

Genetic variation among diverse safflower genotypes for some agro-morphological traits

Naser Sabaghnia^{*}, Hossein Ebrahimi and Mohsen Janmohammadi

Department of Plant Production and Genetics, University of Maragheh, Maragheh, Iran

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Abstract – This study sought to investigate the genetic diversity among 100 safflower genotypes concerning seed yield performance and seventeen morphological traits and yield components. Employing an alpha 10 × 10 lattice design, the two trials were performed in 2022 and 2023, with two replicates. Principal component analyses (PCA) explained 65% and 61% of the variability in the first and second years respectively. In the first year, the yield of a single plant was positively correlated with plant height, lateral capitulum total weight and seed number and weight, and main capitulum seed number and weight. In the second year, the results obtained generally corroborated the first year. In both years, the PC1 and PC2 axes divided genotypes into four main groups which contained 14, 11, 15, and 10 entries respectively. Comparison of the traits of the four clusters demonstrated that Cluster-II and Cluster-IV exhibited the highest single plant yields. These clusters can therefore be considered as potential heterotic groups in crossbreeding programs aimed at producing genotypes with superior performance. About 21 genotypes of 100 studied were identified as good candidates for use in safflower breeding programs.

Keywords: germplasm / principal components analysis / seed yield / yield components

Résumé – Cette étude visait à examiner la diversité génétique de 100 génotypes de carthame concernant le rendement en graines et 17 caractères morphologiques et composantes du rendement. Utilisant un dispositif expérimental de type alpha-lattice 10 × 10, deux essais ont été réalisés en 2022 et 2023, avec deux répétitions. Les analyses en composantes principales (ACP) ont permis d'expliquer 65 % et 61 % de la variabilité au cours de la première et de la deuxième année respectivement. La première année, le rendement d'une plante était positivement corrélé à la hauteur de la plante, au poids total et au nombre et au poids des graines des capitules latéraux, ainsi qu'au nombre et au poids des graines du capitule principal. La deuxième année, les résultats obtenus ont généralement corroboré ceux de la première année. Au cours des deux années, les axes PC1 et PC2 ont divisé les génotypes en quatre groupes principaux qui contenaient respectivement 14, 11, 15 et 10 entrées. La comparaison des caractéristiques des quatre groupes a montré que les groupes II et IV présentaient les rendements les plus élevés. Ces groupes peuvent donc être considérés comme des groupes hétérotiques potentiels dans les programmes de croisement visant à produire des génotypes aux performances supérieures. Environ 21 génotypes sur les 100 étudiés ont été identifiés comme de bons candidats à utiliser dans les programmes de sélection du carthame.

Mots clés : germoplasme / analyse des composantes principales / rendement en graines / composantes du rendement

^{*}Corresponding author: sabaghnia@maragheh.ac.ir

Highlights

- Exploring genetic variation is essential for finding suitable parents for cross breeding programs of safflower.
- Two key traits influenced yield as seed number of lateral capitulum and weight of lateral capitulum, as well as seed number of main capitulum, weight of the lateral capitulum, and seed weight of main capitulum.
- Twenty-one genotypes were identified as the best across the two years based on principal components analysis.

1 Introduction

Safflower, an ancient oilseed crop, is grown for oil production, medicinal applications and also bird feed, food coloring derived from its flowers, and traditional medicine practices. Safflower seeds has an average oil content of approximately 35% and a protein content of around 20%. The quality of safflower oil parallels that of sunflower or groundnut oil owing to the presence of essential unsaturated fatty acids, particularly linoleic acid (Kammili and Yadav, 2022). Despite its compatibility with Iran's climatic conditions and long-standing cultivation history in the region, the cultivated area of safflower does not increase due to the absence of high-yielding cultivars. However, Mexico, Tajikistan, and China show noteworthy yields of approximately 2000, 1600, and 1500 kg ha⁻¹, respectively. In contrast, safflower's performance in Iran hovers around 1300 kg ha⁻¹ (FAOSTAT, 2022). The higher temperatures characteristic of hot climates may diminish the extent of outcrossing (Rudolphi *et al.*, 2008). According to FAOSTAT (2022), global safflower production is estimated to be approximately one million tones. The leading producers are Kazakhstan, accounting for 45% of the production, followed by the Russian Federation at 22%.

Increasing safflower production while maintaining desired quality standards necessitates breeding efforts based on a broad spectrum of plant materials through geographical or genetic barriers to crossbreeding. Recognizing genetic diversity and preserving plant genetic resources facilitate their optimal utilization in breeding programs. Identifying desired genotypes accurately begins with assessing the diversity of different plant materials, including native populations or existing cultivars. Pourdad and Singh (2002), investigated 35 safflower genotypes under semi-arid conditions, and found a strong correlation between yield and capitulum seed number or number of capitula per plant. Similarly, Dwivedi *et al.* (2005) grouped numerous safflower genotypes based on their geographical origin and morphological traits. Safavi *et al.* (2013) evaluated a diverse array of Iranian and foreign safflower genotypes, assessing various morphological traits. They found significant variation among genotypes, corroborating the rich diversity of safflower germplasm in Iran.

Bahmankar *et al.* (2017) identified several key characteristics as effective selection indicators for safflower seed yield breeding programs including capitulum diameter, number of capitula per plant, thousand seed weight. Their analysis revealed that the first PCA axis encompassed yield characteristics, like main capitulum diameter, single plant yield performance, thousand seed weight, and seeds number per capitulum. Minnie *et al.* (2020) conducted a study on genetic variation among 70 safflower genotypes, focusing on yield and observed a positive relation between yield performance and days to flowering and maturity as well as seed number per capitulum. In a study by Lira *et al.* (2021) involving 124 safflower genotypes, remarkable diversity was observed for yield performance, yield components, and phenological traits. The goal of this study was to assess the genetic diversity of morphological traits in safflower and to elucidate their interrelations to develop effective breeding strategies.

2 Materials and methods

2.1 Experiments

In this research, 100 safflower genotypes sourced from the Plant Gene Resources of Canada and the gene bank of the Seed and Plant Improvement Institute of Iran were evaluated. These genotypes originated from diverse geographical locations, and their codes and donor countries are detailed in Table 1. The evaluation was conducted through an alpha lattice experiment setup (10 × 10) with two replicates in 2022 and 2023. The experiments took place at the research farm of Maragheh University, situated at a geographic latitude of 37 degrees and 23 min north and a longitude of 46 degrees and 14 min east. The region experiences a semi-arid and cold high-altitude climate, characterized by an average rainfall of 320 mm and an altitude of 1485 m. After land preparation, seeds were planted in four 2 m rows, with 0.25 m spacing between rows and 10 cm between plants (Fattahi *et al.*, 2018). To facilitate seed establishment after emergence, the plots were irrigated with a sprinkler one day after planting, followed by subsequent irrigations every 10 days by flooding. Before sowing, chemical fertilizers were applied to the field soil to address the minimum organic matter content requirement, with a dosage of 60:30:20 kg ha⁻¹ for nitrogen, phosphorus, and potassium, respectively according to Fattahi *et al.* (2018). Throughout the growth and development stages, standard crop management practices including weeding and pest control were implemented.

2.2 Traits

The data were collected for various morphological traits including plant height (PH), height of the first lateral branch (HFL), height of the first capitulum (HFC), stem diameter (SD), number of lateral branches (NLB), number of main branches (NMB), number of capitula of lateral branches (NCLB), number of capitula of main branch (CMB), number of capitula of plant (NCP), number of seeds of main capitulum (SMC), number of seeds of lateral capitulum (SLC), seed weight of main capitulum (SWMC), seed weight of lateral capitulum (SWL), dry weight of main capitulum with seeds (WMC), weight of lateral capitulum

Table 1. The code and donor country of 100 safflower (*Carthamus tinctorius* L.) genotypes.

Code	Donor Country	Code	Donor Country	Code	Donor Country	Code	Donor Country
G1	Unknown	G26	USA	G51	Unknown	G76	Canada
G2	Unknown	G27	Pakistan	G52	Unknown	G77	Canada
G3	Iran	G28	unknown	G53	Egypt	G78	Canada
G4	Unknown	G29	France	G54	Iran	G79	Canada
G5	Turkey	G30	Iran	G55	USA	G80	Canada
G6	Unknown	G31	USA	G56	Unknown	G81	Canada
G7	Iran	G32	USA	G57	Iran	G82	Canada
G8	Unknown	G33	Iran	G58	USA	G83	Canada
G9	Unknown	G34	Iran	G59	Unknown	G84	Canada
G10	Iran	G35	Iran	G60	Iran	G85	Canada
G11	Iran	G36	Iran	G61	Iran	G86	Iran
G12	Unknown	G37	Unknown	G62	Unknown	G87	Iran
G13	Portugal	G38	Unknown	G63	Iran	G88	Iran
G14	Iran	G39	Iran	G64	Unknown	G89	Iran
G15	Unknown	G40	Unknown	G65	Canada	G90	Iran
G16	Iran	G41	Iran	G66	Canada	G91	Iran
G17	Unknown	G42	USA	G67	Canada	G92	Iran
G18	Iran	G43	Unknown	G68	Canada	G93	Iran
G19	Turkey	G44	Palestine	G69	Canada	G94	Iran
G20	Syria	G45	Iran	G70	Canada	G95	Iran
G21	Iran	G46	Turkey	G71	Canada	G96	Iran
G22	Unknown	G47	Unknown	G72	Canada	G97	Iran
G23	Cyprus	G48	Iran	G73	Canada	G98	Iran
G24	Iran	G49	China	G74	Canada	G99	Iran
G25	Mexico	G50	Unknown	G75	Canada	G100	Iran

with seeds (WLC), weight of single plant (WSP), and yield of single plant (YSP). Recording of some traits like WMC and WLC was performed because their measuring is quicker, without having to thrash out the seed. Additionally, the thousand-seed weight (TSW) was determined by analyzing three samples from each experimental plot. These traits were measured based on [Dajue and Mündel \(1996\)](#).

2.3 Statistical analysis

Due to pest infestation, five genotypes were excluded in the first year, resulting in data recorded for only 95 genotypes. However, in the second year, all 100 genotypes were included in the study. Normality of the data was verified using the Anderson-Darling test implemented in Minitab software ([Minitab Institute, 2005](#)). Subsequently, principal component analyses (PCA) were conducted using Statistica software ([StatSoft Institute, 2011](#)) to decrease the dimension of the data and explore the underlying structure among correlated traits. For visual representation of the results, the values of the first two axes plotted against each other showed the interrelationships among genotypes and traits, facilitating the interpretation of the results and identification of potential patterns or clusters within the data.

3 Results and discussion

Axes 1 and 2 of the PCA explained 65% of variation in the first year (52% and 13% respectively) and 61% in the second year

Table 2. The Eigen analysis of the correlation matrix, Kaiser-Meyer-Olkin index of sampling adequacy and Bartlett's test of sphericity.

	The first year		The second year	
	PCA1	PCA2	PCA1	PCA2
Eigenvalue	9.38	2.29	8.61	2.24
Proportion	0.52	0.13	0.48	0.13
Cumulative	0.52	0.65	0.48	0.61
KMO†	0.697		0.706	
BTS‡	1942.7		1908.5	
df	153		153	
Sig.	0.000		0.000	

†Kaiser-Meyer-Olkin index.

‡Bartlett's Test of Sphericity.

(48% and 13% respectively) ([Tab. 2](#)). The Kaiser-Meyer-Olkin (KMO) statistics of sampling adequacy was 0.697 and 0.706 for the first and second years, respectively, indicating that PCA was an appropriate model for the dataset. Additionally, Bartlett's test of sphericity was significant for both experimental years, further affirming the suitability of PCA for the safflower dataset ([Tab. 2](#)). The substantial amount of explained variation across both years suggests the presence of additive as well as crossover types of interactions for genotype-by-trait reactions. Similar observations have been reported in other studies conducted on safflower ([Ebrahimi *et al.*, 2023](#)) as well as in other crops such as maize ([Shojaei *et al.*, 2020](#)), sorghum ([Welderufael *et al.*, 2023](#)), and

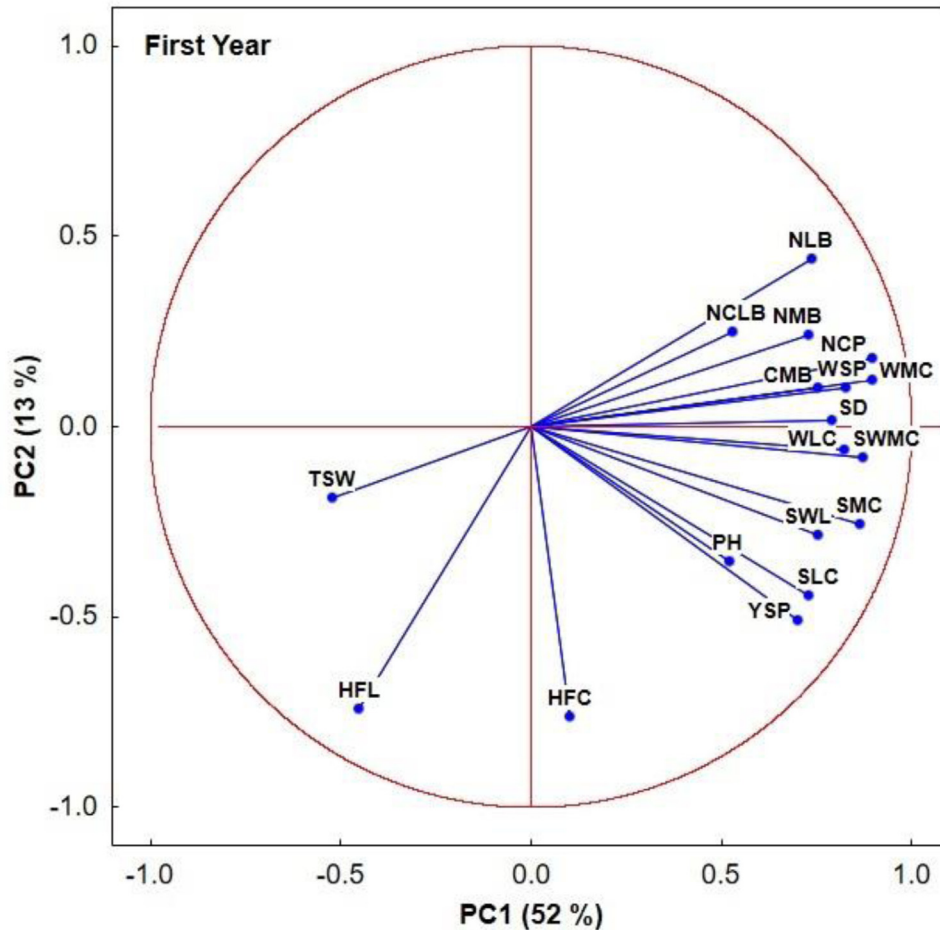


Fig. 1. Plot of PC1 versus PC2, showing associations among traits in the first year. Traits are: plant height (PH), height of the first lateral branch (HFL), height of the first capitulum (HFC), stem diameter (SD), number of lateral branches (NLB), number of main branches (NMB), number of capitula of lateral branches (NCLB), number of capitula of main branch (CMB), number of capitula of plant (NCP), seeds of main capitulum (SMC), seeds of lateral capitulum (SLC), seeds' weight of main capitulum (SWMC), seeds' weight of the lateral capitulum (SWL), weight of main capitulum (WMC), weight of lateral capitulum (WLC), thousand-seed weight (TSW), weight of single plant (WSP) and yield of single plant (YSP).

rapeseed (Bakhshi *et al.*, 2023). These findings confirmed the relatively complex nature of studied traits especially seed yield performance, so utilization of indirect selection from breeding materials ignoring genotype-by-trait interactions is not possible.

Positively associated traits were the number of lateral branches (NLB) and the number of capitula of lateral branches (NCLB) in the year 2022 (Fig. 1). Additionally, there were positive associations between yield of a single plant (YSP) and plant height (PH) and lateral capitulum seed number (SLC), and also between lateral capitulum seed weight (SWL) and main capitulum seed number (SMC) (Fig. 1). Similarly, Bahmankar *et al.* (2014) found a significantly positive relation between yield of single plant and the number of seeds per capitulum. In the first year, lateral capitulum weight (WLC) was positively associated with main capitulum seed weight (SWMC), while main branch capitula number (CMB), weight of single plant (WSP), and weight of the main capitulum (WMC) were closely correlated (Fig. 1). Comparable results have been reported by Beyyavas and Dogan, (2022) using different safflower germplasms. The vector plot of the PCA

graph provides a concise overview of the associations between traits based on their angles. In the first year, most traits were positively associated, as evidenced by angles smaller than 90° (Fig. 1).

In the first year of trials, the angle between NLB and NCLB and YSP, PH, and SLC was only slightly larger than 90° , indicating that they were independent (Fig. 1). Similarly, height of the first capitulum (HFC) was not related to WLC and SWMC, or HFC to TSW, and height of the first lateral branch (HFL) was also independent of TLC (Fig. 1). Ebrahimi *et al.* (2023) found no correlation between the above-mentioned traits in 64 safflower genotypes.

NLB and NCLB were negatively correlated with TSW in the first year (angles larger than 90°) (Fig. 1), suggesting that lateral branches and their capitula were related to smaller seeds. Kizil *et al.* (2008) reported similar negative correlations between number of lateral branches and thousand-seed weight. The seed yield of a single plant varied between 3.27 and 5.36 g in the first year, consistent with the results of Pascual-Villalobos and Alburquerque (1995), who found yield of single

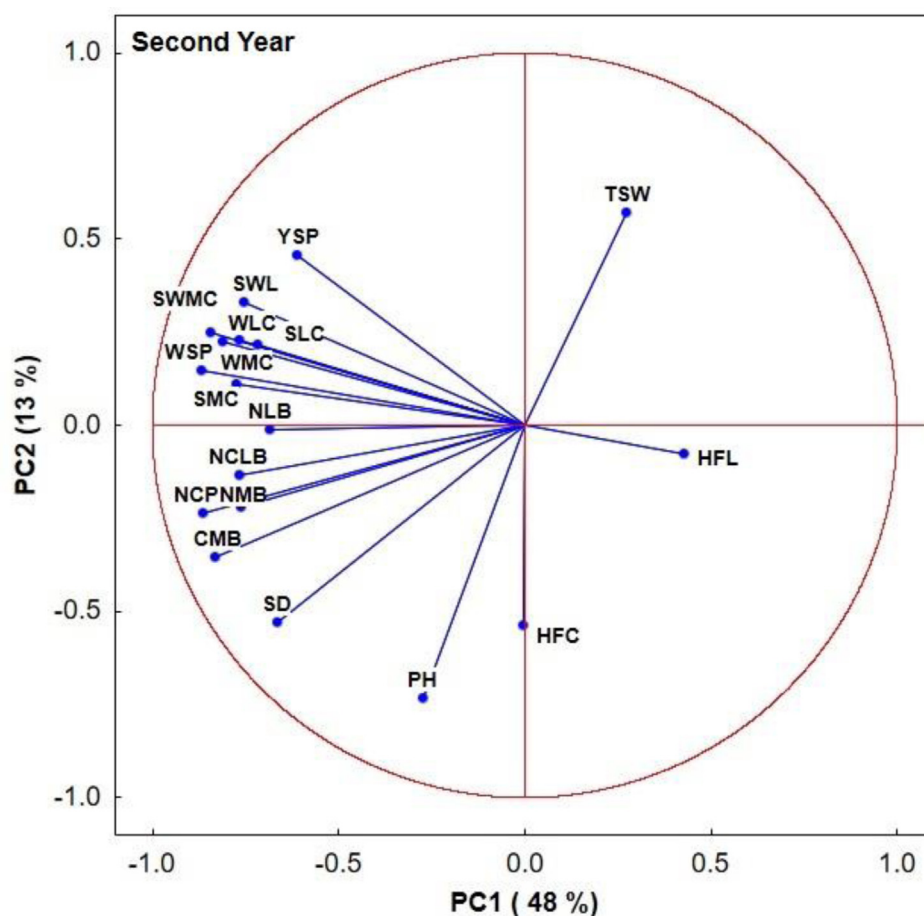


Fig. 2. Plot of PC1 versus PC2, showing associations among traits in the second year. Traits are: plant height (PH), height of the first lateral branch (HFL), height of the first capitulum (HFC), stem diameter (SD), number of lateral branches (NLB), number of main branches (NMB), number of capitula of lateral branches (NCLB), number of capitula of main branch (CMB), number of capitula of plant (NCP), seeds of main capitulum (SMC), seeds of lateral capitulum (SLC), seeds' weight of main capitulum (SWMC), seeds' weight of the lateral capitulum (SWL), weight of main capitulum (WMC), weight of lateral capitulum (WLC), thousand-seed weight (TSW), weight of single plant (WSP) and yield of single plant (YSP).

plant ranging from 2.5 to 10.5 g while [Omidi-Tabrizi \(1999\)](#) reported a seed yield per plant of 12–13 g, highlighting the considerable influence of environmental conditions on this trait.

The PC1 versus PC2 graph for the second year revealed several positive associations between YSP and SWL and other traits observed ([Fig. 2](#)). Indirect selection of the most favorable genotypes can be performed in positions where the same trait is observed consistently in different environmental conditions ([Kumar *et al.*, 2008](#)). Thus, utilizing SLC followed by SMC and SWL could be beneficial for breeding seed yield performance in varying environmental conditions.

While numerical correlation coefficients and PCA graphic interpretation were mostly consistent, some unpredictability is possible because the main axes of a PCA do not describe all variation, as confirmed by [Sabaghnia *et al.* \(2016\)](#) in spinach. In the second year, the angles between PH and WLC, SLC, and SWL, between YSP and SD, between NLB and HFC, between HFL and NCLB, and between TSW and HFL indicated their independence ([Fig. 2](#)). Negative correlations appeared between TSW and PH, HFL and SMC and WSP ([Fig. 2](#)).

In the first year, the PC1 axis effectively segregated genotypes into two main groups on the left and right, and taking into consideration PC2, divided them into four distinct groups, with 26 genotypes in Group-I, 25 in Group-II, 24 in Group-III, and 20 in Group-IV ([Fig. 3](#)). The mean values of each of the four groups are presented in [Table 3](#), with the highest yield of single plants (YSP) attributed to Group-IV. Genotypes in this group exhibited higher values than the other three groups for most of the traits measured. These genotypes are therefore considered promising candidates for use as breeding programs to improve seed yield in safflower. Following Group-IV, the genotypes of Group-II displayed high yield of single plant (YSP) and had higher values than Group-I and Group-III for all measured traits, except for height of the first lateral branch (HFL) and thousand-seed weight (TSW) ([Tab. 3](#)). Group-I only performed better than Group-II for HFL and TSW, better than Group-III for SD, NLB, NMB, NCLB, CMB, and NCP, and better than Group-IV for TSW ([Tab. 3](#)). Thus, this group may complement the weaknesses of Group-II and Group-IV in terms of thousand-seed weight.

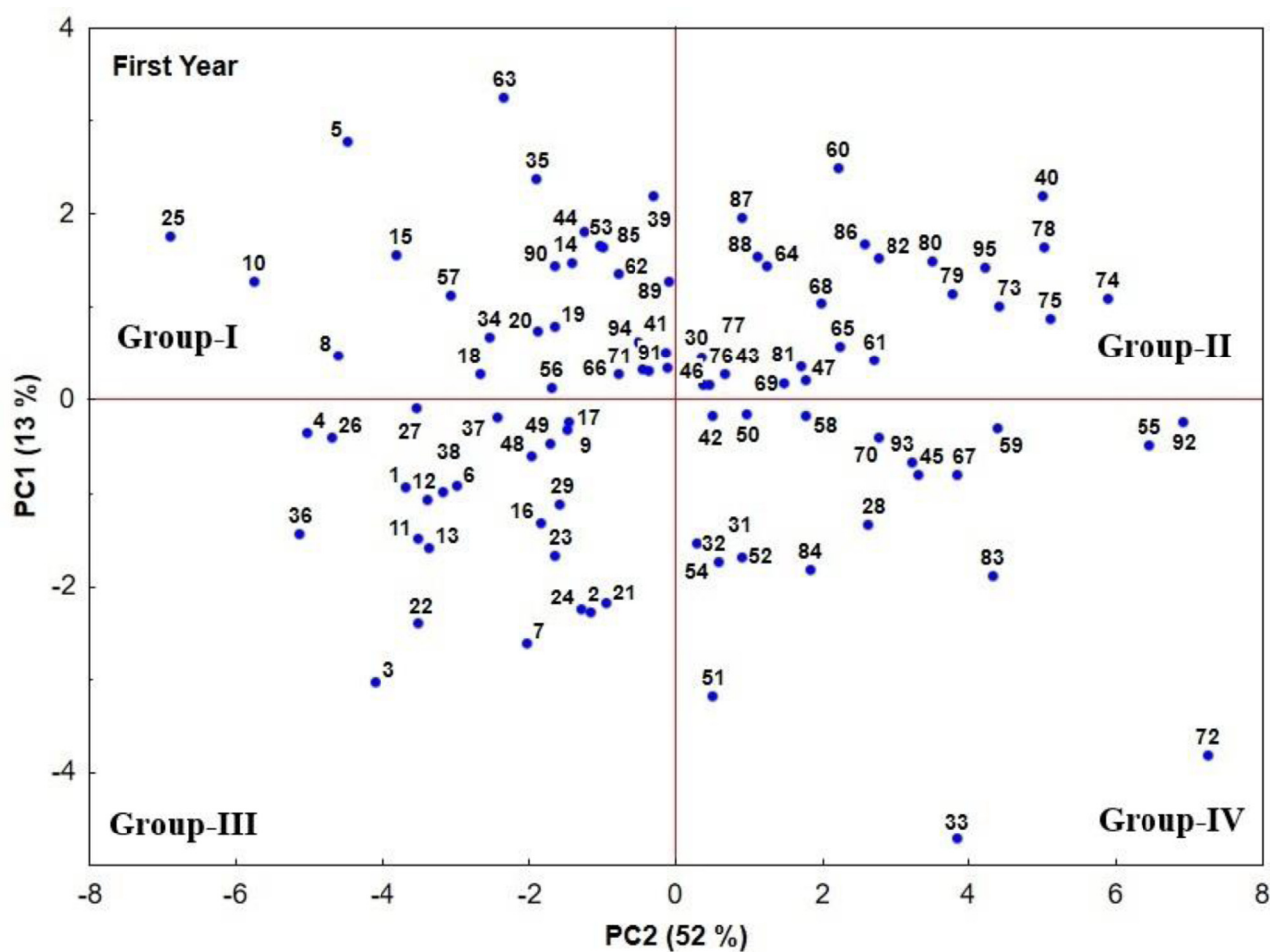


Fig. 3. Plot of PC1 versus PC2, showing dispersion of 95 safflower genotypes in the first year.

Table 3. Means of measured traits for four genotypic groups in the first year.

	Group-I	Group-II	Group-III	Group-IV
PH	59.4	62.1	61.4	66.1
HFL	28.4	25.7	35.6	31.1
HFC	43.5	44.1	49.9	50.5
SD	7.19	8.15	6.92	8.25
NLB	3.91	4.86	3.17	4.28
NMB	4.17	4.94	3.73	4.81
NCLB	0.95	1.11	0.89	1.09
CMB	1.33	1.67	1.16	1.63
NCP	10.2	14.7	8.3	14.2
SMC	164.4	238.4	179.7	272.6
SLC	80.2	117.1	96.0	147.3
SWMC	6.92	10.45	7.12	10.69
SWL	3.39	5.14	3.80	5.69
WMC	15.7	21.2	13.3	20.5
WLC	7.83	11.72	7.95	12.08
WSP	35.0	45.4	31.9	43.4
TSW	32.4	30.3	34.1	30.8
YSP	3.27	4.45	3.95	5.36

For traits' abbreviations, please refer to the text.

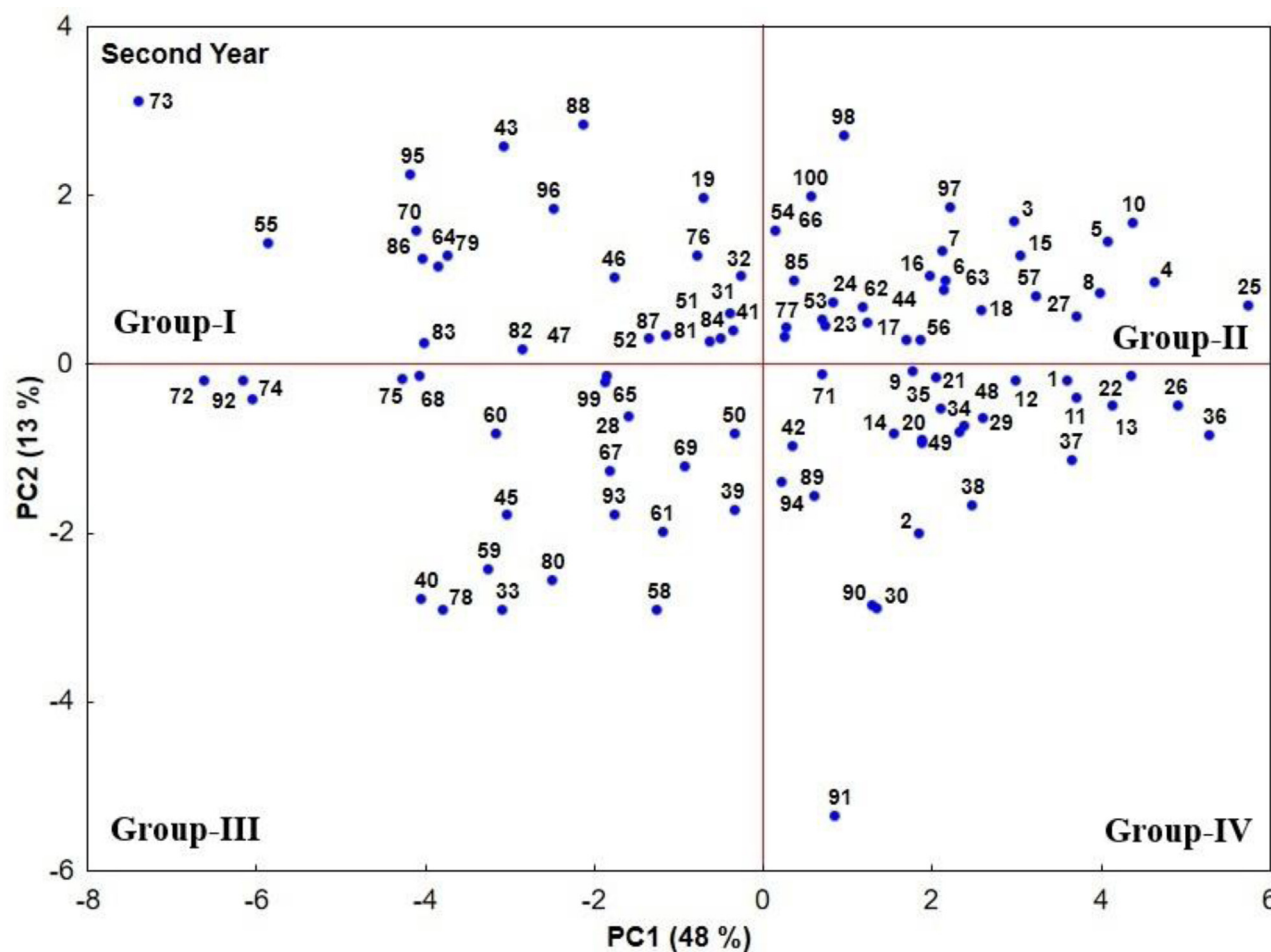


Fig. 4. Plot of PC1 versus PC2, showing dispersion of 100 safflower genotypes in the second year.

Table 4. Means of measured traits for four genotypic groups in the second year.

	Group-I	Group-II	Group-III	Group-IV
PH	54.3	52.7	62.8	58.6
HFL	22.8	24.2	21.5	26.7
HFC	37.7	36.2	41.9	42.4
SD	7.66	6.57	8.31	7.34
NLB	3.78	2.78	3.94	2.84
NMB	3.97	3.21	4.41	3.38
NCLB	1.23	0.84	1.32	0.86
CMB	1.60	1.02	1.93	1.20
NCP	13.9	7.8	16.0	8.7
SMC	250.7	175.6	252.9	159.9
SLC	134.4	84.9	113.2	80.4
SWMC	11.66	8.17	11.75	7.24
SWL	6.54	4.03	5.18	3.58
WMC	23.2	16.9	24.5	14.9
WLC	13.73	9.84	12.48	8.06
WSP	50.4	37.3	50.9	31.2
TSW	39.9	41.5	34.9	38.1
YSP	6.55	4.85	5.36	4.07

For traits' abbreviations, please refer to the text.

In the second year (Fig. 4), 24 genotypes were detected as Group-I, 28 as Group-II, 22 as Group-III, and 26 as Group-IV. The average of these four groups (Tab. 4) indicated that the highest yield of single plant (YSP) was attributed to Group-I, with these genotypes exhibiting higher values than Group-II for all measured traits except HFL and TSW, in contrast to the results of the first year.

We observed that PC1 was associated with yield components and seed yield performance, and the positive scores indicated the positive association between PC1 and identified traits (Toker and Cagiran, 2004). This suggests that these traits may be influenced by similar gene effects, making them advantageous for selecting the most favorable individuals.

The composition of four genotypic groups across two years revealed that genotypes of Group-I in the first year were relatively similar to Group-II in the second year, with 14 overlapping genotypes, forming Cluster-I. These genotypes appeared to be less affected by environmental effects and demonstrated low genotype by environment interaction, suggesting that their characteristics and responses are more stable. Similarly, genotypes of Group-II in the first year were relatively similar to Group-I in the second year, sharing 11 common genotypes, constituting Cluster-II. Likewise, genotypes of Group-III in the first year were relatively similar to Group-IV in the second year, sharing 15 common genotypes,

Table 5. Means of measured traits for four clusters across two years.

	Cluster-I	Cluster-II	Cluster-III	Cluster-IV
PH	53.4	55.5	60.0	67.8
HFL	25.2	23.9	32.3	26.8
HFC	37.7	39.5	47.2	48.3
SD	6.52	7.70	7.02	8.33
NLB	3.35	4.39	2.88	3.92
NMB	3.71	4.63	3.45	4.66
NCLB	0.87	1.15	0.82	1.21
CMB	1.12	1.68	1.05	1.92
NCP	8.4	14.9	7.7	15.7
SMC	155.1	244.3	167.8	291.0
SLC	78.2	125.6	89.5	136.8
SWMC	6.97	11.67	6.87	11.55
SWL	3.55	6.17	3.68	5.56
WMC	15.5	23.1	13.2	22.7
WLC	8.35	12.81	7.77	12.29
WSP	34.9	47.6	30.1	44.4
TSW	36.9	36.5	36.1	32.2
YSP	3.69	5.75	4.02	5.83

For traits' abbreviations, please refer to the text.

forming Cluster-III. Finally, genotypes of Group-IV in the first year were relatively similar to Group-III in the second year, with 10 overlapping genotypes, constituting Cluster-IV. The mean values for these four clusters are provided in Table 5, which shows that genotypes of Cluster-II and Cluster-IV exhibited the highest yield of single plant (YSP) and higher values for the traits studied compared to Cluster-I, except for thousand-seed weight (TSW). Clusters-II and -IV displayed higher values than Cluster-III for all traits except for HFL, HFC, and TSW. Both Cluster-II and Cluster-IV are promising candidates for improving traits such as number of capitula of plant (NCP), number of main branches (NMB), number of capitula of lateral branches (NCLB), and yield of single plant (YSP), making them suitable for breeding yield components and seed yield. However, Cluster-II outperformed Cluster-IV for traits such as PH, HFL, HFC, SD, CMB, SMC, and SLC, while Cluster-IV showed superiority over Cluster-II in NLB, CMB, SWMC, SWL, WMC, WLC, WSP, and TSW. Therefore, they can be considered distinct groups and could be incorporated into breeding programs to obtain genotypes with high performance in the target traits.

This study revealed significant genetic diversity within the safflower germplasm examined, offering valuable insights for breeders to select parents and desirable genotypes in safflower breeding programs. The PCA, a useful multivariate tool, facilitated the simplification of data sets and reduction of principal variables into uncorrelated components, aiding in the identification of relationships among traits in a multi-trait system such as crop plant growth (Kumar *et al.*, 2022). Evaluating genetic diversity through morphological traits remains a useful, straightforward, and practical approach. The study identified two key traits that significantly influenced yield: lateral capitulum seed number (SLC) and weight (SWL), consistent across both years. Other useful traits, main capitulum seed number (SMC), the lateral capitulum total

weight (WLC), and main capitulum seed weight (SWMC) emerged as potential selection indices. Significant genetic diversities were reported among safflower genotypes, particularly in yield components like number of capitula per plant and number of seeds per capitulum (Shinwari *et al.*, 2014; Kemal and Hailu, 2019). In the current study, significant genetic variation was found among 100 safflower genotypes based on their agronomic properties under cool upland semi-arid conditions. Eleven genotypes from Cluster-II and ten genotypes from Cluster-IV were identified as the best performers across the two experimental years. Among these 21 genotypes, seven originated from the germplasm of the Plant Gene Resources of Canada, while the remaining 15 genotypes were sourced from the gene bank of the Seed and Plant Improvement Institute of Iran, 7 were of Iranian origin, one originated from the USA, one (from Turkey), and five had unknown origins.

4 Conclusion

The extensive genetic diversity observed across various safflower traits suggests promising prospects for selecting an optimal combination of traits. Among the 100 examined genotypes, 21 were identified as particularly desirable, forming two distinct groups suitable for crossbreeding as different groups for future programs. Key traits influencing seed yield included lateral capitulum total weight and seed number and weight and main capitulum seed number and weight. These traits are potential selection indices in safflower breeding programs, enabling breeders to enhance seed yield and overall crop performance.

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Conflicts of interest

The authors declare that they have no conflicts of interest in relation to current paper.

Author contribution statement

Naser Sabaghnia: Conceptualization, methodology, supervision, writing-review & editing. Hossein Ebrahimi: Investigation. and Mohsen Janmohammadi: Methodology, review – editing.

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