

Investigation of Genetic Variation in *Carthamus tinctorius* L. Genotypes Using Agro-Morphological Traits

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ABSTRACT

In order to study the genetic variation and relationships among traits, an experiment was carried out on 15 genotypes of *Carthamus tinctorius* L. under field conditions in randomized complete block design with 4 replications in Payam Noor University, Zavareh. Agro-morphological characters, including seed yield/plant, biological yield, number of capitula per plant, number of seed per capitula, 1000- grain weight, number of secondary branches, capitula weight, oil yield and harvest index were measured. Results of the analysis of variance showed significant differences among genotypes for all studied traits ($p \leq 0.01$). High values of phenotypic and genotypic coefficients of variation were obtained for most traits, indicating high variability in the traits under study. Seed yield/plant had significant high and positive correlations with capitula number per plant, seed number per capitula, biological yield and oil yield. Principal component analysis showed three factors that justified 94.33% of the total variation. Cluster analysis grouped the 15 genotypes within 4 clusters, each of which having 9, 2, 1 and 3 genotypes. The clustering pattern of the genotypes revealed that geographic diversity was not related to agronomic diversity. These results could be useful in choosing genotypes for intercrossing to develop improved cultivars.

Keywords: Principal components analysis, Cluster analysis, Genetic variation, Correlation coefficients and Safflower.

INTRODUCTION

Safflower (*Carthamus tinctorius* L.) is one of the oldest oilseed crops and is widely grown under hot and dry climate of the Middle East (Knowles, 1995). Harlan (1992) proposed seven diversity centers for safflower germplasm evolution including the Far East, India-Pakistan, the Middle East, Egypt, Sudan, Ethiopia and Europe.

Safflower has some agronomic advantages such as drought resistance and adaptation to arid and semiarid climatic conditions (Weiss, 2000). Iran has one of the richest germplasm sources of safflower. For instance, out of the 2042 safflower genotypes deposited at the Western Regional Plant Introduction Station, Pullman, WA, USA, 199 are from Iran (De

Haro *et al.*, 1997; Jaradat and Shahid, 2006).

Evaluating yield components and their interrelationships as well as detecting suitable selection indices are very important in safflower breeding program, especially the direct components of yield that are related to the various morphological characters regarded as indirect components of yield. Corleto *et al.* (1997) reported that the most important yield component in safflower is the number of capitula per plant. Bagheri *et al.* (2001) showed that the seed yield/plant had significant and positive correlation with number of seed/plant, number of capitula/plant and seed weight. Omidi *et al.* (2009) indicated that the number of capitula/plant, biomass and oil yield are associated with the increase of seed yield/plant in safflower and concluded that selection for number of capitula/plant was effective to improve seed yield.

Digming and Yuguang (1993) in a study of 30 safflower cultivars, reported that the number of effective branches, main stem diameter, 1000- seed weight, oil content and angle of the first branch were the six principal components. Yasdi Samadi and Abdemishani (1989) studied 168 safflower genotypes using cluster analysis and reported that studied genotypes were grouped within five clusters and concluded that similarity between populations maybe is due to similar genetic basis.

The present study was conducted to assess the genetic diversity of among different safflower genotypes as well as determine the relationship among yield and their components using agromorphological traits.

MATERIALS AND METHODS

The plant materials consisted of 15 genotypes collected from various local regions of Iran (Table 1). This experiment

was carried out at the Research Farm of Payam Noor University, Zavareh (32°32' N and 51°32' E, 1,630 m asl) on a typical Haplargid soil with a texture of clay loam, pH 7.5 and organic matter content of 1%, in 2009. A randomized complete block design with four replications was used. Each plot consisted of three rows 40 cm apart and 1.5 m in length. Fertilizers were applied at 100 kg N/ha and 100 kg P/ha prior to sowing and 75 kg N/ha top dressed at shooting stage. The crop was irrigated as needed.

Plant height recorded from ground level to the top of main stem at maturity. Number of secondary branches, number of capitula per plant, number of seed per capitula, 1000- seed weight, seed yield/plant and biological yield were measured on five plants in the middle row and their average was calculated for each plot.

Analysis of variance of data for agromorphological traits was performed using General Linear Model of SAS program (SAS Institute 1997). Phenotypic correlations among traits were calculated Pearson method (Farshadfar, 2001). Phenotypic and genotypic coefficients of variation (PCV, GCV) were calculated (Singh, 1991).

Then the data were used to generate a genetic distance matrix based on Euclidean distance measure by using SPSS statistical package, and clustering of genotypes was performed using Ward method (Johnson, 1998).

RESULTS

Analysis of variance, phenotypic and genotypic coefficients of variation

Analysis of variance demonstrated that the differences among genotypes were highly significant ($p \leq 0.01$) for all traits (Table 2). Variation among the genotypes

for most traits can be divided into genotypic and phenotypic components.

The phenotypic and genotypic coefficients of variation (PCV and GCV) are presented in Table 2. Phenotypic coefficients of variation (PCV) ranged from 16.85% in number of seed per capitula to 45.19% in seed yield/plant and

genotypic coefficients of variation (GCV) ranged from 13.97% in 1000-seed weight to 25.75% in seed yield/plant. Seed yield/plant, biological yield, number of capitula/plant and oil yield had higher genetic coefficients of variation than other traits.

Table 1. Safflower genotypes used and their origin

Genotype	City- province
1	Kashan - Esfahan
2	Najaf abad - Esfahan
3	Ardestan - Esfahan
4	Meimeh - Esfahan
5	Mobarakeh - Esfahan
6	Garmsar - Semnan
7	Kerman - Kerman
8	Karaj - Tehran
9	Zabol – Sistan & Blochestan
10	Hamadan - Hamadan
11	Shiraz - Fars
12	Shahrekord – Chaharmahal bakhtiari
13	Rasht - Gilan
14	Esfahan - Esfahan
15	Boshehr - Boshehr

Table 2. Mean of squares, phenotypic and genotypic coefficients of variation for the studied traits.

Characters	Genotype DF = 14	Error DF = 45	GCV%	PCV%
Seed yield/plant	471.23**	17.52	25.75	45.19
Biological yield	712.15**	47.91	15.92	36.85
No. Capitula/plant	122.39**	7.18	14.56	39.45
No. Seed /capitula	762.41**	3.19	15.45	16.85
1000- grain weight	9.52**	2.65	13.97	17.42
No. Secondary branches	52.79**	3.67	21.29	24.52
Capitula weight	39.42**	2.51	18.27	19.95
Oil yield	64.12**	0.97	24.85	37.21
Harvest index	14.29**	11.52	23.12	24.55

**Significant at 0.01 probability level

Phenotypic correlations

Phenotypic correlation of seed yield/plant with other traits are shown in Table 3. These values also confirmed that seed yield/plant is significantly correlated with number of capitula per plant (0.89), number of seed number per capitula (0.78), biological yield (0.75), oil yield (0.72) and

harvest index (0.69). 1000-seed weight had negative and significant correlation with number of capitula per plant (-0.82) and seed number/plant capitula (-0.75). There was also a positive correlation between number of secondary branches and biological yield (0.79) and number of capitula/plant (0.75).

Table 3. Correlation coefficients between some agro-morphological traits of safflower

Traits	Seed yield/plant	Biological yield	No. Capitula/plant	No. seed/capitula	1000 seed weight	No. secondary branches	Capitula weight	Oil yield	Harvest index
Seed yield/plant	1								
Biological yield	0.75**	1							
No. capitula/plant	0.89**	0.32	1						
No. seed/plant	0.78**	0.27	-0.79**	1					
1000 seed weight	0.42	0.39	-0.82**	-0.75**	1				
No. Secondary branches	0.49*	0.79**	0.75**	-0.53*	0.29	1			
Capitula weight	0.39	0.25	0.14	-0.32	0.21	0.14	1		
Oil yield	0.72**	0.13	-0.42*	0.27	0.13	0.18	0.26	1	
Harvest index	0.69**	0.21	0.85**	0.75**	0.42*	0.15	0.23	0.16	1

* and ** Significant at 0.05 and 0.01 probability levels, respectively.

Table 4. Factor analysis for all traits in safflower

Traits	PC1	PC2	PC3
Seed yield/plant/plant	0.92	0.14	-0.08
Biological yield	0.85	0.09	-0.15
No. capitula/plant	0.89	0.14	-0.23
No. seed /capitula	0.28	0.79	-0.15
1000- grain weight	-0.52	0.35	-0.24
No. secondary branches	0.41	-0.18	0.72
Capitula weight	0.23	0.94	-0.26
Oil yield	0.74	0.35	-0.29
Harvest index	0.71	0.57	0.11
Eigen value	7.23	2.49	1.95
Variance %	59.23	22.63	12.47
Cumulative variance %	59.23	81.86	94.33

Principal component analysis

The results showed that three principal components cumulatively explained 94.33% of total variability (Table 4). The first principal component (PC1) explained 59.23% of total variability. Among the vectors of PC1, seed yield/plant, number of capitula/plant, biological yield, oil yield and harvest index had higher values. The second principal component (PC2) explain about 22.63% of total variability. Among the vectors of PC2, capitula weight and number of seed per capitula have higher loading factor. The third principal component (PC3) explain about 12.47% of total variability. Among the vectors of PC3, No. secondary branches had higher loading factor than other loading factors.

Cluster analysis

Clustering based on agro-morphological traits clustered the genotypes into four main groups including 9, 2, 1, 3 genotypes, respectively (Figure 1). Cluster 1 included Kerman, Shiraz, Mobarekeh, Zabol, Ardestan, Karaj, Meimeh, Garmsar and Najafabad genotypes. Kashan and Hamadan genotypes were grouped in cluster 2. Cluster 3 included Boshehr genotype. Cluster 4 possessed three genotypes from Rasht, Esfahan and Shahrekord.

Genotypes classification based on PC1 and PC2 genotypes confirmed grouping based on cluster analysis so that in scater diagram of PC1 and PC2 were separated as the 4 groups of cluster analysis (Figure 2).

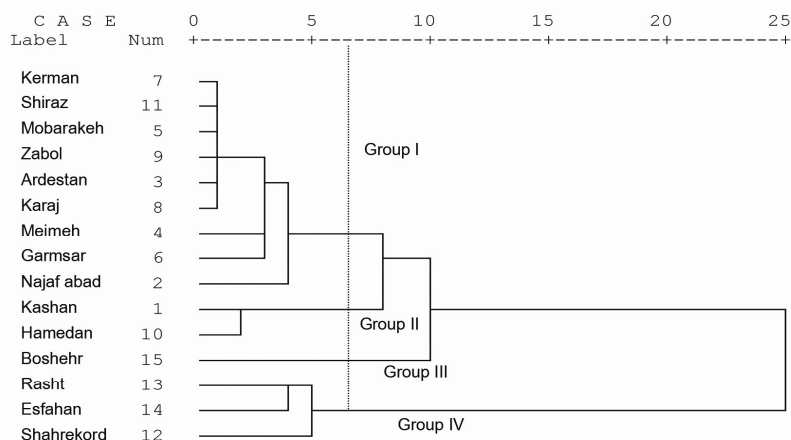


Figure 1. Dendrogram of cluster analysis for 15 safflower genotypes based on agro-morphological traits

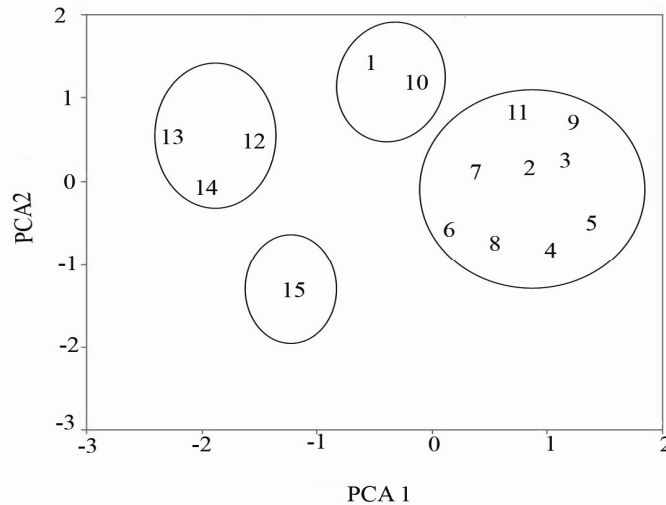


Figure 2. Biplot graphical display of safflower genotypes based on PCA.

DISCUSSION

Performance of a long term breeding program usually needs to obtain some information about the amount and nature of genetic variation and correlation between traits in order to practice selection hybridization for a programme. In general, results of this research showed a considerable genetic variation for most of the agro-morphological traits as seed yield/plant and its components. These results are in agreement with those obtained by Ramazani *et al.* (2006) in safflower cultivar, Salmon (2004) and Dandrea (2002) in *Chamomilla recutita* genotypes. For all traits, phenotypic coefficients of variation were higher than genotypic coefficients, that it may be due to environmental effect. These variations help us to select different genotypes with desirable characteristics.

The result of phenotypic correlations showed that the most important yield components were No. capitula/plant, No. seed number/capitula, biological yield and oil yield. These results are in agreement with those obtained by Ashri *et al.* (1974), Lakha *et al.* (1992), Bagavan

and Ravilkumar (2001) and Amini *et al.* (2008).

Due to limitation of photosynthesis material in safflower, it is expected that by increasing No. capitula/plant and/or No. seed/capitula, decreases 1000-seed weight which is in agreement with the result of Necdet and Esendel (2006) and Amini *et al.* (2007). Tavakoli (2002) showed that 1,000-seed weight had the least correlation coefficient with yield and concluded that 1000-seed weight is less influenced by environmental conditions and its control is more genetically. There is a positive and significant correlation between No. secondary branches and No. capitula/plant which are in agreement with the result of Zand (1995) and Akbari *et al.* (2007).

Considering the results of principal component analysis, the first principal component was mostly related seed yield/plant and its components. According to the correlation results, there was positive and high correlation among all traits in this factor, Therefore, this factor can have an important role as selection index in breeding programs for production of cultivars with high seed yield. The second and third principal components were entitled as capitula yield and

branching, respectively. Amini *et al.* (2007) in the study of 32 safflower genotypes, identified six principal components that explain 81.81% of total variation among traits.

The result of different reports showed that with increase of genetic distance, the percentage of heterosis will increase in intercrossing programs (Jafari *et al.*, 2007; Jaradat *et al.*, 2006). Grouping of genotypes based on genetic distance is effective in a breeding program when several traits investigate simultaneously (Jafari *et al.*, 2007). Genotypes 1 and 12 from Kashan and Shahrekord had the most genetic distance, and therefore high heterosis percentage is expected from their cross. Genotypes 7 and 11 from Kerman and Shiraz had the least genetic similarity.

According to obtained results from cluster analysis, genotypes of safflower from different regions located in the same group which have a low coefficient of correlation between genetic and geographic distances. This can be due to the exchange of plant materials across the

regions during the history of safflower cultivation. Zeinali (2003) and Mehdikhani *et al.* (2006) reported similar results in mint and chamomilla genotypes, respectively. Omid *et al.* (1999) in study of 100 safflower cultivars and cluster analysis based on morphological traits and its origin, reported that studied cultivars clustered in 6 and 13 different groups, respectively. Also concluded that grouping based on traits related to seed yield/plant is more effective than based on their origine.

CONCLUSION

In general, our results indicated the presence of comparable genetic potentials among Iranian safflower genotypes to develop desirable cultivars via intercrossing.

Although results of this investigation provided information about the potential in genetic variability among Iranian safflower genotypes but evaluation of more germplasm is needed for effective improvement of breeding program.

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