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Relationships among morpho-phenological traits using principal components analysis in safflower

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Abstract

Safflower (*Carthamus tinctorius* L.) is an oilseed crop which is adapted to semi-arid region of the world. The objective of this study was to use statistical method of principal components analysis to evaluate the relationship between morphological, phenological traits and yield performances of 20 different safflower genotypes. Plant characters such as day to initiate flowering (DIF), day to 50% flowering (50% DF), day to maturity (DM), plant height (PH), main head diameter (MHD), heads per plants (HP), seeds per head (SH), 1000-seed weight (SW) and seed yield per Plants (SYP) were main selected measurements for the data analysis. The information derived from principal components analysis could classify these characters into three groups based on the amount of variables among plant characters. These events enable to justify 80% of the all of variability within the genotypes. Number of head per plant, SW, SH, DF as well as DM are putative morphological markers which can be considered as the desirable tools for screening elite safflower genotypes for yield improvement in breeding of safflower.

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Introduction

Safflower (*Carthamus tinctorius* L.) is an oilseed crop and belongs to the family Compositae or Asteraceae (Abd El-Latteif, 2012, Weiss, 2000, Jaradat and Shahid, 2006). Oilseed crops are the main sources of edible oils with healthy diet and compared to synthetic and animal oils have become more popular with high demand among consumers. Such expectation reinforces plant researchers to concentrate their works toward promoting of oil production in the edible oilseed crops. Beside its oil demand, safflower has been cultivated for many other different reasons in India, the Near East, the Middle East and China (Esendal, 2001, Knowles, 1969). It has been grown primarily to use for its colorful petals as a food coloring, oil extraction and obtaining textile dye in the Far East, Central and North Asia, America, North Africa and Europe for centuries (Shabana, 2013, Salamati *et al.,* 2011, Majidi *et al.*, 2011). A precise agricultural practice in combination with plant breeding would be a great attempt to boost crop production in safflower. A successful breeding program usually depends on the choice of selection indices for improving plant vigor in order to promote seed yield quality (Samonte *et al.*, 1998). For promotion of seed yield and oil content in safflower genotype, one has to develop a selection criteria in which are able to bear highly efficient source of genetic variation within selected characters (Golkar *et al.*, 2011). Relationships among phonological and morphological characters in safflower have been studied with calculation of principal components analysis in safflower (Mozafari *et al.*, 2006, Ahmadzadeh *et al.*, 2008, Mokhtasi *et al.*, 2006, Khan *et al.*, 2009). Mozafari and Asadi stated that 87% of total variation for the seed yield could be explained by four first component and eigen value more than one was used to assign the principal components into PC1, PC2, PC3 and PC4 (Mozafari and Asadi ,2006). Khan *et al.*, has reported that first four principal components accounted for 68.4% of the total variation for the seed yield (Khan *et al.*, 2009). The aim of this study was to use of the principal components analysis to evaluate the relationship among phonological and morphological characters in certain of safflower genotypes in order to elucidate the best selection index for yield improvement in breeding of safflower.

Material and methods

Plant material and growth condition

Twenty genotypes of the safflower including; 6 Iranian genotypes and 14 exotic genotypes (Table 1) provided from Institute of Plant Genetics and Crop Plant Research (IPK) in Gatersleben of the Germany were sown in spring 2011 at Research Farm of the Researches Center for Agriculture and Natural Resources located in Yasuj (51^{0} 31´ E and 30^{0} 41´ N, 1734 m asl), Iran (Table1). Yasuj located in cold climates and possess cold to moderate cold weather. The soil of research field had a loamy texture. Genotypes were set to grow in a trail study of randomized completed blocks design with three replications. Each plot had four rows with 3m length and with spacing of 50cm; seeds were sown by hand with 5cm distance in rows. Recommended crop management practices were implemented to raise the crops to desirable growth stages. Plots were kept weed, pest and disease free till harvesting time.

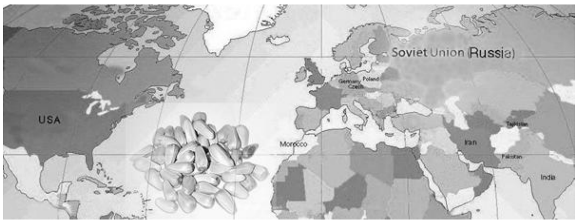

Fig. 1. geographical distribution of safflower genotypes.

Studied characters and its measuring method

Plant characters measurements were including: Days to initiated flowering (DIF), Days to 50% flowering (DF 50%), Days to maturity (DM) on basis field observations, while plant height (PH), number of head per plant (HP), number of seed per head (SH), 1000- seed weight (SW) (g), main head diameter (MHD) (mm) and seed yield per plant (SYP) (g) were recorded using seven randomly selected plants from each plot.

Statistical analysis

Principal components analysis was estimated using SAS 9.1 program using seed yield as dependent variable and the remaining characters as independent variables.

Table 1. List of names and origin of safflower genotypes.

Genotype	Origin	Genotype	Origin
Khatam Yazd	Iran	C130	Morocco
Goldasht	Iran	C132	Germany
Sina411	Iran	C161	Soviet Union
Local Isfahan	Iran	C24	Morocco
Isfahan 14	Iran	C151	Pakistan
IL111	Iran	C83	Tajikistan
C19	Polish	C9	Republic of Czech
C160	Soviet Union	C56	USA
C173	Indian	C55	Polish
C124	Pakistan	C159	Germany

Results and discussion

Principal component analysis precisely classified nine characters into three groups and Eigen value more than one was used to assign the principal components into PC1, PC2 and PC3. These components justified almost overall 80% of the total genetic variation (Table 2). The estimation of the first component was contained basic component of seed yield which was loading value of MHD, SYP, SW as well as seeds per head respectively (Table 2). The positive loading values of these characters were 0.54, 0.52, 0.45 and 0.32, which showed positive direction of the relationship between the components and the variables. So, it can be interpreted that the above mentioned characters may be contained the same genes that could become useful for selection in breeding program to produce desirable safflower genotypes. With regarded to the high amount of characters loading value in the first component, this component could be called as yield and yield component. This finding was confirmed with same result in a report by Ahmadzade *et al.* (Ahmadzade *et al.*, 2008). The second component could explain 32% from sum of the genetic variation in plant population (Table 2) and had showed positive loading value of 0.54, 0.53, and 0.38 for DIF, 50% DF and day to maturity characters, respectively. These characters were powerfully pertinent to phonological characters thus, the component named phonological component. The third component was capable of explaining only 14% of the total genetic variation which might become less important for safflower breeding improvement. Based on results obtained via the principal components analysis, has been observed that characters such as MHD, SW, SH, DIF as well as DM are the best and the most important plant materials in safflower breeding. Therefore according to principal components analysis result that 1000-seed weight, main head diameter, number of seed per head, days to initiated flowering and days to maturity on seed yield per plant had positive direct effect in the first and secondary components, it could be concluded that mentioned characters are putative morphological markers which can be considered as the desirable tools for screening elite safflower genotype under the field conditions. These results showed that in order to gain more and accurate aware of the relationships between characters that could have maximum impact on seed yield per plant and as well as elucidate the best selection index for yield improvement of safflower can be using principal components analysis in breeding programmes for promote the yield production in safflower.

Table 2. Eigen value and eigenvectors from the 3-selected principal components axis for evaluation of traits on the twenty safflower genotypes.

Characters studied	PC1	PC2	PC3
DIF	-0.130	0.530	-0.070
50%DF	-0.060	0.540	-0.290
DM	0.220	0.380	-0.190
HP	0.200	0.210	0.610
PH	0.060	0.360	0.510
MHD	0.540	-0.060	-0.100
SH	0.320	-0.260	0.250
SW	0.450	0.002	-0.300
SYP	0.520	0.150	0.010
Eigen value	3.013	2.850	1.256
Proportion variance	%34	%32	%14
Accumulation variance	%34	%66	%80

DIF: Days to initiate flowering; 50%DF: days to 50% flowering; DM: Days to maturity; HP: heads per plant; PH: plant height; MHD: Main head diameter; SH: seeds per head; SW: 1000-seed weight; SYP: seed yield per plant.

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