous characters, were found in 2014 and 2015 seasons. Similar results have been reported by (Frandsen, 1986).

Table 2. Plant height (cm) at cutting time for eight teosinte genotypes in 2014 season

Genotypes	2014 season			
	1st C	2nd C	3rd C	Mean
1	105.3	120.7	94.7	106.9
2	106.0	123.7	100.7	110.1
3	122.0	135.0	116.7	124.3
4	114.3	137.7	116.7	122.9
5	102.0	114.7	94.0	103.6
6	103.7	105.3	87.0	98.7
7	104.3	117.0	91.0	104.1
8	96.0	118.7	84.7	99.8
Mean	106.7	121.6	98.2	-
L.S.D. (5%)	Cuts, C = 2.17	G = 2.11		
		C * G = 6.6		
CV(%)		2.04		

Table 3. Stem diameter (mm) at cutting time for eight teosinte genotypes in 2014 season

Genotypes	2014 season			
	1st C	2nd C	3rd C	Mean
1	8.7	14.7	7.7	10.3
2	7.7	14.0	8.3	10.0
3	7.7	16.0	11.3	11.7
4	9.3	16.3	12.7	12.8
5	8.3	13.0	7.7	9.7
6	10.7	15.3	11.0	12.3
7	9.3	13.0	8.3	10.2
8	8.7	12.3	8.7	9.9
Mean	8.8	14.3	9.4	-
L.S.D. (5%)	Cuts, C = 0.32	G = 0.58		
		C * G = 1.02		
CV(%)		5.67		

Table 4 . Number of leaves / plant at cutting time for eight teosinte genotypes in 2014 season

Genotypes	2014 season			
	1st C	2nd C	3rd C	Mean
1	9.0	10.7	7.3	9.0
2	7.3	12.3	8.3	9.3
3	9.3	17.3	10.3	12.3
4	10.0	18.0	11.3	13.1
5	8.3	13.3	7.3	9.7
6	8.3	12.0	9.0	9.8
7	8.7	11.0	8.3	9.3
8	7.7	11.3	7.0	8.7
Mean	8.5	13.2	8.6	-
L.S.D. (5%)	Cuts, C = 0.70	G = 0.71		
		C * G = 1.23		
CV(%)		7.40		

Table 5. Leaves area / plant (cm^2) at cutting time for eight teosinte genotypes in 2014 season

Genotypes	2014 season			
	1st C	2nd C	3rd C	Mean
1	2917.5	3670.0	1304.9	2630.8
2	1855.4	3735.2	2530.9	2707.2
3	3520.1	7779.4	4055.5	5118.4
4	3900.3	8659.7	4093.9	5551.3
5	2385.1	4127.4	803.2	2438.6
6	3080.7	3037.4	1549.5	2555.9
7	2818.6	2611.2	1285.9	2238.6
8	2255.6	3527.7	1150.5	2311.3
Mean	2841.6	4643.5	2096.7	-
L.S.D. (5%)	Cuts, C = 259.11	G = 286.98		
		C * G = 157.34		
CV(%)		9.44		

Table 6. Dry matter at cutting time for eight teosinte genotypes in 2014 season

Genotypes	2014 season			
	1st C	2nd C	3rd C	Mean
1	18.0	18.4	18.9	18.4
2	17.2	21.9	21.6	20.2
3	18.9	22.3	22.2	21.1
4	18.6	21.4	22.7	20.9
5	18.8	18.1	18.4	18.5
6	18.6	18.8	19.2	18.9
7	18.6	18.6	18.3	18.5
8	18.1	17.7	18.1	17.9
Mean	18.3	19.6	19.9	-
L.S.D. (5%)	Cuts, C = 0.07	G = 0.13		
		C * G = 0.16		
CV(%)		0.72		

Table 7. Fresh yield (ton/fed) at cutting time fore eight teosinte genotypes in 2014 season

Genotypes	2014 season			
	1st C	2nd C	3rd C	Total
1	6.7	12.7	2.8	22.2
2	6.4	21.8	4.8	33.0
3	9.2	23.4	5.8	38.4
4	9.3	22.8	5.8	37.9
5	6.3	16.3	3.7	26.3
6	9.2	18.7	4.7	32.6
7	7.7	15.5	3.8	27.0
8	6.8	13.3	3.5	23.6
Mean	7.7	18.1	4.3	-
L.S.D. (5%)	Cuts, C = 0.07	G = 0.10		
		C * G = 0.16		
CV(%)		1.05		

Broad sense heritability :

Data in Tables (20 and 21) showed the phenotypic coefficient variance (PCV(%)), genetic ($\delta^2 g$), environment ($\delta^2 e$), phenotypic variations ($\delta^2 p$), broad sense heritability (h^2b%) and mean estimates for plant height (pH), stem diameter (SD), number of leaves / plant (NL), leaves area (LA), dry matter (DM), fresh yield (fy), dry yield (Dy), fresh leaves / stem (FL/s) and dry leaves / stem (DL/s).

The heritability percentages were high in fresh yield, dry matter, leave area, plant height, stem diameter (99.9,

99.8, 99.5, 99.5 and 99.1, respectively) while fresh leaves / stem (FL/S) had the lowest value of h^2b (86.2%).

Heritability ranged from (86.2 to 99.9%) and was considered important in selection of different teosinte genotypes. The high heritability values indicated that the predominance of additive gene action in the expression of the traits, which could be improved through single cycle of slection. These results are in agreement with those of Manggoel *et al.* (2012) and Rashwan (2010).

Tables (20 and 21) show the genotypic ($\delta^2 g$) and phenotypic variation ($\delta^2 P$). Genotypic coefficient of variation (Gcv), phenotypic coefficient of variance (Pcv), broad sense heritability (h^2). Generally, PCV had higher values than that of Gcv, which indicated some environmental implication a long side genotypic reasons of variation, observed among genotypes used in this study.

Phenotypic variance was higher than the genetic variance for all morphological traits. This observed variation might be due to environmental factors rather than genetic ones. Similar results have been reported by Nwosu *et al.* (2013). The heritability in broad sense was significantly higher for all the traits under investigation, it ranged from (86.2 to 99.9%). in 2014 season. Also it ranged from (95.6 to 99.9%) in 2015 season and was considered important in selection of different teosinte genotypes from a population (Manggoel *et al*. 2012), (Sharma and Singhania, 1992) and (Rashwan, 2010). The high h^2 values indicate that the predominace of additive gene action in the expression of the traits, which could be improved through a signal cycle of selection.

SDS – PAGE technique gave a huge help for evaluation teosinte genotypes, Generally, highly genetic variation was detected for the eight genotypes (Figures 1, 2 and 3).

Data in Tables (25 and 28), showed the total soluble protein, studying via SDS – PAGE technique, all teosinte genotypes reflected variable distinguishable protein fragments, on one hand, genotype I of teosinte was superior in protein band number with 21 fragments.

Table 8. Dry yield (ton/fed) at cutting time for eight teosinte genotypes in 2014 season

Genotypes	2014 season			
	1st C	2nd C	3rd C	Total
1	1.2	2.3	0.53	4.03
2	1.1	3.7	1.1	6.9
3	1.7	5.2	1.3	8.2
4	1.7	4.8	1.3	7.8
5	1.2	2.9	0.69	4.7
6	1.7	3.5	0.91	6.1
7	1.4	2.8	0.71	4.9
8	1.2	2.4	0.64	4.2
Mean	1.4	3.5	0.89	-
L.S.D. (5%)	Cuts, C = 0.02	G = 0.02		
		C * G = 0.16		
CV(%)		1.2		

Table 9. Fresh leaves / stem(%) at cutting time for eight teosinte genotypes in 2014 season

Genotypes	2014 season			
	1st C	2nd C	3rd C	Mean
1	168.9	77.1	63.1	103.0
2	213.9	62.1	62.0	112.7
3	293.1	82.1	74.2	149.8
4	307.4	86.4	71.2	155.0
5	179.1	66.3	46.1	97.1
6	214.6	68.7	58.5	113.9
7	126.1	86.3	65.8	92.7
8	132.4	75.5	53.6	87.2
Mean	204.4	75.5	61.8	-
L.S.D. (5%)	Cuts, C = 19.0	G = 27.0		
		C * G = 46.84		
CV(%)		24.9		

Table 10. Dry leaves / stem (%) at cutting time for eight teosinte genotypes in 2014 season

Genotypes	2014 season			
	1st C	2nd C	3rd C	Mean
1	235.2	126.5	142.8	168.2
2	254.8	85.8	113.2	151.2
3	402.4	153.6	136.9	230.9
4	395.1	151.6	108.2	218.3
5	250.7	105.8	98.1	151.5
6	332.8	98.3	93.6	174.9
7	210.7	106.7	113.4	143.6
8	208.8	111.4	104.9	141.7
Mean	286.3	117.4	113.8	-
L.S.D. (5%)	Cuts, C = 0.80	G = 2.29		
		C * G = 3.97		
CV(%)		1.39		

Table 11. Plant height (cm) at cutting time for eight teosinte genotypes in 2015 season

Genotypes	2015 season			
	1st C	2nd C	3rd C	Mean
1	111.0	117.7	81.3	103.3
2	106.3	122.3	95.7	108.1
3	116.0	136.3	112.7	121.7
4	111.3	135.7	109.3	118.7
5	103.0	121.7	85.7	103.4
6	106.7	115.3	101.0	107.6
7	101.0	112.0	98.7	103.8
8	96.3	118.0	88.7	101.1
Mean	106.4	122.3	96.6	-
L.S.D. (5%)	Cuts, C = 1.21	G = 1.43		
		C * G = 2.47		
CV(%)		1.38		

Table 12. Stem diameter (mm) at cutting time for eight teosinte genotypes in 2015 season

Genotypes	2015 season			
	1st C	2nd C	3rd C	Mean
1	11.3	16.0	8.6	12.0
2	8.6	18.3	12.0	13.0
3	13.3	20.6	14.3	16.1
4	13.0	21.3	15.6	16.6
5	9.3	13.3	8.6	10.4
6	12.3	15.0	11.3	12.8
7	11.0	13.6	8.3	11.0
8	11.6	16.0	8.6	12.1
Mean	11.3	16.7	10.9	-
L.S.D. (5%)	Cuts, C = 0.97	G = 0.62		
		C * G = 1.07		
CV(%)		4.99		

Table 13. Number of leaves / plant at cutting time for eight teosinte genotypes in 2015 season

Genotypes	2015 season			
	1st C	2nd C	3rd C	Mean
1	9.3	12.0	8.0	9.7
2	9.0	13.6	10.3	11.0
3	10.3	15.3	11.6	12.4
4	11.0	18.6	15.0	14.8
5	9.6	11.6	9.0	10.1
6	9.3	12.3	8.3	10.0
7	8.3	11.6	7.6	9.2
8	8.0	10.6	7.0	8.5
Mean	9.3	13.2	9.6	-
L.S.D. (5%)	Cuts, C = 0.56	G = 0.77		
		C * G = 1.34		
CV(%)		7.58		

Table 14. Leaves area / plant (cm^2) at cutting time for eight teosinte genotypes in 2015 season

Genotypes	2015 season			
	1st C	2nd C	3rd C	Mean
1	2993.5	4387.1	1569.7	2983.4
2	2804.4	4804.2	1779.1	3129.2
3	4925.1	6952.7	3517.1	5131.7
4	5369.1	8902.3	4658.5	6310.0
5	3135.5	4172.7	1484.7	2931.0
6	3367.2	4514.1	1620.4	3167.3
7	2379.8	3791.0	1269.1	2480.0
8	2325.6	3412.4	1300.0	2346.0
Mean	3412.5	5117.1	2149.8	-
L.S.D. (5%)	Cuts, C =278.63	G = 269.11		
		C * G = 466.55		
CV(%)		7.94		

Table 15. Dry matter at cutting time for eight teosinte genotypes in 2015 season

Genotypes	2015 season			
	1st C	2nd C	3rd C	Mean
1	18.4	18.5	19.1	18.7
2	17.7	21.8	22.6	20.7
3	18.7	22.7	23.8	21.7
4	18.7	21.9	22.6	21.1
5	19.5	19.7	19.7	19.6
6	18.6	18.8	20.0	19.1
7	18.6	18.9	18.7	18.7
8	17.9	19.0	19.1	18.7
Mean	18.5	20.2	20.7	-
L.S.D. (5%)	Cuts, C = 0.10	G = 0.15		
		C * G = 0.23		
CV(%)		0.82		

On the other hand, genotype 4 of teosinte expressed the lowest protein pattern with sixteen fragments.

Results of cluster analysis are, graphically, illustrated in a dendrogram (Fig. 5). Data revelead that the studied traits showed diversity among teosinte genotypes. The data showed the lowest polymorphism level (5.5%) between G3 and G6. On the other hand, the highest level of polymorphism was (15.1 – 23.8%) between GI and G7.

The following level of polymorphism was (9.5 – 11.1%}) for G2 and G8. Also, the data showed the lowest similarity level (80.25%) between G1 and G7.

On the other hand, the highest level of similarity was (94.3%) between G3 and G5. The following level of similarity was (89.7%) for G2 and G8.

The dendrogram showed the relationships among the eight teosinte genotypes. The genotypes were divided into three main groups and to sub-groups. The genotypes (1 and 8) were in one group. While genotypes (3, 4, 5, 6 and 7) were in different groups and genotype (2) in another group as shown in (Fig. 5) cluster.

Table 16. Fresh yield (ton/fed) at cutting time for eight teosinte genotypes in 2015 season

Genotypes	2015 season			
	1st C	2nd C	3rd C	Total
1	6.8	11.6	2.8	21.2
2	6.3	20.8	4.2	31.3
3	9.4	21.2	5.7	36.3
4	9.3	22.2	5.8	37.3
5	6.6	11.6	3.0	21.2
6	9.2	16.7	4.4	30.3
7	7.8	15.6	3.2	26.6
8	7.4	14.4	3.6	25.4
Mean	7.8	16.7	4.1	-
L.S.D. (5%)	Cuts, C = 0.10	G = 0.10		
		C * G = 0.16		
CV(%)		1.11		

Table 17. Dry yield (ton/fed) at cutting time for eight Teosinte genotypes in 2015 season

Genotypes	2015 season			
	1st C	2nd C	3rd C	Total
1	1.2	1.6	0.54	3.3
2	1.1	4.5	0.96	6.5
3	1.7	4.8	1.36	7.8
4	1.7	4.8	1.32	7.8
5	1.2	2.3	0.59	4.1
6	1.7	3.1	0.88	5.6
7	1.4	2.9	2.40	6.7
8	1.3	2.7	0.70	4.7
Mean	1.4	3.3	1.1	-
L.S.D. (5%)	Cuts, C = 1.6	G = 2.2		
		C * G = 3.97		
CV(%)		1.1		

Table 18. Fresh leaves/stem (%) at cutting time for eight teosinte genotypes in 2015 season

Genotypes	2015 season			
	1st C	2nd C	3rd C	Mean
1	133.3	76.4	53.4	87.7
2	1 62.4	57.9	56.4	92.2
3	168.2	83.3	71.0	107.5
4	196.4	66.3	75.3	112.7
5	164.0	67.0	53.5	94.8
6	152.7	60.9	58.3	90.6
7	168.2	86.1	53.1	102.4
8	201.0	76.4	62.3	113.2
Mean	168.2	71.7	60.4	-
L.S.D. (5%)	Cuts, C = 2.1	G = 2.4		
		C * G = 4.23		
CV(%)		2.5		

Table 19. Dry leaves / stem (%) at cutting time for eight teosinte genotypes in 2015 season

Genotypes	2015 season			
	1st C	2nd C	3rd C	Mean
1	272.1	152.5	122.3	182.3
2	244.2	111.5	125.3	160.3
3	354.5	176.3	140.8	223.8
4	395.1	181.8	164.9	247.3
5	223.3	119.1	97.0	146.4
6	274.6	109.9	98.8	161.1
7	200.2	123.4	113.7	145.7
8	223.2	116.7	124.2	154.7
Mean	273.4	136.4	123.3	-
L.S.D. (5%)	Cuts, C = 20.6	G = 22.4		
		C * G = 38.98		
CV(%)		13.2		

Table 20. Genetics ($\delta^2 g$), environment ($\delta^2 e$) and phenotypic ($\delta^2 p$) variations, phenotypic coefficient variance (PCV(%)), broad sense heritability (h^2b%) and mean estimates for PH, SD, (NL), LA, DM, FY, DY, FL/S and DL/S during 2014 season

Traits	$\delta^2 g$	$\delta^2 e$	$\delta^2 p$	GCV	PCV %	h^2b%	mean
PH	867.7	4.94	372.65	0.27	2.04	99.43	108.79
SD	12.86	0.37	13.23	0.33	5.66	97.2	10.86
NL/Plant	23.56	0.56	24.12	0.47	7.40	97.7	10.15
DM	13.82	0.01	13.84	0.19	0.72	99.8	19.32
FY	38.9	0.0112	38.99	0.61	1.05	99.9	10.06
DY	2.67	0.01	2.682	0.82	1.21	99.4	1.97
FL/S	5033.5	806.69	5840.06	0.62	2.49	86.2	113.95
DL/S	10551.2	5.82	10557.1	0.57	1.39	99.9	178.5

Table 21. Genetics ($\delta^2 g$), environment ($\delta^2 e$) and phenotypic ($\delta^2 p$) variations, phenotypic coefficient variance (PCV(%)), broad sense heritability (h^2b%) and mean estimates for PH, SD, (NL), LA, DM, FY, DY, FL/S and DL/S during 2015 season

Traits	$\delta^2 g$	$\delta^2 e$	$\delta^2 p$	GCV	PCV %	h^2b%	mean
PH	524.4	2.26	526.63	0.21	1.38	99.5	108.48
SD	45.15	0.42	45.57	0.51	4.99	99.1	13.02
NL/Plant	36.79	0.66	37.45	0.56	7.58	98.23	10.75
DM	13.19	0.02	13.22	0.18	0.82	99.8	19.8
FY	38.25	0.01	38.27	0.64	1.11	99.9	9.60
DY	2.61	0.04	2.65	0.71	10.57	98.4	2.27
FL/S	924.5	6.59	931.1	0.30	2.56	99.2	100.2
DL/S	12423.1	558.7	12981.8	0.63	13.29	95.6	177.7

Table 22. Genetic correlation (r_G) between plant height (PH), stem diameter (SD), number of leaves (NL), (LA), (DW), (FW), (DL/S) and (FL/S) in 2014 season

Correlations (2014)

		PH	SD	LEAVES/PL	NO.OF L/PL	LA	DW	FW	FL/STEM	DL/STEM
PH	Pearson Correlation	1	0.678**	0.808**	0.866**	0.483**	0.784**	0.796**	0.126	.106
	Sig. (2-tailed)		0.000	0.000	0.000	0.000	0.000	0.000	0.292	0.377
	N	72	72	72	72	72	72	72	72	72
SD	Pearson Correlation	0.678**	1	0.851**	0.726**	0.449**	0.851**	0.849**	-0.370**	-0.400**
	Sig. (2-tailed)	0.000		0.000	0.000	0.000	0.000	0.000	0.001	0.001
	N	72	72	72	72	72	72	72	72	72
LEAVES/PL	Pearson Correlation	0.808**	0.851**	1	0.919**	0.523**	0.865**	0.885**	-0.192-	-0.211-
	Sig. (2-tailed)	0.000	0.000		0.000	0.000	0.000	0.000	0.107	0.075
	N	72	72	72	72	72	72	72	72	72
NO.OF L/PL	Pearson Correlation	0.866**	0.726**	0.919**	1	0.568**	0.763**	0.798**	0.035	0.059
	Sig. (2-tailed)	0.000	0.000	0.000		0.000	0.000	0.000	0.769	0.625
	N	72	72	72	72	72	72	72	72	72
LA	Pearson Correlation	0.483**	0.449**	0.523**	0.568**	1	0.320**	0.429**	-0.287*	-0.270*
	Sig. (2-tailed)	.000	.000	.000	.000		.006	.000	.014	.022
	N	72	72	72	72	72	72	72	72	72
DW	Pearson Correlation	0.784**	0.851**	0.865**	0.763**	0.320**	1	0.990**	-0.111-	-0.153-
	Sig. (2-tailed)	0.000	0.000	0.000	0.000	0.006		0.000	0.353	0.199
	N	72	72	72	72	72	72	72	72	72
FW	Pearson Correlation	0.796**	0.849**	0.885**	0.798**	0.429**	0.990**	1	-0.138-	-0.171-
	Sig. (2-tailed)	0.000	0.000	0.000	0.000	0.000	0.000		0.248	0.150
	N	72	72	72	72	72	72	72	72	72
FL/STEM	Pearson Correlation	0.126	-0.370**	-0.192-	0.035	-0.287*	-0.111-	-0.138-	1	0.936**
	Sig. (2-tailed)	0.292	0.001	0.107	0.769	0.014	0.353	0.248		0.000
	N	72	72	72	72	72	72	72	72	72
DL/STEM	Pearson Correlation	0.106	-0.400**	-0.211-	0.059	-0.270*	-0.153-	-0.171-	0.936**	1
	Sig. (2-tailed)	0.377	0.001	0.075	0.625	0.022	0.199	0.150	0.000	
	N	72	72	72	72	72	72	72	72	72

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

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

Table 23. Genetic correlation (r_G) between plant height (PH), stem diameter (SD), number of leaves (NL), (LA), (DW), (FW), (DL/S) and (FL/S) in 2015 season

Correlations (2015)

		pH	SD	NL/P	LA/P	DM	FY	DY	FL/S	DL/S
pH	Pearson Correlation	1	0.870**	0.804**	0.882**	0.343**	0.859**	0.453**	-0.022-	0.144
	Sig. (2-tailed)		0.000	0.000	0.000	0.003	0.000	0.000	0.854	0.231
	N	71	71	71	71	71	71	71	71	71
SD	Pearson Correlation	0.870**	1	0.877**	0.857**	0.538**	0.861**	0.474**	-0.204-	-0.027-
	Sig. (2-tailed)	0.000		0.000	0.000	0.000	0.000	0.000	0.088	0.823
	N	71	71	71	71	71	71	71	71	71
NL/P	Pearson Correlation	0.804**	0.877**	1	0.900**	0.601**	0.753**	0.357**	-0.248*	-0.020-
	Sig. (2-tailed)	0.000	0.000		0.000	0.000	0.000	0.002	0.037	0.870
	N	71	71	71	71	71	71	71	71	71
LA/P	Pearson Correlation	0.882**	0.857**	0.900**	1	0.365**	0.817**	0.389**	0.054	0.293*
	Sig. (2-tailed)	0.000	0.000	0.000		0.002	0.000	0.001	0.655	0.013
	N	71	71	71	71	71	71	71	71	71
DM	Pearson Correlation	0.343**	0.538**	0.601**	0.365**	1	0.234*	0.052	-0.489**	-0.301*
	Sig. (2-tailed)	0.003	0.000	0.000	0.002		0.050	0.665	0.000	0.011
	N	71	71	71	71	71	71	71	71	71
FY	Pearson Correlation	0.859**	0.861**	0.753**	0.817**	0.234*	1	0.475**	-0.106-	-0.024-
	Sig. (2-tailed)	0.000	0.000	0.000	0.000	0.050		0.000	0.381	0.845
	N	71	71	71	71	71	71	71	71	71
DY	Pearson Correlation	0.453**	0.474**	0.357**	0.389**	0.052	0.475**	1	-0.146-	-0.077-
	Sig. (2-tailed)	.000	.000	.002	.001	.665	.000		.223	.525
	N	71	71	71	71	71	71	71	71	71
FL/S%	Pearson Correlation	-0.022-	-0.204-	-0.248*	0.054	-0.489**	-0.106-	-0.146-	1	0.833**
	Sig. (2-tailed)	0.854	0.088	0.037	0.655	0.000	0.381	0.223		0.000
	N	71	71	71	71	71	71	71	71	71
DL/S%	Pearson Correlation	0.144	-0.027-	-0.020-	0.293*	-0.301*	-0.024-	-0.077-	0.833**	1
	Sig. (2-tailed)	0.231	0.823	0.870	0.013	0.011	0.845	0.525	0.000	
	N	71	71	71	71	71	71	71	71	71

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

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

On the other hand, less similarity was found between G1 and G7. Therefore, there is a diversity among the genotypes. Cluster analysis is considered a valuable tool for subdividing the number of genotypes in groups in clouding similarity and dissimilarity genotypes.

The genotypes might be classified into three distinguished groups, Also, it might help in breeding programs. These results are in agreement with *Gad*, Ehak, *et al.* (1988) Sultan *et al.* (2016)and Khatab *et al.* (2016). Figures (1, 2 and 3) and Table (34) illustrates the total soluble protein fractions of teosinte genotypes. 100, 81, 69, 66, 52, 42, 37.2 and 34 KDa protein bands were common between G1 and G2. On the other hand, 107, 77, 63, 50, 47, 41, 39.5, 39, 34.5 and 34 KDa, were recorded as common protein fragments between G3 and G4. Interestingly, 107, 77, 63, 50, 47, 45, 40, 39.5, 39, 37, 34.5, 34 and 29 KDa were in common between G5 and G6. Moreover, 117, 88, 63, 44 and 38.5 KDa were in common between G7 and G8 as shown in Table (34).

As a result for genetic similarity it was clarified for teosinte genotypes, based on total soluble protein fractionation via SDS – PAGE techiique. As shown in

Figure (5), G2 of teosinte showed a high dissimilarity and located in separate individual cluster.

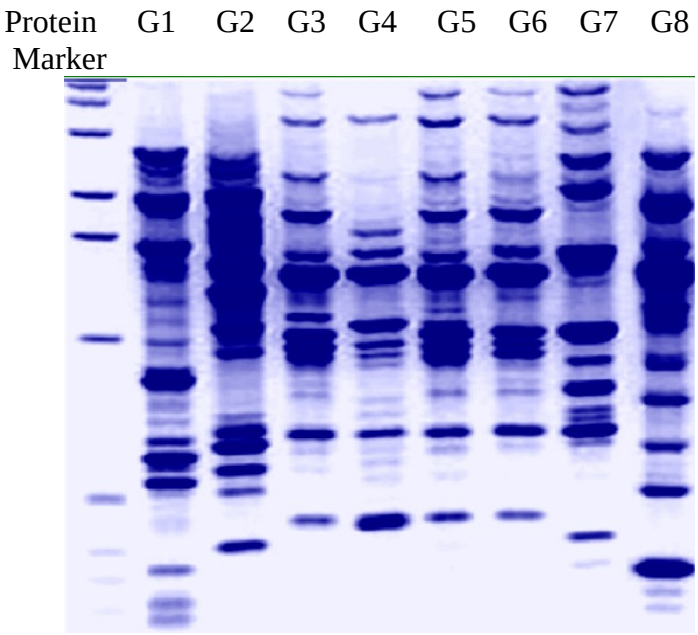

Figure 1. Protein fingerprinting patterns foe eight teosinte genotypes

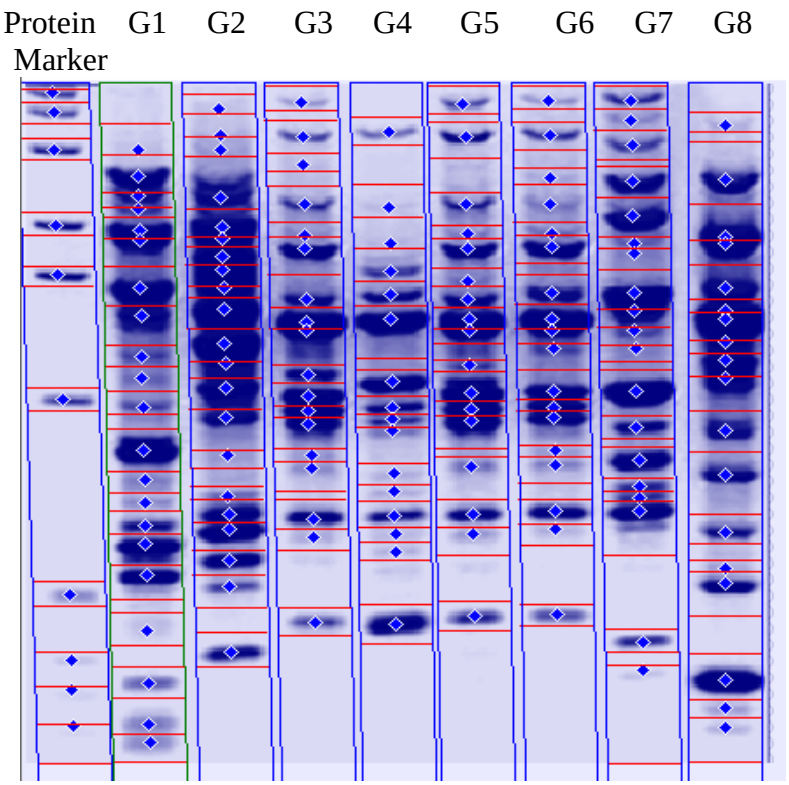

Figure 2. Computerized detection for protein patterns for eight teosinte genotypes

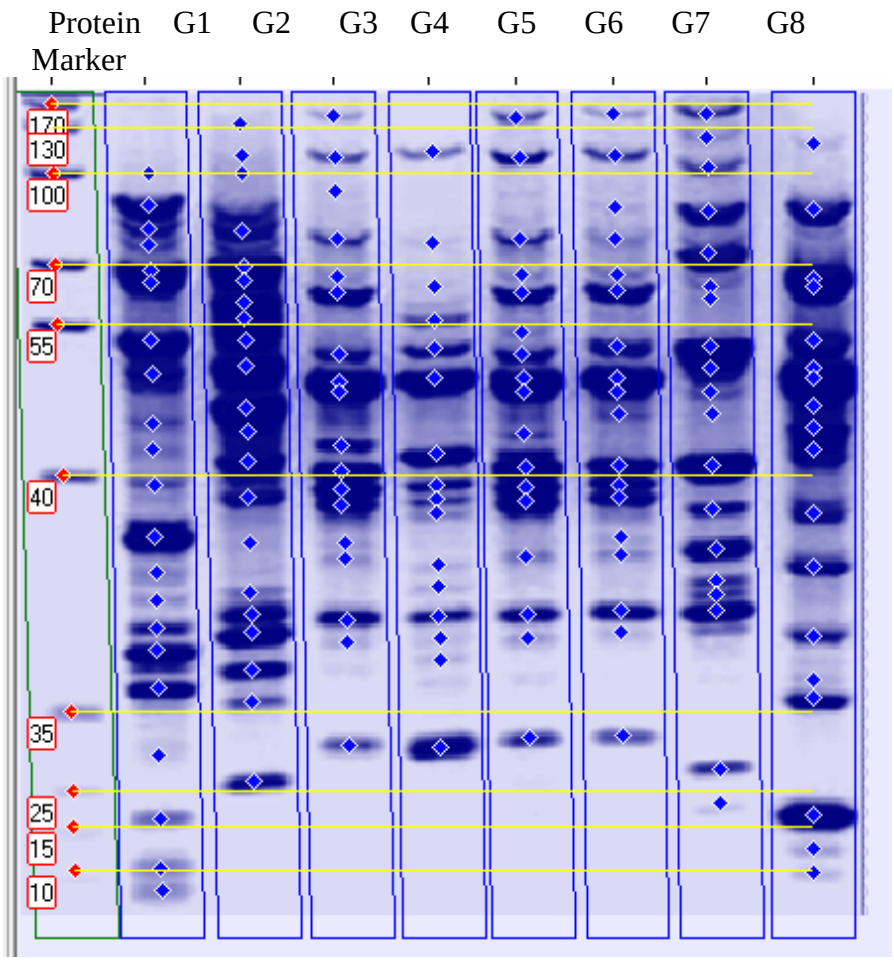

Figure 3. Computerized detection of molecular weight for eight teosinte genotypes

Table 24.Data analysis of protein patterns parameters for protein marker

Band No	Position	Peak Height	Area	Band %	Lane %	MW	Rf
1	6	105.42	266.00	8.02	4.72	170.000	0.016
2	17	103.66	456.00	10.30	6.07	130.000	0.044
3	38	141.55	456.00	12.43	7.32	100.000	0.098
4	79	157.24	494.00	14.74	8.68	70.000	0.204
5	107	170.16	418.00	14.63	8.61	55.000	0.276
6	176	127.16	494.00	12.17	7.16	40.000	0.455
7	284	63.37	494.00	8.53	5.02	35.000	0.734
8	320	29.84	722.00	6.45	3.79	25.000	0.827
9	337	19.71	798.00	6.51	3.83	15.000	0.871
10	357	17.47	836.00	6.22	3.66	10.000	0.922

Table 25. Data analysis of protein patterns parameters for the first teosinte genotype

Band No	Position	Peak Height	Area	Band %	Lane %	MW	Rf
1	38	38.18	646.00	1.47	1.41	100.000	0.098
2	52	204.16	798.00	7.95	7.63	89.511	0.134
3	63	167.50	304.00	3.55	3.40	81.224	0.163
4	70	136.71	228.00	2.21	2.12	76.135	0.181
5	82	219.14	456.00	6.29	6.04	68.090	0.212
6	88	202.42	570.00	6.73	6.46	64.490	0.227
7	114	222.16	836.00	10.87	10.43	52.219	0.295
8	129	187.37	836.00	9.64	9.25	47.426	0.333
9	152	133.39	456.00	3.89	3.73	42.637	0.393
10	164	103.29	494.00	3.36	3.23	41.085	0.424
11	180	127.76	494.00	3.52	3.38	*39.118*	*0.465*
12	204	214.34	912.00	10.41	9.99	38.617	0.527
13	220	82.34	456.00	2.36	2.27	38.217	0.568
14	233	72.39	380.00	1.59	1.53	37.927	0.602
15	246	171.26	456.00	3.50	3.36	37.556	0.636
16	256	214.50	684.00	7.99	7.66	37.148	0.661
17	273	206.05	722.00	6.27	6.02	36.061	*0.105*
18	304	30.55	684.00	1.40	1.34	31.478	*0.186*
19	333	100.39	646.00	2.33	2.24	17.090	0.860
20	356	80.18	760.00	2.57	2.47	10.142	0.920
21	366	70.47	608.00	2.11	2.03	7750	0.946

Table 26. Data analysis of protein patterns parameters for the second teosinte genotype

Band No	Position	Peak Height	Area	Band %	Lane %	MW	Rf
1	15	36.39	418.00	0.80	0.77	136.136	0.039
2	29	50.61	456.00	1.13	1.09	107.620	0.075
3	38	66.61	418.00	1.60	1.53	100.000	0.098
4	64	192.42	1102.00	9.67	9.27	80.485	0.165
5	80	228.45	608.00	7.75	7.43	69.355	0.207
6	87	215.66	190.00	2.52	242	65.070	0.225
7	97	223.84	380.00	5.12	4.91	59.636	0.251
8	104	221.03	456.00	6.27	6.01	56.308	0.269
9	114	215.05	228.00	3.02	2.90	52.219	0.295
10	126	231.74	684.00	9.37	8.98	48.267	0.326
11	145	232.47	684.00	9.35	8.96	43.813	0.375
12	156	202.74	342.00	4.17	4.00	42.059	0.403
13	169	216.53	646.00	7.91	7.59	40.584	0.437
14	186	197.82	874.00	6.84	6.56	39.357	0.481
15	207	69.18	380.00	1.52	1.46	38.530	0.535
16	229	104.79	266.00	1.36	1.30	38.020	0.592
17	239	207.79	494.00	5.05	4.84	37.773	0.618
18	248	221.29	570.00	5.89	5.64	37.485	0.641
19	265	205.00	532.00	4.50	4.31	36.645	0.685
20	279	129.82	684.00	2.68	2.57	35.523	0.721
21	316	181.71	722.00	3.48	3.34	27.058	0.817

High genetic similarity was found within 3, 4, 5, 6 and 7 genotypes of teosinte.

SDS – PAGE technique, as an accurate indicator methodology, added more support for diagnosis different of microflora in clover by Liu *et al.* (2007) Morover, Azab *et al.* (2011) added more support to the presented results Via SDS – PAGE analysis for the water doluble protein in the six Egyptian clover. It revealed a total number of Lg band S, with molecular

weights (MW), ranging from about 12-24 to 121.2 KDa, and these six Egyptian clover genotypes could much be uniquely identified with genotype protein markers.

Table 27. Data analysis of protein patterns parameters for the third teosinte genotype

Band No	Position	Peak Height	Area	Band %	Lane %	MW	Rf
1	11	55.21	532.00	1.65	1.52	150.303	0.028
2	30	109.71	684.00	3.51	3.22	106.561	0.078
3	46	41.26	380.00	1.35	1.24	94.055	0.119
4	68	137.50	760.00	6.03	5.53	77.567	0.176
5	85	85.74	304.00	2.29	2.10	66.254	0.220
6	92	203.53	798.00	10.18	9.34	62.253	0.238
7	120	191.42	684.00	8.81	8.08	50.120	0.310
8	133	230.34	456.00	9.35	8.58	46.390	0.344
9	138	219.97	760.00	12.50	11.47	45.224	0.357
10	162	191.97	380.00	5.83	5.35	41.308	0.419
11	174	216.18	456.00	8.19	7.52	40.154	0.450
12	182	213.42	266.00	5.35	4.91	39.590	0.470
13	189	197.50	646.00	8.96	8.22	39.201	0.488
14	207	65.00	266.00	1.60	1.46	38.530	0.535
15	214	69.58	646.00	3.03	2.78	38.352	0.553
16	242	188.55	646.00	6.41	5.88	37.686	0.625
17	252	45.18	418.00	1.50	1.38	37.328	0.651
18	299	123.87	608.00	3.47	3.19	32.698	0.773

Table 28. Data analysis of protein patterns parameters for the fourth teosinte genotype

Band No	Position	Peak Height	Area	Band %	Lane %	MW	Rf
1	28	94.39	608.00	3.29	2.88	108.766	0.072
2	69	43.55	684.00	2.84	*2.48*	76.848	0.178
3	89	49.11	646.00	3.28	2.87	63.919	0.230
4	105	150.21	684.00	7.54	6.60	55.864	0.271
5	118	203.05	532.00	8.87	7.76	50.792	0.305
6	131	236.82	1102.00	21.99	19.25	46.896	0.339
7	166	229.21	570.00	11.97	*10.48*	40.876	*0.429*
8	180	202.34	380.00	7.02	6.14	39.718	*0.465*
9	187	158.32	266.00	4.26	3.73	39.303	*0.483*
10	193	96.63	760.00	5.18	4.53	39.016	*0.499*
11	217	*48.42*	456.00	2.15	1.88	38.283	0.561
12	227	50.29	342.00	1.67	*1.46*	38.065	0.587
13	240	177.39	570.00	6.27	*5.49*	37.745	0.620
14	250	40.37	304.00	*1.40*	1.23	*37.409*	*0.646*
15	260	41.66	380.00	1.56	1.37	36.943	0.672
16	300	199.37	836.00	10.71	9.38	*32.478*	*0.775*

Table 29. Data analysis of protein patterns parameters for the fifth teosinte genotype

Band No	Position	Peak Height	Area	Band %	Lane %	MW	Rf
1	12	99.79	608.00	3.07	2.64	146.572	0.031
2	30	156.00	760.00	5.57	4.78	106.561	0.078
3	68	*14242*	684.00	*640*	5.50	77.567	0.176
4	84	86.37	304.00	2.36	2.03	66.858	0.217
5	92	189.89	608.00	8.31	7.13	62.253	0.238
6	110	100.61	380.00	3.60	3.09	53.763	0.284
7	120	192.84	456.00	6.97	5.99	50.120	0.310
8	131	226.37	456.00	9.81	*8.43*	46.896	0.339
9	138	212.03	304.00	5.98	5.14	45.224	0.357
10	157	143.29	228.00	3.04	2.61	41.925	*0.406*
11	172	219.68	646.00	12.01	10.31	40.318	*0.444*
12	181	209.87	304.00	6.34	*5.44*	39.653	*0.468*
13	188	200.84	684.00	9.90	8.50	39.251	*0.486*
14	213	83.84	874.00	4.39	3.77	38.375	0.550
15	239	*181.42*	608.00	6.09	5.23	37.773	0.618
16	250	56.68	570.00	2.06	1.77	*37.409*	*0.646*
17	296	137.26	608.00	4.08	3.50	33.296	0.765

Table 30. Data analysis of protein patterns parameters for the sixth teosinte genotype

Band No	Position	Peak Height	Area	Band %	Lane %	MW	Rf
1	10	66.55	494.00	2.03	1.79	154.128	0.026
2	29	137.97	608.00	4.57	4.02	107.620	0.075
3	53	56.39	342.00	1.81	1.59	88.751	0.137
4	68	95.84	798.00	6.02	5.30	77.567	0.176
5	84	101.97	266.00	2.43	2.14	66.858	0.217
6	91	210.89	570.00	9.20	8.09	62.800	0.235
7	117	195.66	608.00	9.11	8.01	51.138	0.302
8	131	235.42	532.00	11.53	10.15	46.896	0.339
9	138	205.47	304.00	5.62	4.94	45.224	0.357
10	148	146.74	532.00	6.61	5.82	43.282	0.382
11	171	222.32	646.00	10.25	9.02	40.404	0.442
12	180	209.82	228.00	4.11	4.15	39.718	0.465
13	186	210.00	722.00	10.02	8.81	39.357	0.481
14	204	65.42	266.00	1.65	1.45	38.617	0.527
15	212	84.05	532.00	3.14	2.16	38.400	0.548
16	238	200.16	532.00	6.59	5.80	37.800	0.615
17	248	44.55	456.00	1.54	1.35	37.485	0.641
18	295	119.03	456.00	3.18	2.80	33.476	0.162

Table 31. Data analysis of protein patterns parameters for the seventh teosinte genotype

Band No	Position	Peak Height	Area	Band %	Lane %	MW	Rf
1	10	146.87	494.00	3.52	3.34	154.128	0.026
2	21	81.29	456.00	*246*	2.34	120.070	0.054
3	35	131.82	608.00	4.33	4.12	102.214	0.090
4	55	*196.45*	646.00	7.25	6.89	87.234	0.142
5	74	207.95	836.00	10.35	9.84	73.341	0.191
6	89	*118.47*	228.00	2.00	1.90	63.919	0.230
7	95	98.24	456.00	3.32	3.16	60.659	0.245
8	117	230.61	836.00	11.21	10.66	51.138	0.302
9	127	204.89	380.00	5.30	5.04	47.980	0.328
10	138	140.50	380.00	3.58	*3.40*	45.224	0.357
11	148	97.21	342.00	*2.49*	2.37	43.282	0.382
12	171	233.32	988.00	*12.44*	11.83	*40.404*	*0.442*
13	191	186.32	494.00	5.06	4.81	39.105	0.494
14	209	208.89	646.00	*7.40*	7.04	*38.476*	*0.540*
15	224	143.50	304.00	65	2.50	38.130	0.579
16	230	216.03	190.00	1.98	1.88	37.998	0.594
17	238	148.76	1140.00	9.00	8.55	37.800	0.615
18	310	142.14	494.00	*2.19*	2.65	29.566	0.801
19	326	24.45	2090.00	2.89	*2.15*	21.382	0.842

Table 32. Data analysis of protein patterns parameters for the eighth teosinte genotype

Band No	Position	Peak Height	Area	Band %	Lane %	MW	Rf
1	24	46.74	418.00	1.12	1.09	114.421	0.062
2	54	182.05	1330.00	9.29	8.99	87.992	0.140
3	86	214.18	760.00	8.27	8.00	65.658	0.222
4	89	209.79	494.00	6.12	5.92	63.919	0.230
5	114	195.42	722.00	8.41	8.14	52.219	0.295
6	127	225.16	304.00	4.31	4.17	47.980	0.328
7	131	230.18	570.00	8.71	8.43	46.896	0.339
8	144	195.42	266.00	3.48	3.36	44.000	0.372
9	154	202.92	494.00	6.60	6.39	42.340	0.398
10	164	188.79	722.00	7.31	7.07	41.085	0.424
11	193	170.95	874.00	7.44	7.20	39.016	0.499
12	218	189.16	1292.00	8.37	8.10	38.261	0.563
13	249	167.42	646.00	4.11	3.97	37.448	0.643
14	269	50.55	228.00	0.72	0.70	36.371	0.695
15	278	191.50	950.00	5.02	4.86	35.619	0.718
16	331	230.82	950.00	8.18	7.91	18.266	0.855
17	347	54.50	380.00	1.08	1.04	11.689	0.897
18	358	41.47	950.00	1.47	1.42	9.750	0.925

Table 33. Data matrix for eight teosinte genotypes

Name	MW	Lane2	Lane3	Lane4	Lane5	Lane6	Lane7	Lane8	Lane9
Band1	151.283	0	0	1	0	1	1	1	0
Band2	136.136	0	1	0	0	0	0	0	0
Band3	117.245	0	0	0	0	0	0	1	1
Band4	107.425	0	1	1	1	1	1	0	0
Band5	100.738	1	1	0	0	0	0	1	0
Band6	94.055	0	0	0	0	0	0	0	0
Band7	88.372	1	0	0	0	0	1	1	1
Band8	80.855	1	1	0	0	0	0	0	0
Band9	77.137	1	0	1	1	1	1	0	0
Band10	73.341	0	0	0	0	0	0	1	0
Band11	68.723	1	1	0	0	0	0	0	0
Band12	65.865	1	1	1	0	1	1	0	1
Band13	63.177	0	0	1	1	1	1	1	1
Band14	60.147	0	1	0	0	0	0	1	0
Band15	56.086	0	1	0	1	0	0	0	0
Band16	53.763	0	0	0	0	1	0	0	0
Band17	52.219	1	1	0	0	0	0	0	0
Band18	50.662	0	0	1	1	1	1	1	0
Band19	48.076	0	1	0	0	0	0	1	1
Band20	46.900	1	0	1	1	1	1	0	1
Band21	45.224	0	0	1	0	1	1	1	0
Band22	43.594	0	1	0	0	0	1	1	1
Band23	42.240	1	1	0	0	1	0	0	1
Band24	41.088	1	0	1	1	0	0	0	1
Band25	40.373	0	1	1	0	1	1	1	0
Band26	39.680	1	0	1	1	1	1	0	0
Band27	39.294	0	1	1	1	1	1	0	0
Band28	39.046	0	0	0	1	0	0	1	1
Band29	38.554	1	1	1	0	0	1	1	0
Band30	38.376	0	0	1	0	1	1	0	0
Band31	38.253	1	0	0	1	0	0	0	1
Band32	38.130	0	0	0	0	0	0	1	0
Band33	38.028	0	1	0	1	0	0	1	0
Band34	37.927	1	0	0	0	0	0	0	0
Band35	37.763	0	1	1	1	1	1	1	0
Band36	37.446	1	1	1	1	1	1	0	1
Band37	37.148	1	0	0	0	0	0	0	0
Band38	36.943	0	0	0	1	0	0	0	0
Band39	36.645	0	1	0	0	0	0	0	0
Band40	36.371	0	0	0	0	0	0	0	1
Band41	36.061	1	0	0	0	0	0	0	0
Band42	35.571	0	1	0	0	0	0	0	1
Band43	33.386	0	0	0	0	1	1	0	0
Band44	32.588	0	0	1	1	0	0	0	0
Band45	31.478	1	0	0	0	0	0	0	0
Band46	29.566	0	0	0	0	0	0	1	0
Band47	27.058	0	1	0	0	0	0	0	0
Band48	21.382	0	0	0	0	0	0	1	0
Band49	17.678	1	0	0	0	0	0	0	1
Band50	11.689	0	0	0	0	0	0	0	1
Band51	9.946	1	0	0	0	0	0	0	1
Band52	7.750	1	0	0	0	0	0	0	0

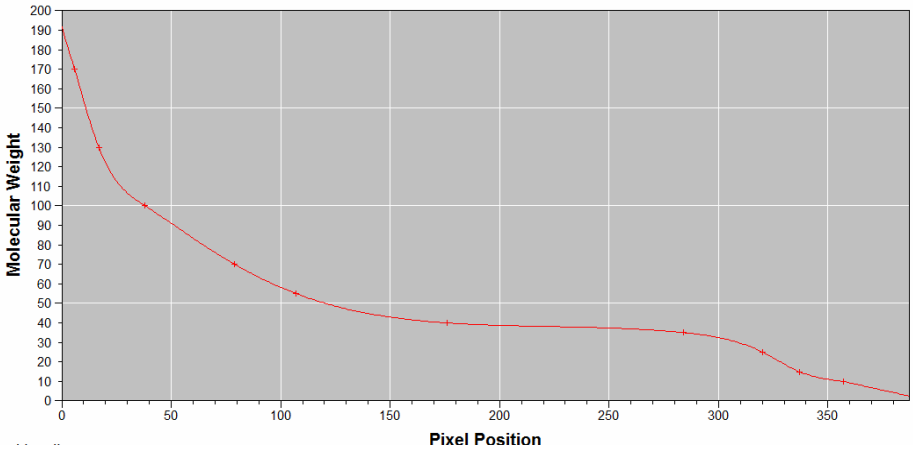

Figure 4. Molecular weight calculation method

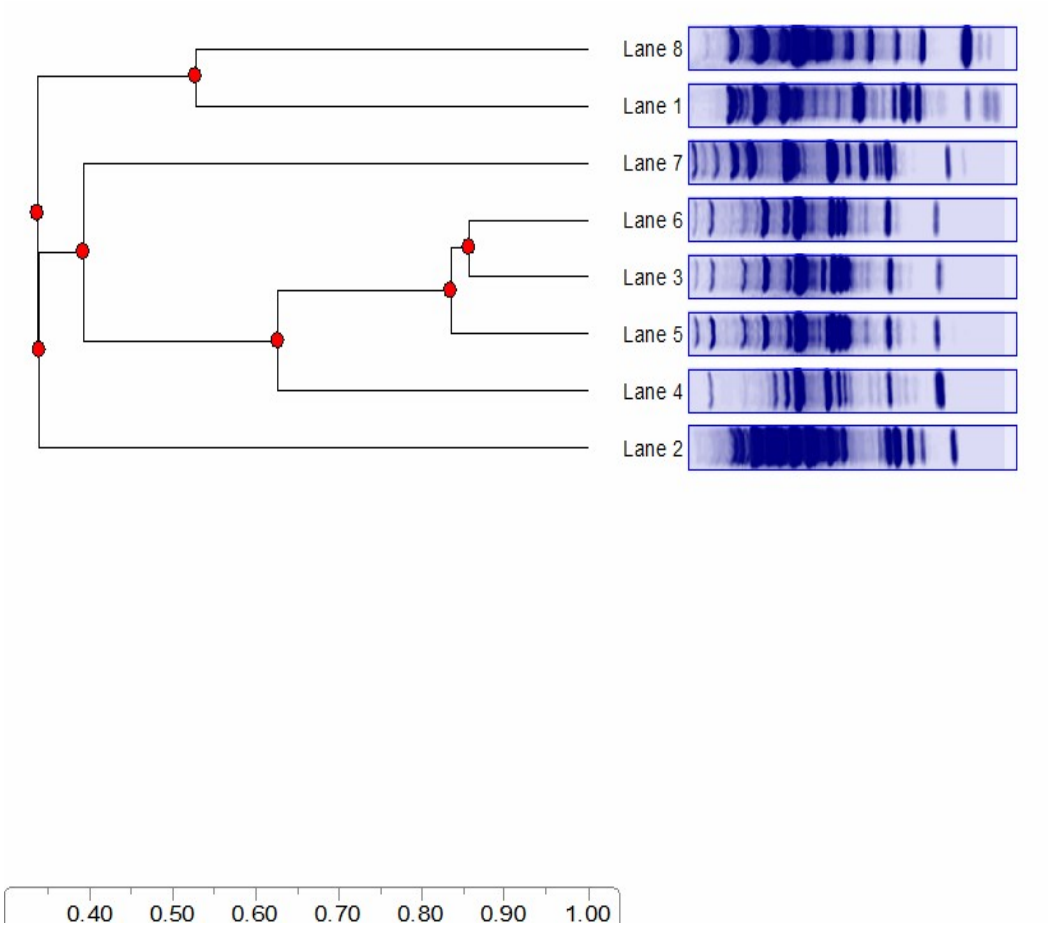

Figure 5. Phyllogenetic tree according to SDS-PAGE results

Table 34.Protein fraction comparision for eight teosinte **genotypes**

Fractions	Teosinte Genotypes protein fractions (KDa)							
	1	**2**	**3**	**4**	**5**	**6**	**7**	**8**
1	-	151	-	-	151	151	151	-
2	-	138	-	-	-	-		-
3	-		-	-	-	-	117	117
4	-	107	107	107	107	107	-	-
5	100	100		-	-	-	100	-
6	-	-	94	-	-	-		-
7	88	-		-	-	88	88	88
8	81	81		-	-	-	-	-
9	77	-	77	77	77	77	-	-
10	-	-	-	-	-	-	73	-
11	69	69	-	-	-	-		-
12	66	66	66	-	66	66		66
13	-	-	63	63	63	63	63	63
14	-	60	-		-	-	60	-
15	-	56	-	56	-	-	-	-
16	-	-	-	-	54	-	-	-
17	52	52	-	-		-	-	52
18	-	-	50	50	50	50	50	
19	-	48	-	-	-	-	48	48
20	47	-	47	47	47	47	-	47
21	-	-	45	-	45	45	45	-
22	-	44	-	-		44	44	44
23	42	42	-	-	42	-	-	42
24	41	-	41	41	-	-	-	41
25		40	40	-	40	40	40	-
26	39.5	-	39.5	39.5	39.5	39.5	-	-
27	-	39	39	39	39	39	-	-
28	-	-	-	38.5	-	-	38.5	38.5
29	37.5	37.5	37.5	-	-	37.5	37.5	-
30	-	-	37		37	37	-	-
31	36.5	-	-	36.5	-	-	-	36.5
32	-	-	-		-	-	36	-
33	-	35.5	-	35.5	-	-	35.5	-
34	35	-	-		-	-	-	-
35	-	34.5	34.5	34.5	34.5	34.5	34.5	-
36	34	34	34	34	34	34	-	34
37	33.5	-	-		-	-	-	-
38	-	-	-	33	-	-	-	-
39	-	32.5	-	-	-	-	-	-
40	-	-	-	-	-	-	-	32
41	31.5	-	-	-	-	-	-	-
42	-	31	-	-	-	-	-	31
43	-	-	-	-	29.5	29.5	-	-
44	-	-	29	29	-	-	-	-
45	28.5	-	-	-	-	-	-	-
46	-	-	-	-	-	-	28	-
47	-	27	-	-	-	-	-	-
48	-	-	-	-	-	-	21	-
49	18	-	-	-	-	-	-	18
50	-	-	-	-	-	-	-	12
51	10	-	-	-	-	-	-	10
52	8	-	-	-	-	-	-	

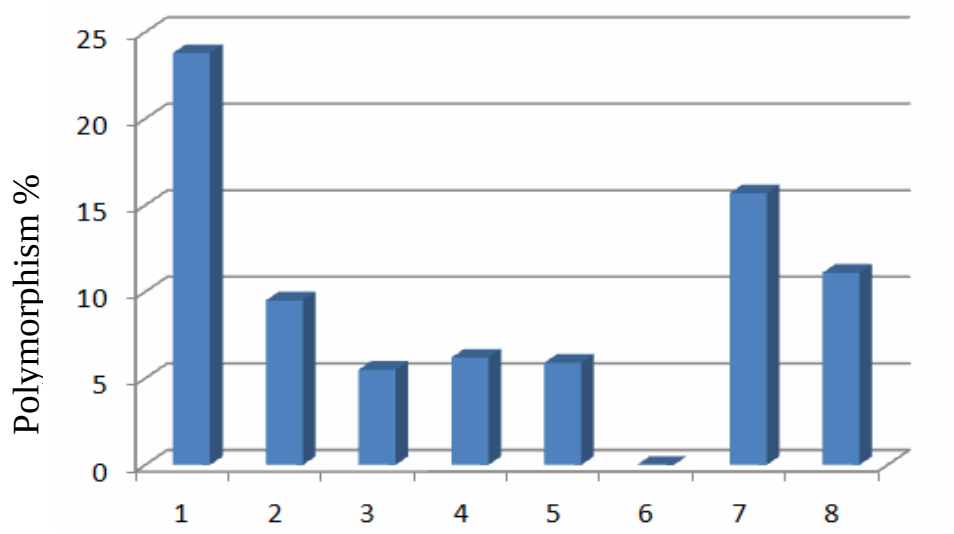

Figure 6. Polymorphism (%) for eight teosinte genotypes

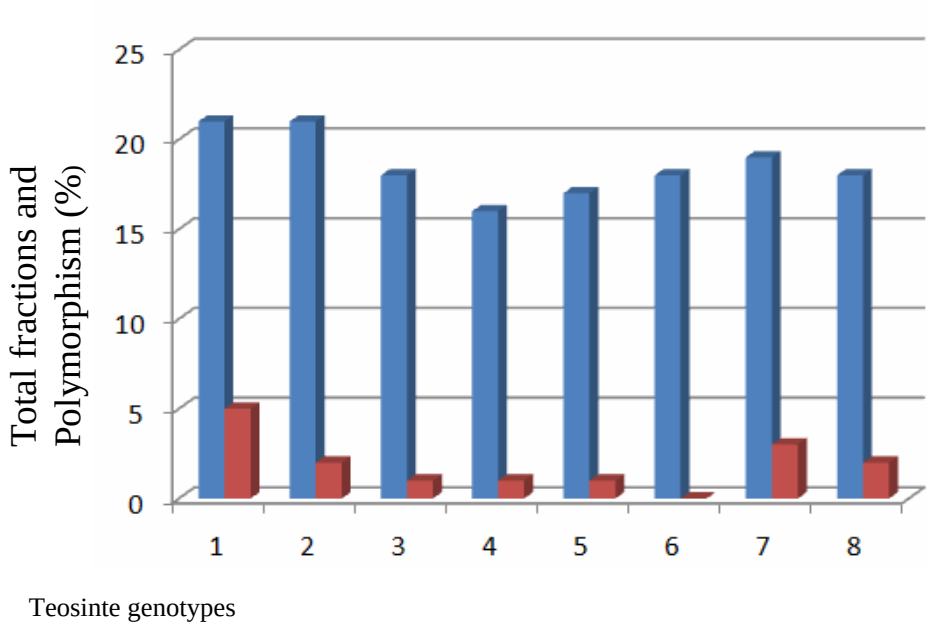

Figure 7. Total fractions and Polymorphism (%) for eight teosinte genotypes

Where:

Total fractions

Polymorphism (%).

Table 35. Total fractions and polymorphism (%) for eight teosinte genotypes

Teosinte genotypes	Total fractions	Monomorphic fractions	Polymorphic fractions	Polymorphism (%)
1	21	16	5	23.8
2	21	19	2	9.5
3	18	17	1	5.5
4	16	15	1	6.2
5	17	16	1	5.9
6	18	18	0	0
7	19	16	3	15.7
8	18	16	2	11.1

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الملخص العربي

تقييم بعض التراكيب الوراثية المبشرة من الذرة الريانة للصفات المورفولوجية والثوابت الوراثية تحت الظروف المصرية

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يعتبر تحليل التباين بين التراكيب الوراثية المختلفة للصفات المختلفة وتقدير درجات الارتباط بالمحصول ودرجة التوريث ودرجة القرابة من الأهمية بما كان لنجاح برامج التربية المختلفة، تمت إقامة التجربة الخاصة بهذه الدراسة في محطة بحوث الجميزة الزراعية ومركز البحوث الزراعية خلال موسمي صيفي ٢٠١٤، ٢٠١٥م لتقييم (ثمانية) تراكيب وراثية من الذرة الريانة متضمنة الصنف المحلي من الذرة الريانة وانتخاب أفضلها حيث أظهرت النتائج أن التركيب الوراثي (٣) والتركيب الوراثي (٤) تفوقا على باقي التراكيب الوراثية في موسمي ٢٠١٤ و ٢٠١٥ لكل الصفات المدروسة، وأظهرت النتائج وجود فروق معنوية بين التراكيب المختبرة خلال كل الصفات المدروسة وهذا يوضح إمكانية الانتخاب واستخدام برامج التربية اعتماداً على هذه الصفات، مستخدماً تلك التراكيب الوراثية خاصة رقمي (٣ و٤) كما كانت هناك فروقاً كبيرة بين التراكيب الوراثية لمعظم الصفات المدروسة وراثياً من خلال درجة التوريث بمفهومها الواسع حيث أظهرت النتائج أن درجة التوريث تراوحت ما بين (٨٦,٢ إلى ٩٩,٩%) لصفة المحصول الأخضر (FY) وصفة عدد الأوراق بالساق (NL/S).

وأظهرت تقنية تحليل البروتين (SDS – PAGE) التباين بين التراكيب الوراثية من حيث المحتوى البروتيني الكلي الذائب وأظهرت أيضاً اختلافات الـ Bands الخاصة بالبروتين في التراكيب الوراثية المدروسة حيث تراوح عدد الـ Bands من ١٦ إلى ٢١ Bands في كل من التركيب الوراثي رقم (٣) والتركيب الوراثي رقم (١) وكذلك التشابه الوراثي في شكل البروتين والأوزان الجزئية لكل من التركيب الوراثي رقم (٣) والتركيب الوراثي رقم (٤).

كذلك أظهرت درجة القرابة الوراثية انتماء كل من التراكيب الوراثية (٣، ٤، ٥، ٦، ٧) إلى مجموعة واحدة وهذا يدل على التشابه من الناحية الوراثية ودرجة القرابة الوراثية بينهم.

توصي نتائج هذه الدراسة بوضع التراكيب الوراثية رقمي ٣ و٤ كتراكيب وراثية مبشرة جديدة من الذرة الريانة تتميز بصفات محصولية علفية جيدة.

الكلمات الدالة : الذرة الريانة – التباين الوراثي – تحليل البروتيني SDS – PAGE – المكافئ الوراثي بالمفهوم الواسع.