

Agro-Morphological and Chemical Traits Diversity in Nine Maize (*Zea mays* L.) Genotypes

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ABSTRACT

Diversity of traits is a major need of any plant breeding program that concerns the natural evolution and causes sustainable plant production under various environments. Phenotypic variations based on agro-morphological and chemical traits of nine maize genotypes were studied under field and laboratory conditions during 2015 at the experimental farm of the Faculty of Agricultural Sciences, Qlyasan in Iraq. The genotypes differed significantly for all traits studied. Fajr 260 was the tallest plant. Talar was the latest genotype for number of days to tasseling and silking while Es-Solito 635 needed the maximum number of days for harvesting. The best performances of number of kernels per row, the number of kernels per ear and kernels yield were observed by genotypes Btaris and Cantapbis. Plant height, number of kernels per row, ear weight and kernel weight per ear were the most influential characters that conferred to the genetic diversity. Data indicated a wide range of variation among maize genotypes for traits of oil and protein contents. Talar had the maximum kernel oil and ash content; whereas, Iranian genotypes exhibited the lowest values of all chemical composition traits. The results of the principal component analysis (PCA) showed that the first two components accounted for more than 62.35% of total variation. Cluster analysis based on 23 traits exhibited three distinct clusters. High similarity was observed between Cantapbis and Bataris. At the same time, ZP434xA and Talar were more differentiated from others. This information about the genetic diversity may be utilized in the future maize breeding programs.

Keywords: Maize, Agro-morphological traits, diversity.

INTRODUCTION

Maize (*Zea mays* L.) is considered as a member of the family Poaceae. Maize is a highly polymorphic, annual diploid species with ten chromosomes, including both wild teosinte and cultivated maize. Maize is considered as the third most important cereal crop after wheat and rice around the world. It is covered 4.8% of the total cropped

area and attributed by 3.5% of world crops value of agricultural output (Ahmad *et al.*, 2011). Many million people in the world consume maize as an important food, and 40% of the world's maize is grown in the United States. However, the cultivation lands and production of maize in Kurdistan is limited. It is primarily utilized for livestock feed. In general, the cultivated genotypes in Kurdistan have low-quality nutrition. It is important to focalize research of maize genotypes on the regions where modern genotypes can adopt and benefit the local rural society. These research studies are important for supervising the menaces of maize diversity and for a better understanding of economic, social and cultural factors that have an effect on the maize growth and

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divergences (Vaz Patto *et al.*, 2007). The agro-morphological and molecular markers methods can be a foundation for acknowledgment of geographic diversity and indication.

As in other crops, agro-morphological characteristics were used to interpret the genetic semblance and the assortment of maize races. Therefore, the divergence studies that are subjected to agro-morphological characters usually showed different results, and the estimation of these traits have to grow the plants until complete maturity for diagnostic purposes. An agro-morphological marker is any visible phenotype, for which alleles at individual loci segregate in a Mendelian manner. The use of markers as an assisting tool to select the genotypes with beneficial traits had started in the breeding program long time ago and there is crucial need to optimize the efficiency of hybrid combinations and to produce new inbred lines, presenting of maize genotypes from different origins. Furthermore, genotypes organization and conservation in breeding programs documented the information of genetic relationships among genotypes of well parental selection (Melchinger *et al.*, 1991; Bernardo, 2002). In which, the specific objectives of this study were to:

- Assess and compare the agro-morphological and chemical traits diversity in maize populations (Local and Iranian).
- Classify the genotypes into relatively homogeneous groups based on phenotypic data.

Materials and Methods

Plant materials

The nine maize genotypes used in this study were; Es-Solito, Medium 791, Dhqan, Fajr 260, Btaris, Cantabpis, Talar, MSIxB, and ZP434xA. Es-Solito, Medium 791, Dhqan, Fajr 260, Btaris and Cantabpis genotypes were produced from College of Agriculture, the University of

Kurdistan, Sianandaj, Iran, while the local genotypes: Talar, MSIxB and ZP434xA were collected by Ministry of Agriculture in Kurdistan region-Iraq.

Soil preparation, experimental design, and sowing

Field work was carried out in Qlyasan Research Station, Faculty of Agricultural Sciences, University of Sulaimani, Iraq with latitude 35°32'30"N, longitude 45°21'00"E and 738 masl, during the spring in 2015. The trial was carried out on a total plot size of 300 m². The land used for the trial was cleared and plowed. Ridges were made manually using hoes. Randomized complete block design (RCBD) layout with three replications was used. Planting was done on 4th April 2015. For each genotype, three grains per hill were planted. Thirty plants per plot were kept in three rows with 3 m long. The distance between two rows and two plants was 0.75 m and 0.25 m, respectively. The experiment was fertilized with the urea (20%N), superphosphate (20%P₂O₅), and potassium (20%K) with 50kg/do, respectively as first does at planting, and second does as a urea 80kg/do after 40 days from germination. The crosses between self-plant were made, each cross was made in 10 ears as well as the self-pollination was made for each genotype. The ten ears per plot for each genotype were harvested at maturity.

Data collection

The measurements were taken as a mean of 10 randomly selected plants in each plot for each genotype.

A. Vegetative characters and phenological characters

- **Plant height (PH):** it was measured by the mean of the height of plant (cm) from the soil surface to the base of tasseling at flowering stage.
- **Days to 50% tasseling (DT):** it was recorded by the number of days from sowing up to 50% of the plants showing tassel emergence.
- **Days to 50% silking (DS):** it was counted by the

number of days from planting up to 50% of the plants display silk emergence.

- **Days to harvesting (DH):** it was calculated by the number of days from sowing to physiological maturity.

B. Reproductive characters

- **The distance of ear from the soil surface (DES):** it was the distance (cm) between ear and soil surface.

- **Number of ears/plant (NEP):** it was counted by the average of the number of ears per plant.

- **Ear length (EL):** it was determined as the average distance of ear (cm) from the base to the tip of ten randomly de-husked cobs per plot.

- **Number of row/ear (NRE):** it was measured by the average of the number of rows per ear.

- **Ear diameters (ED):** it was determined as the mean of the width of the ear (cm) of ten randomly de-husked cobs per plot.

- **Number of kernels/row (NKR):** the actual count of the average of the number of kernel per row of the ear.

- **Number of kernels/ear (NKE):** this was measured as the average number of kernels per ear.

- **Ear weight (EW):** this was measured as the mean of weight (g) of ear harvested per plant, and recorded at 15.5% kernel moisture content.

- **Kernel weight/ear (KWE):** this was determined as the mean weight (g) of kernels per ear.

- **300 kernels weight (TKW):** it was recorded from a three samples (300 grains/sample) of the freshly harvested ear, as the average of weight (g) at 12.5% moisture content.

- **Kernel yield (KY):** the fresh weight of ten harvested ears for each plot was taken at 15.5% kernel moisture and converted to (ton /ha).

- **Kernel length (KL):** this was determined as the

mean of length (mm), from the base to the tip, of 50 randomly selected kernels per plot.

- **Kernel width (KW):** this was counted as the average width (mm) of 50 randomly selected kernels per plot.

- **Plant height/ear height index (PH/EL):** it was formed by the dividing of plant height on the ear length.

- **Ear height/ear diameter index (EH/ED):** it was counted by dividing of ear height on ear diameter.

- **Kernel length/kernel width index (KW/KL):** it was calculated by dividing of kernel length on kernel width.

C. Proximate composition traits

• Measurement of kernel oil content (KOC%)

Ten gram of maize kernel was ground into fine powder with mortar and pestle. The oil content of maize seeds was obtained by complete extraction using the Soxhlet extractor (Konté, USA). Three gram of each powdered seed sample was put into a porous thimble and placed in a Soxhlet extractor, using 150 cm³ of n-hexane (with a boiling point of 40-60° C) as an extracting solvent for 6 hours. The oil was obtained after the solvent was removed. The oil content was calculated as follows: % oil content= (weight of oil/weight of the sample) *100.

• Measurement of kernel ash content (KAC%)

Five grams of the dried ground sample was weighed into a dry porcelain dish and then heated in a muffle furnace at 550°C for 24 hours and then cooled in desiccators and weighed. The content of ash was calculated by this formula: % ash = (weight of ash/ weight of sample) *100.

• Measurement of kernel protein content (KPC%)

The total protein in grain was determined by the method of Chow *et al.* (1980).

Statistical data analysis

The software JMP version 7 and XLSTAT version 11

were used for statistical analysis like one-way analysis of variance and Duncan multiple range test at 5% level (ANOVA-RCBD). The principal component analysis (PCA) (Eriksson *et al.*, 1999) was determined to assess the relationship between the variables (Traits and Genotypes). Depending on the means of agro-morphological and chemical composition characters, the dendrogram was produced by using the Euclidean distances and unweighted pair-group method with the arithmetic mean (UPGMA) analysis method.

Results and Discussion

Analysis of variance and pair-wise comparison displayed significant variations between tested maize genotypes. Agro-pheno-morphological characteristics are still benefit for primary estimation because they are fast, simple and can be used as a general approach for evaluating genetic variation among morphologically discernible genotypes.

Evaluation of vegetative and phenological characters

To determine the difference presenting among collected genotypes from different origins, different statistical analyzes were achieved, and the results are showed after that. Results collected from ANOVA and pair-wise comparison displayed significant variations between maize genotypes for all vegetative and phenological traits (Table 1). The values of plant height were varied from 182.067- 220.200 cm, respectively (Table 2). The maximum value of plant height was recorded by Fajr 260T while the minimum value of plant height was exhibited by Dhqan. These results indicated that these two Iranian genotypes are highly adapted to specific environmental conditions, and thus, they could be

a valuable source of genetic variability. These results also documented the existence of genetic diversity in the evaluated genotypes. Ihsan *et al.* (2005) also showed significant genetic variations for plant height traits between other maize genotypes. Agro-morphological markers have been used in studies of maize landraces by several researchers (Ruiz de Galarreta & Alvarez, 2001; Lucchin *et al.*, 2003; Ortiz *et al.*, 2008). Similar results have recorded elsewhere (Idris and Abualli, 2011 and Kamara *et al.*, 2003). They have displayed significant variability in different maize populations in term of growth traits. Also, Nazir *et al.* (2010); Salami *et al.* (2007) showed great significant variation in plant height in various maize genotypes. The nine maize genotypes diverged significantly for number of days to 50% tasseling, days to 50% silking, and days to harvesting. The means of number of days to tasseling, days to silking, and days to harvesting was expressed from 62.965-79.833, 68.420-83.111, and 112.833-133.833 (Table 2). Dhqan has the lowest scores for tasseling and silking, 62.965 and 68,420 days, respectively, and could be considered as with intermediate yields. Es-Solito 635 expressed the maximum number of days to maturity (133.833 days). Local genotype Talar gave the highest periods for 50% tasseling (79.833 days), silking, and (83.111 days). These differences might be due to their variations in genetic background and climatic factors. These results have been confirmed by other studies. Fehr (1993) demonstrated that the level of performance of various genotypes might not be the same if they were sown in various environments and will grow to depend on their genetic power. These results also in consistence with the findings of Naushad *et al.* (2007); Akbar *et al.* (2008); Nazir *et al.* (2010).

Table 1. Mean squares of the analysis of variance of agro-morphological and chemical composition characters in nine maize genotypes.

Characters	DF			Mean square		
	Replications	Genotypes	Error	Replications	Genotypes	Error
Plant height	2	8	16	37.96	435.356**	60.957
Days to 50% tasseling	2	8	16	27.85	78.320**	19.733
Days to 50% silking	2	8	16	27.18	63.054*	16.839
Days to harvesting	2	8	16	28.69	124.903**	10.836
Distance of ear from the soil surface	2	8	16	377.724	300.285**	62.826
Number of ears/plant	2	8	16	0.084	0.258**	0.045
Ear length	2	8	16	0.169	6.972**	0.819
Number of rows/ear	2	8	16	0.373	3.082*	0.431
Ear diameter	2	8	16	0.11	0.190*	0.057
Number of kernels/ear	2	8	16	1789.839	9223.896*	2459.844
Number of kernels/row	2	8	16	11.286	50.162**	10.425
Ear weight	2	8	16	52.573	969.187**	105.622
Kernel weight/ear	2	8	16	37.79	802.649**	86.059
300 kernel weight	2	8	16	2.287	85.648*	30.892
Kernel yield	2	8	16	1.951	17.598**	2.32
Kernel length	2	8	16	0.171	0.458*	0.151
Kernel width	2	8	16	0.077	0.349*	0.097
Plant height/Ear height	2	8	16	0.237	3.666**	0.268
Ear height/Ear diameter	2	8	16	0.04	0.0810*	0.028
Kernel length/Kernel width	2	8	16	0.031	0.117**	0.027
Kernel oil content	2	8	16	0.049	1.854**	0.121
Kernel ash content	2	8	16	0.002	0.0207*	0.006
Kernel protein content	2	8	16	0.000048	0.0308**	0.00076

Table 2. Mean value, pair-wise comparison and some statistical descriptions of vegetative and phenological traits measured for nine maize genotypes.

Genotypes	PH	DT	DS	DH
Es-Solito 635	189.250 ^c	67.520 ^{bc}	70.417 ^{bc}	133.833 ^a
Medium 791	191.600 ^c	74.326 ^{ab}	77.875 ^{ab}	124.569 ^b
Dhqan	182.067 ^c	62.965 ^c	68.420 ^c	116.625 ^{cd}
Fajr 260	220.200 ^a	65.423 ^c	70.298 ^{bc}	112.833 ^d
Btaris	206.233 ^{ab}	69.812 ^{bc}	75.305 ^{bc}	122.104 ^{bc}

Genotypes	PH	DT	DS	DH
Cantabpis	195.067 ^{bc}	66.695 ^{bc}	71.500 ^{bc}	123.222 ^b
Talar	206.600 ^{ab}	79.833 ^a	83.111 ^a	130.534 ^a
MSI xB	209.900 ^{ab}	69.604 ^{bc}	74.506 ^{bc}	121.778 ^{bc}
ZP 434 xA	206.867 ^{ab}	66.604 ^{bc}	71.736 ^{bc}	119.763 ^{bc}
Minimum	182.067	62.965	68.420	112.833
Maximum	220.200	79.833	83.111	133.833
Mean	200.865	69.198	73.685	122.807
Standard deviation	12.046	5.109	4.585	6.452

PH: Plant height (cm), DT: Days to 50% tasseling, DS: Days to 50% silking and DH: Days to harvesting. Data superscripted by the same letter are not significantly different at the 0.05 level using Duncan multiple range test.

Evaluation of reproductive characters

The significant genotypic effects were presented for all reproductive characters; kernels yield being complex trait is highly influenced by various environmental factors including biotic and abiotic factors. Reproductive characters were also the most important trait in maize that should be taken during the selection of favorable genotypes. As shown in Table 1, the significant genotypic effects were presented for all reproductive studied traits. The variations in present investigations were due to divergent maize genotypes in genetic makeup. The distance of ear from the soil surface, number of ears/plant, ear length, number of rows/ear, ear diameter, number of kernels/ear, number of kernels/row, ear weight, kernel weight/ear, 300 kernel weight, and kernels yield ranged from 77.033-100.500 cm, 1.433-2.333, 18.227-22.383 cm, 13.986-16.233, 6.099-6.795, 360.375-504.933, 24.007-35.209, 102.912-145.688 g, 82.144-122.122 g, 58.893-74.097g, and 5.912-13.207 (ton/ha), respectively (Table 3).

The lowest distance of ear from the soil surface, number of ear/plant, ear length, number of row/ear, ear diameter, number of kernels/ear, number of kernels/row, ear weight, kernel weight/ear, 300 kernel weight, kernels

yield, kernel length, and kernel width were performed by Es-Solito 635, Talar, Fajr 260, Es-Solito 635, Fajr 260, MSIxB, Talar, Fajr 260, MSIxB, ZP 434xA, Cantabpis, Talar, Medium 791, Talar, Talar, Dhqan, respectively. As shown in the (Table 2), the best performances of reproductive characters were observed by Medium 791, Dhqan, Cantabpis, Btari, Cantabpis, Dhqan and Es-Solito 635, respectively. It was noticed that Talar genotype was inferior in the traits of: number of ears/plant, kernel weight per ear, kernel yield and kernel length, Whilst the genotype Cantabpis superseded all genotypes for the traits of: ear diameter, ear weight, kernel weight per ear and kernels yield and followed by Btari for the traits of: ear length, 300-kernel weight, and kernels yield. The differences in yield components indicated that the capability of genotype diverges with their genetic constituent (Pohlman and Sleper, 1995). Therefore, it is suggested that these genotypes have to be tested in different ecological zones of Iraq. These results are in line with the findings of Sokolov and Guzhva (1997); Ajmal *et al.* (2000); Zahid *et al.* (2004); Olakojo and Olaoye (2005); Ahmad *et al.* (2011).

Table 3. Mean value, pair-wise comparison and some statistical descriptions of reproductive and proximate composition characters collected from nine maize genotypes.

Genotypes	DES	NEP	EL	NRE	ED	NKE	NKR	EW
Es-Solito 635	77.033 ^d	1.567 ^{de}	19.450 ^{bc}	13.986 ^b	6.525 ^{ab}	386.543 ^{bc}	27.261 ^{bc}	108.012 ^b
Medium 791	100.000 ^{ab}	1.667 ^{cde}	21.625 ^a	14.206 ^b	6.652 ^a	500.524 ^a	35.209 ^a	130.601 ^a
Dhqan	78.133 ^d	1.900 ^{bcd}	18.490 ^c	14.867 ^b	6.370 ^{ab}	504.933 ^a	33.945 ^a	131.664 ^a
Fajr 260	81.933 ^{cd}	1.933 ^{abcd}	18.227 ^c	14.500 ^b	6.099 ^b	386.504 ^{bc}	27.176 ^{bc}	102.912 ^b
Btaris	85.300 ^{bcd}	2.067 ^{ab}	22.383 ^a	14.433 ^b	6.705 ^a	470.867 ^{ab}	32.897 ^{ab}	145.031 ^a
Cantabpis	81.533 ^{cd}	2.167 ^{ab}	20.787 ^{ab}	15.200 ^{ab}	6.795 ^a	478.188 ^{ab}	31.574 ^{ab}	145.688 ^a
Talar	99.833 ^{ab}	1.433 ^e	19.057 ^c	16.233 ^a	6.704 ^a	391.633 ^{bc}	24.007 ^c	106.050 ^b
MSIxB	96.033 ^{abc}	2.033 ^{abc}	18.606 ^c	14.722 ^b	6.154 ^b	360.375 ^c	24.498 ^c	107.331 ^b
ZP 434xA	100.500 ^a	2.333 ^a	18.605 ^c	14.453 ^b	6.369 ^{ab}	423.726 ^{abc}	29.667 ^{abc}	103.903 ^b
Minimum	77.033	1.433	18.227	13.986	6.099	360.375	24.007	102.912
Maximum	100.500	2.333	22.383	16.233	6.795	504.933	35.209	145.688
Mean	88.922	1.900	19.692	14.733	6.486	433.699	29.582	120.132
Standard deviation	10.004	0.293	1.524	0.666	0.252	55.449	4.089	17.974

DES: Distance of ear from the soil surface (cm), NEP: Number of ears/plant, EL: Ear length (cm), NRE: Number of rows/ear, ED: Ear diameter (cm), NKE: Number of kernels/ear, NKR: Number of kernels/row and EW: Ear weight (g). Data superscripted by the same letter are not significantly different at the 0.05 level using Duncan multiple range test.

Table 3. continued

Genotypes	KWE	300KW	KY	KL	KW	PH/EL Index	EL/ED Index	KL/KW Index	KAC	KOC	KPC
Es-Solito 635	83.318 ^c	67.010 ^{abc}	6.532 ^{de}	9.424 ^{cd}	5.493 ^a	9.746 ^{cd}	2.985 ^{bc}	1.736 ^d	1.311 ^c	6.396 ^{cd}	6.360 ^e
Medium 791	104.734 ^b	58.893 ^c	8.757 ^{cd}	10.332 ^{ab}	4.547 ^{cd}	8.866 ^d	3.250 ^{ab}	2.281 ^{ab}	1.355 ^{bc}	6.472 ^{cd}	7.030 ^d
Dhqan	105.306 ^{ab}	61.073 ^{bc}	10.029 ^{bc}	10.439 ^a	4.398 ^d	9.851 ^c	2.903 ^c	2.374 ^a	1.372 ^{bc}	6.593 ^{bcd}	7.201 ^d
Fajr 260	83.391 ^c	62.333 ^{bc}	8.074 ^{cde}	9.801 ^{abcd}	4.776 ^{bcd}	12.083 ^a	2.992 ^{bc}	2.058 ^{bc}	1.470 ^{ab}	7.214 ^b	8.230 ^b
Btaris	120.269 ^{ab}	74.097 ^a	12.395 ^{ab}	10.209 ^{ab}	5.162 ^{ab}	9.220 ^{cd}	3.346 ^a	1.978 ^{bcd}	1.377 ^{bc}	6.148 ^{cd}	7.830 ^{bc}
Cantabpis	122.122 ^a	71.583 ^{ab}	13.207 ^a	10.117 ^{abc}	5.194 ^{abc}	9.384 ^{cd}	3.059 ^{abc}	1.952 ^{cd}	1.327 ^{bc}	5.980 ^d	5.501 ^f
Talar	82.144 ^c	63.580 ^{bc}	5.912 ^e	9.365 ^d	5.088 ^{abc}	10.840 ^b	2.842 ^c	1.845 ^{cd}	1.556 ^a	8.550 ^a	7.032 ^d
MSI xB	86.936 ^c	62.173 ^{bc}	8.855 ^{cd}	9.735 ^{abcd}	4.865 ^{bcd}	11.286 ^{ab}	3.036 ^{abc}	2.004 ^{bcd}	1.472 ^{ab}	6.760 ^{cb}	8.960 ^a
ZP 434 xA	84.974 ^c	59.430 ^c	9.949 ^{bc}	9.673 ^{bcd}	4.845 ^{bcd}	11.177 ^{ab}	2.920 ^c	2.005 ^{bcd}	1.475 ^{ab}	6.174 ^{cd}	7.460 ^{cd}
Minimum	82.144	58.893	5.912	9.365	4.398	8.866	2.842	1.736	1.311	5.980	5.501
Maximum	122.122	74.097	13.207	10.439	5.493	12.083	3.346	2.374	1.556	8.550	8.960
Mean	97.022	64.464	9.301	9.899	4.93	10.273	3.037	2.026	1.413	6.699	7.230
Standard deviation	16.357	5.343	2.422	0.391	0.341	1.145	0.212	0.235	0.083	0.786	0.337

KWE: Kernel weight/ear (g), 300KW: 300 kernel weight (g), KY: Kernels yield (ton/hectare), KL: Kernel length (mm) and KW: Kernel width (mm) KOC: Kernel oil content (%), KAC: Kernel ash content (%), KPC (%).Data superscripted by the same letter are not significantly different at the 0.05 level using Duncan multiple range test.

Evaluation of chemical traits

Significant variations among maize genotypes for proximate composition: content of kernel oil, ash, and protein were detected (Table 1). The mean values of the kernel oil, kernel ash, and kernel protein contents were 5.980-8.550%, 1.311-1.556%, and 5.501-8.960%, respectively. As presented in the (Table 3), the results indicated that local maize genotype 'Talar' had maximum kernel oil and ash contents (8.550% and 1.556%, respectively); whereas Iranian genotypes exhibited the lowest values of all chemical composition traits. All these genotypes identified by high oil content could be used as a source material in a programs of breeding. Kernel oil content is considered as a quantitative trait that is controlled by numerous genes with small effects (Dudley, 1977). The data in this part of results mentioned a wide range among maize genotypes for traits: oil and protein contents. Previously, several chemical composition traits were studied by Moulin *et al.* (2003). Berardo *et al.* (2009) analyzed 1245 maize varieties from various countries. They observed that the protein content diverges from 7.39 to 15.42%. These results are in agreement with results from Berardo *et al.* (2009) who reported different ranges of divergence (5.26 and 7.17%) in kernel protein content for different maize genotypes. Also, different maize genotypes concentrated the different amount of their kernel oil content ranged from 0.04 to 12.3% which are highly supported in the study of Has *et al.* (2009). Further different ranges of kernel protein contents from 8 to 11% in different maize genotypes at the University of Illinois was recorded (Smith, 1990).

Phenotypic characterization of maize genotypes

Different methods were used for characterization of genotypes, and multivariate analysis was the most appropriate for them. Data mining was a very useful method for selection, exploration and modeling of hug datasets to detect novel trends to make the explaining

more attractive and decisive. Multivariate analyses were performed for data mining. Some multivariate analysis methods such as principle component analysis (PCA) and agglomerative hierarchical clustering (AHC) were used for genotypes clustering (Fernandez, 2002). Depending on the percentage of variance, eight principle components were produced. The PCA convert the 23 variables or traits to 8 independent combinations. These eight principle components formed 100% of the total variation among maize genotypes. The two principal components PC1 and PC2 revealed 62.350% of the original phenotypic variation. The value of the contribution of first and second components was 40.210 and 22.140%, respectively.

Regarding the distribution of genotypes on PCA plot, genotypes that were subsisted away from the center of the plot in the positive trends of distinct traits demonstrated their best performance whereas; the genotypes that were outmost from the center of the plot in the negative orientation of traits displayed their weak performance. The Iranian genotypes showed a wide variability in phenotypic traits among them. Three groups of maize genotypes with different genetic constituents were highlighted on scatter plot: the first group composed of Es-Solito 655, Talar, MSIxB and Fajr 260. The second group included Medium 791, Cantabpis, Btarris and Dhqan, whereas the last group comprised ZP 434xA. On the other hand, the results of phenotypic variation of some traits for Talar genotype were opposite to those recorded for Dhqan genotype. Ruiz de Galarreta and Alvarez (2001) described and classified seven groups of the Northern Spain maize landraces using a similar approach based on the morphological characterization of crop accessions. These results are also in consistence with that reported by Brandolini and Brandolini (2001) and Ruiz de Galarreta and Alvarez (2001) who used the morphological traits to classify of Spanish and Italian maize landraces respectively. N'da *et al.* (2015) classified 600 accessions of maize into five

clusters based on 22 traits.

Based on the average values of 23 morphological traits, cluster analysis was performed using Euclidean distance and UPGMA method (Figure 2). The maximum distance analysis was carried out by Dhqan and Talar which means that low similarity presented between them as these genotypes were collected from different parents and origins. In contrast, the minimum dissimilarity was stated between Btaris and Cantabpis. These two genotypes might be introduced from the same region. Variation in these results might be due to different environmental conditions where the genotypes had been grown. Also, the constructed dendrogram confirm the results of PCA in the classification

of genotypes. The agglomerative hierarchical clustering classified the nine genotypes into three major groups. In which, the first group consisted of Es-Solito 655, Talar, MSIxB and Fajr 260. The second group contained Medium 791, Cantabpis, Btaris and Dhqan. Whereas, the last group included ZP 434xA. As indicated in Figures 1 and 2, Talar genotype was the most far distant genotype compared to others. The two Iranian genotypes Cantabpis and Btaris showed more similarity. Concerning the genotypes dispersion could be noticed that most Iranian genotypes were dispersed on the scatter plot. This result indicated that there was a great divergence among Iranian genotypes.

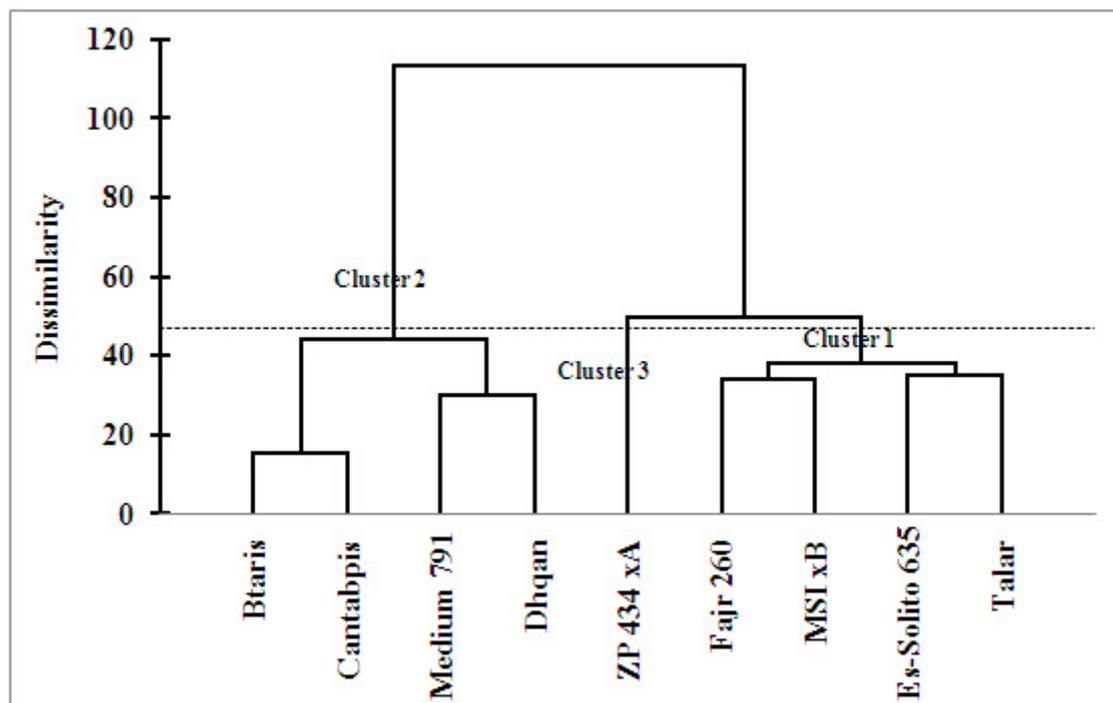


Figure 1: Cluster analyzes of maize genotypes depending on phenotypic characters using Euclidean distance and Unweighted pair-group method average (UPGMA).

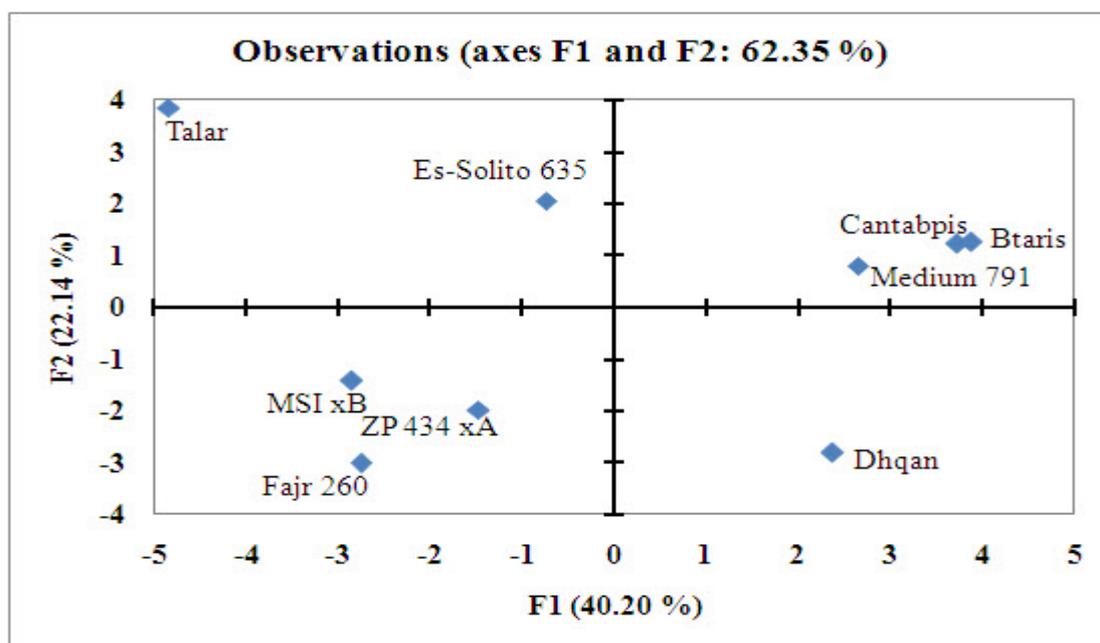


Figure 1: Principle component analysis (PCA) plot showing the distribution of maize genotypes on scatter plot based on the phenotypical data.

Conclusion

The nine maize genotypes studied have displayed a significant variation in term of agro-morphological and chemical compositions characteristics. The local genotype, Talar, needed more days to flowering, maturity and was superior in kernel oil content to other genotypes.

PCA and cluster analysis divided nine maize genotypes into three clusters. At the same time, ZP434xA were more differentiated from others genotypes. This study had identified two Iranian genotypes (Btaris and Cantabpis) as high yield potential.

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دراسة السمات الزراعية - المورفولوجية والكيميائية في تسعة أنماط من الذرة

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ملخص

تتبع الصفات هو حاجة رئيسية لأي برنامج تربية النباتات التي تتعلق بالتطور الطبيعي وتسبب إنتاج النباتات المستدامة في ظل بيئات مختلفة. تم دراسة الاختلافات النمطية المستندة إلى الصفات الزراعية - المورفولوجية والكيميائية لتسعة أصناف وراثية من الذرة تحت الظروف الحقلية والمختبرية خلال عام 2015 في كلية العلوم الزراعية، قليسان في العراق. اختلفت التركيب الوراثية معنويا لجميع الصفات الدروسة. أظهر التركيب الوراثي المحلي Fajr 260 أعلى قيمة لارتفاع النبات. احتاج التركيب الوراثي Talar إلى أعلى عدد من الايام للتزهير الذكري والانثوي، بينما احتاج Es-Solito 635 إلى عدد أيام أكثر للنضج. فيما ما يتعلق بصفات مكونات الحاصل، فإن أعلى عدد الحبوب/عرنوص، عدد الحبوب/صف وحاصل الحبوب سجلت من قبل الطرز Cantapbis و Btaris. وقد لوحظت ارتفاع النبات، وعدد من الحبوب في الصف، وزن العرنوص و وزن الحبوب في العرنوص كانت الصفات الأكثر تأثيرا التي تمنح للتنوع الجيني. وأشارت البيانات إلى وجود الاختلافات بين الأنماط الجينية للذرة لصفات الزيت ومحتويات البروتين. سجلت Talar الحد الأقصى لمحتوى الزيت والرماد، في حين أظهرت الأنماط الجينية الإيرانية أدنى القيم لجميع صفات التركيب الكيميائي. وأظهرت نتائج تحليل المكونات الرئيسية أن المكونين الأولين يمثلان أكثر من 62.35% من إجمالي التغير. وأظهر التحليل العنقودي المستند إلى 23 صفة، ثلاث مجموعات متميزة. وقد لوحظ تشابه كبير بين Cantapbis و Btaris. وفي الوقت نفسه، كانت ZP434xA و Talar أكثر تميزا عن الآخرين. ويمكن استخدام هذه المعلومات عن التنوع الجيني في برامج تربية الذرة في المستقبل.

الكلمات الدالة: الذرة، الصفات الزراعية- المورفولوجية، التنوع.

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