



## ORIGINAL ARTICLE

# Genetic diversity and Classification of Spring Safflower (*Carthamus tinctorius*) Cultivars using Morphological Characters

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### ABSTRACT

Assessment of genetic diversity is primarily useful to utilize the genetic materials through breeding programs. In this survey, genetic diversity of 30 spring genotypes of safflower (*Carthamus Tinctorius*) was assessed by morphological traits. Studying of morphological traits was conducted in two years (2005 and 2006) based on a randomized Complete Block Design with three replications. The results of analyses of variance for each year and combined analysis of data for two years demonstrated that the differences among genotypes were significant for more traits. Cluster analyses by ward method classified the genotypes based on morphological traits in two groups. The first group included 11 genotypes. The second group was divided into two subgroups with 11 and 8 genotypes. According to the results, land races genotypes, lines and improved genotypes were separately grouped as groups or subgroups. The result of principal component analyses introduced three principal components with eigenvalue more than one which contributed 72.92 percent of the total variability.

**Key words:** *Carthamus tinctorius*, Cluster analyses, Genetic diversity, Morphological traits, Principal component analyses.

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### INTRODUCTION

Safflower (*Carthamus tinctorius* L.), a member of the family of Asteraceae, is a multipurpose crop for oil, medicinal and industrial uses [1]. Traditionally, it was first grown for the pigment of flowers in order to color foods and dye cloths. Safflower seed is the harvestable part, either for feeding poultry or to extract its oil content [2]. Development of oil seeds cultivation has an important role to provide the requisite edible oils for human beings [3].

Path analysis has been used by plant breeders to assist in identifying useful selectable traits [4,5]. Partitioning of the correlation coefficient into its components, one component being the path coefficient that measures the direct effect of a predictor variable upon its response variable; the second component being the indirect effect(s) of a predictor variable on the response variable through another predictor variable is the advantage of path analysis [4].

Iran is one of the centers of safflower culture in the old world. Diverse climatic and agricultural conditions of Iran had led to formation of many local population of this crop in the country [6]. Many of these populations possess genotypes with favorable characteristics for agricultural and industrial purposes.

For the effective use of underutilized crops, it is critical to understand the extent and distribution of genetic diversity within species [7]. The first program for breeding, genetic diversity studies in crop plants mostly relied on the evaluation of morphological and agronomic traits [8,9].

Characterization of safflower germplasm so far included agro-morphological studies [1,4, 10] biochemical analyses [11-13] and, recently, molecular markers have been applied [14-16].

The objectives of this research were to evaluate the genetic diversity and classification of spring safflower genotypes using morphological characters.

### MATERIAL AND METHODS

#### Plant material and morphological evaluation:

In this study, 30 spring safflower genotypes were used. Field experiments were carried out at the research station of Faculty of Agriculture, Islamic Azad University- Shabestar branch in 2005 and 2006. These genotypes were planted in the field based on the randomized complete block design with three

replications in each of the years. The genotypes included four lines in each replication. Seeds were sown row to row distance of 40 cm and plant to plant distance of 15 cm. All other agronomic practices were kept uniform. Characters were evaluated on ten randomly selected plants in the mid-rows of plots. The following quantitative morphological variable were grain yield (kg/ha), plant height (cm), number of heads per plant, number of seeds per head, 100 seed weight (g), effective head weight (g), effective heads weight per plant (g), plant weight (g), hectoliter weight (g), biological yield (kg/h), harvest index, days to 50% flowering and days to maturity.

#### Statistical analysis:

Estimated data in 2005 and 2006 years were combined and analysed. The path and correlation analyses following the methods of Dewey and Lu [17] and Snedecor and Cochran [18], respectively. Cluster analyses according to guide liners of SPSS software were performed using morphological data by ward's method. The data were subjected to principal component analysis (PCA) by SAS software [19].

## RESULTS AND DISCUSSION

### Correlation

The correlation among all pairs of variables is shown in Table 1. Grain yield was significantly correlated with plant height ( $r = 0.56^{1**}$ ), hectoliter weight ( $r = 0.602^{**}$ ) and biological yield ( $r = 0.978^{**}$ ). The other characters expressed a non-significant correlation.

Therefore, the function of the each of the traits is assessed in its performance on grain yield. Positive and significant correlation between grain yield and the plant height could be resulted via genotypes ability in competition of light absorption in order to promote the photosynthesis process.

Arslan [20] reported positive and significant relationships between grain yield and traits of plant height, number of heads per plant, branch height, stem diameter, head diameter, number of seeds per head. The reported results by Dingming et al. [21], Zheng [22], Patil et al. [23] and Omidi [24] have supported the present results. These results showed that any positive increase in such characters will suffice the boost in grain yield.

The highest positive correlations were obtained between biological yield with some characters which include; plant height ( $r = 0.621^{**}$ ), day to 50% flowering ( $r = 0.37^*$ ) and day to maturity ( $r = 0.407^*$ ).

In this term, it is notable that the long time maturation of high length plants possibly leads to increase the biological yield performance.

Authenticity of the highly significant positive correlation between biological yield and number of head per plant with seed yield were approved by Mozaffari and Asadi [25] and Omidi [24].

Table 1: Correlation coefficients between characters measured in the mean of combine tow years.

characters	PH	DF	DM	PW	NH	HWP	EHW	NS	HW	SW	GY	BY	HI
PH	-												
DF	0.55**	-											
DM	0.614**	0.435**	-										
PW	0.193	-0.199	0.050	-									
NH	-0.034	-0.234	-0.084	0.688**	-								
HWP	0.045	-0.358	-0.107	0.819**	0.681**	-							
EHW	0.197	-0.154	-0.079	0.546**	0.125	0.699**	-						
NS	0.470*	0.161	0.384	0.450*	0.150	0.476**	0.540**	-					
HW	0.500**	0.606**	0.353*	-0.091	-0.261	-0.069	0.073	0.258	-				
SW	-0.307	-0.322	-0.082	-0.051	-0.165	0.089	0.384*	-0.226	-0.99	-			
GY	0.561**	0.276	0.342	0.304	-0.050	0.227	0.343	0.376*	0.602**	0.195	-		
BY	0.621**	0.369*	0.407*	0.254	-0.039	0.092	0.243	0.354	0.607**	0.128	0.978**	-	
HI	-0.413**	-0.423**	-0.45*	0.241	0.474*	0.624**	0.369*	0.006	-0.120	0.320	-0.016	-0.128	-

\* $p < 0.05$ , \*\*  $p < 0.01$ , Plant Height = PH, Days to 50% Flowering = DF, Days to Maturity = DM, Plant Weight = PW, Number of heads per plant = NH, Heads Weight per Plant = HWP, Effective Head Weight = EHW, Number of seeds per head = NS, Hectoliter Weight = HW, 100 seed weight = SW, Grain yield = GY, Biological Yield = BY and Harvest Index = HI,

### Path analysis

In order to determine the traits with biggest effect on the grain yield, all of the traits (except biologic yield and harvest index: these traits are completely dependent on grain yield), were considered as an independent and grain yield as a dependent variables. In the experiment, the stepwise and forward regression for grain yield indicated four centered traits of plant height, number of seed per plant, plant weight and hectoliter weight at the model.

Consequently, the direct and indirect effects of four examined traits on the grain yield were estimated by path coefficient (table 2). Path coefficient analysis revealed the plant height, number of seed per plant, plant weight and hectoliter weight characters as the traits with highest positive direct effects on grain yield. The plant height, number of seed per plant, hectoliter weight and plant weight seem to be important under this survey. This output suggests the increasing of these characters as the immensely efficient

criteria to improve yield of safflower. Similar results were reported by Ashri *et al*[26], Guo yahai *et al.* [27] and Abel [28].

The indirect effect of the plant height via hectoliter weight and plant weight were positive on grain yield but via number of seed per plant was negative. Nevertheless, the number of seed per plant had positive direct effect on grain yield; it had also negative indirect effects through plant weight and hectoliter weight on grain yield. Mahasi *et al.* [29] measured a high positive direct effect of 100 seeds weight and an indirect negative effect through number of seed per head, effective head weight and number of head per plant on grain yield.

Table 2: The direct (diagonal and bolded) and indirect effects of four traits on grain yield.

Characters	Direct effect	Indirect effect				Correlation confection with grain yield
		PH	PW	HW	NS	
PH	0.383	-	0.056	0.238	-0.115	0.561**
PW	0.292	0.074	-	-0.4320	-0.0191	0.304 <sup>ns</sup>
HW	0.475	0.1915	-0.0266	-	-0.0371	0.602**
NS	0.375	-0.118	-0.0148	-0.047	-	0.195 <sup>ns</sup>

ns=  $p > 0.05$ , \* $p < 0.05$ , \*\*  $p < 0.01$ , Plant Height = PH, Plant Weight = PW, Number of seeds per head = NS, Hectoliter Weight = HW, Adjusted  $R^2 = 0.662$

### Cluster analyses

The cluster analyses based on means of all morphological characters from each genotype shown in Figure 1 and Table 3. Cluster analysis categorized genotypes into two groups. Cluster 1 has 11 genotypes. Cluster 2 has 19 genotypes and could be further divided into two subgroups. Subgroup 1 includes 11 genotypes, (Zargan, LRV.51.141, Esfahan1, Esfahan2, Ch.353, CART.9094, 1457,3- Urmieh, Arak, Kh.34.779, Krdestan2). Subgroup 2 has 8 genotypes (Fariv3.76, Kurdistan1, LRV.51.233, Tabriz2, Tabriz1, Kh.2357, Kh.15.44, Arak2811.2).

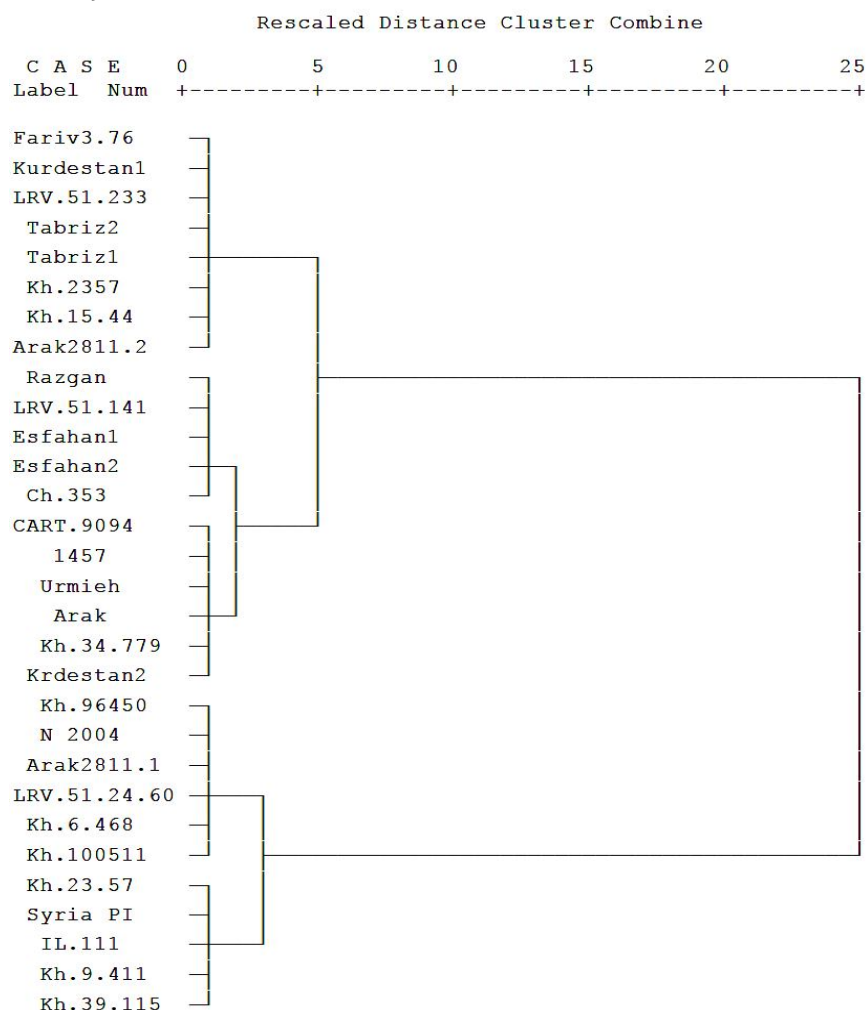


Figure 1: Cluster analysis of genotypes based morphological traits by using Ward's method

Table3: Mean and percent difference from total mean for each cluster based on morphological traits.

harvest index	biological yield	grain yield	100 seed weight	hectoliter weight	number of seeds per head	effective head weight	heads weight per plant	number of heads per plant	plant weight	days to maturity	days to 50% flowering	plant height	Genotype	Cluster
23.92 +0.53	33.71 -0.09	33.81 +0.21	33.65 -0.27	33.71 -0.09	33.81 +0.21	33.65 -0.27	33.71 -0.09	33.81 +0.21	33.65 -0.27	33.71 -0.09	33.81 +0.21	33.65 -0.27	Kh.96450, N 2004, Arak2811.1, LRV.51.24.60, Kh.6.468, Kh.10.0511, Kh.23.57, Syria PI, IL.III, Kh.9.411, Kh.39.115	1
3000.17 +2.43	3629.47 +23.92	3364.59 +14.87	2176.54 -25.68	3629.47 +23.92	3364.59 +14.87	2176.54 -25.68	3629.47 +23.92	3364.59 +14.87	2176.54 -25.68	3629.47 +23.92	3364.59 +14.87	2176.54 -25.68	Zargan, LRV.51.141, Esfahan1, Esfahan2, 9- Ch.353, CART.9094, 1457, Urmieh, 4- Arak, Kh.34.779, Krdestan2, FariV3.76, Kurdestan1, LRV.51.233, Tabriz2, Tabriz1, Kh.2357, Kh.15.44, Arak2811.2	2
1017.40 +3.39	1215.16 +23.19	1131.89 +15.03	728.52 -25.96	1215.16 +23.19	1131.89 +15.03	728.52 -25.96	1215.16 +23.19	1131.89 +15.03	728.52 -25.96	1215.16 +23.19	1131.89 +15.03	728.52 -25.96	Zargan, LRV.51.141, Esfahan1, Esfahan2, 9- Ch.353, CART.9094, 1457, Urmieh, 4- Arak, Kh.34.779, Krdestan2, FariV3.76, Kurdestan1, LRV.51.233, Tabriz2, Tabriz1, Kh.2357, Kh.15.44, Arak2811.2	2-1
3.38 -3.54	3.58 +2.17	3.49 -0.40	3.52 +0.46	3.58 +2.17	3.49 -0.40	3.52 +0.46	3.58 +2.17	3.49 -0.40	3.52 +0.46	3.58 +2.17	3.49 -0.40	3.52 +0.46	Zargan, LRV.51.141, Esfahan1, Esfahan2, 9- Ch.353, CART.9094, 1457, Urmieh, 4- Arak, Kh.34.779, Krdestan2, FariV3.76, Kurdestan1, LRV.51.233, Tabriz2, Tabriz1, Kh.2357, Kh.15.44, Arak2811.2	2-2
81.49 +3.8	81.50 +3.9	81.49 3.90	73.13 -6.76	81.50 +3.9	81.49 3.90	73.13 -6.76	81.50 +3.9	81.49 3.90	73.13 -6.76	81.50 +3.9	81.49 3.90	73.13 -6.76	Zargan, LRV.51.141, Esfahan1, Esfahan2, 9- Ch.353, CART.9094, 1457, Urmieh, 4- Arak, Kh.34.779, Krdestan2, FariV3.76, Kurdestan1, LRV.51.233, Tabriz2, Tabriz1, Kh.2357, Kh.15.44, Arak2811.2	
20.77 +5.6	4.31 +4.4	40.50 +4.89	35.34 -8.47	4.31 +4.4	40.50 +4.89	35.34 -8.47	4.31 +4.4	40.50 +4.89	35.34 -8.47	4.31 +4.4	40.50 +4.89	35.34 -8.47	Zargan, LRV.51.141, Esfahan1, Esfahan2, 9- Ch.353, CART.9094, 1457, Urmieh, 4- Arak, Kh.34.779, Krdestan2, FariV3.76, Kurdestan1, LRV.51.233, Tabriz2, Tabriz1, Kh.2357, Kh.15.44, Arak2811.2	
2.48 -2.36	2.66 +4.72	2.58 +1.58	2.45 -3.54	2.66 +4.72	2.58 +1.58	2.45 -3.54	2.66 +4.72	2.58 +1.58	2.45 -3.54	2.66 +4.72	2.58 +1.58	2.45 -3.54	Zargan, LRV.51.141, Esfahan1, Esfahan2, 9- Ch.353, CART.9094, 1457, Urmieh, 4- Arak, Kh.34.779, Krdestan2, FariV3.76, Kurdestan1, LRV.51.233, Tabriz2, Tabriz1, Kh.2357, Kh.15.44, Arak2811.2	
12.69 +7.91	13.36 +5.45	13.09 +3.31	11.96 -5.60	13.36 +5.45	13.09 +3.31	11.96 -5.60	13.36 +5.45	13.09 +3.31	11.96 -5.60	13.36 +5.45	13.09 +3.31	11.96 -5.60	Zargan, LRV.51.141, Esfahan1, Esfahan2, 9- Ch.353, CART.9094, 1457, Urmieh, 4- Arak, Kh.34.779, Krdestan2, FariV3.76, Kurdestan1, LRV.51.233, Tabriz2, Tabriz1, Kh.2357, Kh.15.44, Arak2811.2	
7.65 +2.82	7.48 +0.54	7.55 +1.48	7.24 -2.69	7.48 +0.54	7.55 +1.48	7.24 -2.69	7.48 +0.54	7.55 +1.48	7.24 -2.69	7.48 +0.54	7.55 +1.48	7.24 -2.69	Zargan, LRV.51.141, Esfahan1, Esfahan2, 9- Ch.353, CART.9094, 1457, Urmieh, 4- Arak, Kh.34.779, Krdestan2, FariV3.76, Kurdestan1, LRV.51.233, Tabriz2, Tabriz1, Kh.2357, Kh.15.44, Arak2811.2	
19.15 +0.42	20.25 +6.19	19.79 +3.78	17.82 -6.55	20.25 +6.19	19.79 +3.78	17.82 -6.55	20.25 +6.19	19.79 +3.78	17.82 -6.55	20.25 +6.19	19.79 +3.78	17.82 -6.55	Zargan, LRV.51.141, Esfahan1, Esfahan2, 9- Ch.353, CART.9094, 1457, Urmieh, 4- Arak, Kh.34.779, Krdestan2, FariV3.76, Kurdestan1, LRV.51.233, Tabriz2, Tabriz1, Kh.2357, Kh.15.44, Arak2811.2	
113.89 +0.32	114.54 +88	114.27 +0.65	112.24 -1.14	114.54 +88	114.27 +0.65	112.24 -1.14	114.54 +88	114.27 +0.65	112.24 -1.14	114.54 +88	114.27 +0.65	112.24 -1.14	Zargan, LRV.51.141, Esfahan1, Esfahan2, 9- Ch.353, CART.9094, 1457, Urmieh, 4- Arak, Kh.34.779, Krdestan2, FariV3.76, Kurdestan1, LRV.51.233, Tabriz2, Tabriz1, Kh.2357, Kh.15.44, Arak2811.2	
84.23 +0.62	87.10 +0.24	84.10 +0.35	83.0 -0.97	87.10 +0.24	84.10 +0.35	83.0 -0.97	87.10 +0.24	84.10 +0.35	83.0 -0.97	87.10 +0.24	84.10 +0.35	83.0 -0.97	Zargan, LRV.51.141, Esfahan1, Esfahan2, 9- Ch.353, CART.9094, 1457, Urmieh, 4- Arak, Kh.34.779, Krdestan2, FariV3.76, Kurdestan1, LRV.51.233, Tabriz2, Tabriz1, Kh.2357, Kh.15.44, Arak2811.2	
86.43 -1.43	92.56 +5.56	89.98 +2.62	83.72 -4.54	92.56 +5.56	89.98 +2.62	83.72 -4.54	92.56 +5.56	89.98 +2.62	83.72 -4.54	92.56 +5.56	89.98 +2.62	83.72 -4.54	Zargan, LRV.51.141, Esfahan1, Esfahan2, 9- Ch.353, CART.9094, 1457, Urmieh, 4- Arak, Kh.34.779, Krdestan2, FariV3.76, Kurdestan1, LRV.51.233, Tabriz2, Tabriz1, Kh.2357, Kh.15.44, Arak2811.2	

In subgroup 1 of cluster 2, genotypes had higher average in the grain yield and biological yield characters in comparison with other genotypes (Table 3). The classification of genotypes (subgroup 1 from cluster 2) was based on grain and biological yield. The greatest deviation percentage from means was found for grain and biological yield followed by the plant height, plant weight and effective head weight respectively. The positive higher deviation percentage mean for grain and biological yield could be attributed to the higher genetic potential and adaptability of the respective genotypes. More genotypes this group were from local genotypes of centre Iran.

Performance of genotypes was more similar for grain yield and biological yield in study.

The deviation mean values of the most traits in subgroup 2 from cluster 2 were not different from total mean.

The genotypes of cluster 1 showed the least amount at all characters. In this cluster, the negative greatest deviation percentage from means was found for number of seed per plant, grain yield and biological yield.

Yazdi – Samadi and Abde – Mishani (1989) by using cluster analysis divided 168 safflower genotypes into five clusters by morphological characters.

### Principal Components Analysis

By applying principal component analysis technique on safflower data, the eigen values and cumulative variances of correlation matrix of safflower plant traits are given in Table 2. It is clear that the first principal component of safflower data accounts 31.79% of total variability percent in the data, while the second principal component accounts 28.29% of the total variability.

The first three principal components which are orthogonal with each other and extract maximum of total variability (about 72.92%). On the basis of correlation between characters and principal component is given in Table 3. In first principal component grain yield, plant height, number of seeds per head, hectoliter weight, biological yield have positive correlation between themselves i.e., varies in same direction. The second principal component; number of heads per plant, effective head weight, effective heads weight per plant, plant weight and harvest index had positive correlation between them and varies in the same direction.

Mozaffari and Asadi [25] reported that on the basis of correlation between principal components and original traits at safflower Mutants, a classification was made to observe the relation between different traits. It was observed that for the first principal component, in irrigated condition height, stem diameter, capitulum diameter, number of seeds in capitulum, capitulum weight, oil content and days to maturity and in drought stress condition capitulum diameter, number of seeds in capitulum, 100 seeds weight, oil content and days to maturity had positive correlation between themselves and varies in the same aspect.

Associations among the 30 genotypes were also revealed by PCA (Figure 2). In PCA, 30 genotypes were separated into four groups, in which groups 2 and 3 have all the genotypes from clusters 1 (Figure 1) and group 1 and 4 have all the genotypes from cluster 2 of the dendrogram (Figure 1).

Overall, the grouping pattern from PCA corresponded well with the clustering pattern of the dendrogram.

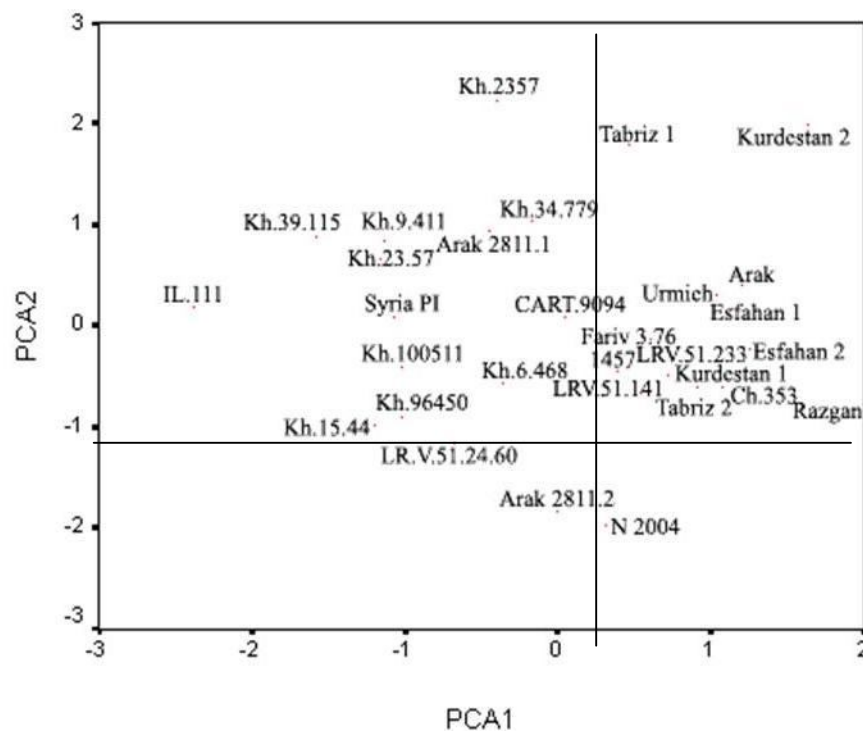


Figure2. Scatter plot PC1 and Pc2 in 30 safflower genotypes

Table 4: Eigen value, proportion and cumulative explained by the first three PC

Principal component	Eigen value	Proportion	Cumulative
PC1	4.13232	31.79	31.79
PC2	3.67806	28.29	60.08
PC3	1.66906	12.84	72.92

Table 3: Vector loadings explained by the first three PC

Traits	PC1	PC2	PC3
plant height	0.844*	-0.167	0.215
days to 50% flowering	0.573	-0.562	0.162
days to maturity	0.632*	-0.285	0.179
plant weight	0.346	0.775*	0.308
number of heads per plant	0.0076	0.692*	0.467
heads weight per plant	0.207	0.937*	0.128
effective head weight	0.355	0.685*	-0.286
number of seeds per head	0.639*	0.374	0.262
hectoliter weight	0.701*	-0.269	-0.236
100 seed weight	-0.126	0.252	-0.838*
grain yield	0.827*	0.151	-0.385
biological yield	0.856*	0.0025	-0.328
harvest index	0.265	0.735*	-0.261

## CONCLUSION

This survey revealed plant height, number of seeds per head and hectoliter weight were significantly correlated with the grain yield as well as a positive direct effect on the grain yield. Some of the traits such as plant weight and 100 seed weight had positive but non-significant correlation with grain yield, but their direct effect on the grain yield was higher and positive. Therefore, grain yield improvement could be achieved by using traits of plant height, hectoliter weight and 100 seeds weight as the efficient selectable phenotypic markers.

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