

Electronic Journal of Plant Breeding



Research Article

Genetic analysis in sunflower germplasm across the four states falling under the semi-arid environments of India

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Abstract

The present research focuses on the identification of stable trait specific genetic resources across the five semi-arid environments located in the four states of India. The study illustrated the existence of a wide range of variations for most of the characters among the sunflower genotypes, which provides opportunities for genetic gain through selection or hybridization. Genotype x Environment (G x E) interaction was significant for all traits except for days to 50 % flowering, maturity days and 100-seed weight which means different genotypes responded differently to environments for the rest of the traits. Based on *per se* performance across the locations GMU 296 and HOHAL 30 can be considered as high yielding and high oil content accessions. Based on biplot, stability and *per se* performance genotypes GMU 806, GMU 635, GMU 296, GMU 802 and check DRSF113, can be considered as a medium to high yielding with medium oil content and medium maturity genotypes across the environments and can be considered as an ideal genotype across semi-arid environments. Character association indicated that among the seven traits, seed yield per plant had a significant negative association with oil content. The traits 50 % flowering and maturity days fall under one group and showed the more or less similar type of pattern in the expression of the traits by heat map approach. Based on diversity analysis identified genotypes from the second cluster can be utilized for the development of high yielding, medium oil content and medium duration diverse gene pool in sunflower for semi-arid environments.

Key words: Stability Analysis, Correlation, PCA, Sunflower

INTRODUCTION

In India, sunflower is the most important oilseed crop with the production of 2.11 lakh tonnes and productivity of 738 kg/ha during 2018-19 (Anonymous, 2019). The varieties and hybrids with early to medium maturity are widely preferred by sunflower growers (Dudhe *et al.*, 2017). Hence, to identify breeding material with high

yielding and medium duration from working germplasm is of prime importance. Germplasm is key initial material to plan a successful breeding programme. Knowledge of genetic variation and genetic relationships between conserved germplasm is important for efficient germplasm preservation, characterization and subsequent use by

breeders. The variability present in the germplasm for the desired trait is important to develop new varieties and hybrids. For instance, the most important goal of sunflower breeding is to develop genotypes with high seed yield and oil content (Dudhe *et al.*, 2009) along with resistance to biotic and abiotic stresses. The study on genetic variability of germplasm collection was a very important activity in the identification of different genotypes (Siddiqi *et al.*, 2012). Prior knowledge on the nature and magnitude of variability and heritability in a population is one of the prerequisites for a successful breeding program in selecting genotypes with desirable characters (Dudley and Moll, 1969). It is therefore, of great importance for breeders to know the heritability of the agronomical characters to improve the yield of the crop effectively. Heritability value alone may not provide clear predictability of the breeding value. Heritability in conjugation with genetic advance over a mean (GAM) is more effective and reliable in predicting the resultant effect of selection (Patil *et al.*, 1996; Ramesh *et al.*, 2013). The correlation coefficient gives an idea about the traits that directly affect the seed yield. Among a set of germplasm genetic divergence provides background for selection and development of new genetically diverse inbred. Multivariate statistical techniques like cluster analysis (CA) and principal component analysis (PCA) use different methods based on morphological or molecular markers and help breeders in selecting appropriate genotypes which meet the objectives of the breeding programme (Mohammadi and Prasanna, 2003). Earlier multivariate analysis has been used frequently for genetic diversity analysis in sunflowers (Muppidathi *et al.*, 1995; Mohan and Seetharam 2005; Reddy *et al.*, 2012). In the present study, the diversity of sunflower germplasm was assessed by using a heat map approach. It uses colour variation to study the expression of the traits. Genotype x Environment (G x E) analysis was used to analyze the stability of genotypes and to access the value of test locations. It leads to differences in the performance of genotypes over the environment and reduces the predictability of the performance of genotypes in target environments based on genotype performance in test environments. Since it is impossible to test genotypes in all target environments, plant breeders do indirect selection by growing the material in different test environments. In plant breeding selection of suitable test locations, is important since it accounts for G x E and maximizes gain from selection (Yan *et al.*, 2011). An efficient test location is discriminating and is representative of the target environments for the cultivars to be released. Hence, by considering all the above points the present study was planned to find stable performing medium maturing, high seed yielding along with medium to high oil content sunflower accessions, and to study the genetic variability and diversity of the germplasm in order to select accessions to serve as the genetic base for medium maturing and high yielding varieties and hybrids for semi-dryland conditions.

MATERIALS AND METHODS

A total of 350 sunflower accessions seed were multiplied and evaluated in the augmented block design at the ICAR-IIOR Narkhoda field, Shamshabad, Hyderabad and identified promising accessions for yield and yield attributing traits (Unpublished data). The 35 accessions with dark black and light black seeds along with the high seed yield (>30 g/plant) and mid to high oil content accessions (38-40 %) were selected to constitute the evaluation trial. DRSK-113 is used as a check population and released as a national variety by ICAR-IIOR. These 35 accessions were evaluated in four states of India (Telangana, Andhra Pradesh, Karnataka and Maharashtra) at five semi-arid dryland locations (ICAR-Indian Institute of Oilseeds Research, Rajendrnagar, Hyderabad (17° 22' 31" N 78° 28' 27" E); Regional Agricultural Research Station, Nandyal-Kurnool 15.4853° N, 78.4809° E); Main Agriculture Research Station, University of Agricultural Sciences – Raichur (13.0784° N, 77.5793° E) and in Maharashtra at two locations viz., Oilseeds Research Station, Dr PDKV., Akola (20°42'51.2"N, 77°3'2.21"E) and Oilseeds Research Station, Latur, VNMKV, Parbhani (18°24'53"N 76°36'47"E). At all the selected locations, the mean annual precipitation ranged between 200 and 700 mm and hence falls under semi-dryland environments. The experimental design used was a randomized complete block design. Planting was done in ridges and furrows with two replications per location and spacing of 60 x 30 cm. Hand-weeding and normal management practices were followed. Data were collected on randomly selected 5 plants and observations were recorded on days to 50 % flowering (DFF); maturity days (DM), plant height (PH), head diameter (HD), 100-seed weight (SW), oil content (OC) and seed yield/plant (SY). The plant height and head diameter measured in cm and 100-seed weight, seed yield/plant measured in (g).

Combined analysis using transformed values with interaction term for each location and combined locations was calculated by using the Design Resources Server of IASRI as suggested by Parsad and Gupta (2007). Phenotypic (PCV) and genotypic (GCV) coefficients of variation were calculated as proposed by Singh and Chaudhary (1985). Heritability in the broad sense (H^2) was estimates on genotypic mean described by Allard (1999) and expected genetic advance (GA) and percentage of GA calculated according to Shukla *et al.* (2006).

R version 3.1.3 package diversity and PCA analysis R Core Team (2013). Package 'gplots' was used to draw a heat map for diversity study as suggested (Dudhe *et al.*, 2017). For expressed traits colour variation of red and yellow correspond to low and high diversity while the white colour represents median levels of expression. Correlation between diversity and colors is represented in the color key. The histogram represents a distribution of each value under observation for a particular trait. The biplot was generated by using the 'FactoMineR'

(Factor analysis and data mining with R) package (Husson *et al.*, 2009) with function 'biplot'.

RESULTS AND DISCUSSION

In India majority of the sunflower cultivation area is under semi-arid conditions of Karnataka, Telangana, Andhra Pradesh and Maharashtra states. Multilocation evaluation and characterization of sunflower genotypes facilitate the identification of appropriate trait specific germplasm accessions with a genetically diverse background across the locations. *Per se* performance across locations and other attributes of the material is presented in **Table 1**.

The present study revealed that a good amount of variability was present among the sunflower accessions. Accessions viz., GMU 296 (19.0 g), GMU 635 (18.0g), GMU 806 (17g), GP4 745 (17g), GMU 804 (17g) and GMU 802 (17g) produced on par yield when compared with check DRSF 113 (18g). Selection 2 (36%), HOHAL 30 (37%), PSECO 177 (36%) and GMU 802 (36%) had medium oil content. HOHAL 30 (37.0%) had the highest oil content across locations, while eighteen accessions produced more oil content than check. Check DRSF-113 had 88 days duration. Two more genotypes GMU 355 and GMU 440 recorded 88 days and all other genotypes had of lesser duration than check. In India, medium duration genotypes are mostly preferred which matures within the range of 85-100 days. Hence, in this study, all the genotypes were considered as medium maturing genotypes.

Significant differences among the environments (E) and among the genotypes (G) revealed through combined variance analysis suggesting variability among genotypes and differences among the environments is presented in **Table 2**.

G x E interaction was significant for all traits except days to 50 flowering, maturity days and 100-seed weight which means different genotypes respond differently to different environments for the rest of the traits. Significant variation for G x E interaction for seed yield among sunflower genotypes at more than two environments was reported by Alem *et al.* (2016) and Dudhe *et al.* (2017). Similarly, Mousavi *et al.* (2016) reported significant effects of G x E interaction for 16 genotypes for oil content at four locations in sunflower.

Estimates of various variability parameters viz., phenotypic (PCV) and genotypic coefficient of variability (GCV), genetic advance and broad sense of heritability (H^2) are calculated and classified into high, medium and low (**Table 3**). The magnitudes of phenotypic coefficient of variation (PCV) values were higher than the corresponding (GCV) values indicating these characters are under the influence of environmental effect. The phenotypic coefficient of variability ranged from 3.56 (Maturity days) to 19.74 per cent (Seed yield) and the genotypic

coefficient of variability ranged from 3.03 (Maturity days) and 15.91 per cent (Seed yield). Broad sense heritability estimates were high for plant height (91.85), followed by 100 seed weight (78.29). Genetic advance as per cent of the mean (GAM) was the highest for seed yield/plant (26.41 %) followed by 100 seed weight (21.22 %) and most of the traits showed a moderate amount of genetic advance. The high heritability exhibited for plant height and 100 seed weight indicate that environmental factors did not greatly affect phenotypic variation and may not be rewarding whereas, for days to 50 % flowering it was low. A heritability value includes both additive and non-additive gene action hence cannot provide any information on the amount of progress gained after selection. Therefore, selection of traits with high heritability estimates in a broad sense will be worthy if accompanied with high genetic advance as per cent of means (Ramesh *et al.*, 2013; Dudhe *et al.*, 2017). In this study, high heritability associated with high genetic advance as per cent of mean were recorded for seed yield/plant, indicating the minor role of environment on seed yield and a role of additive gene action. Similar observations were also reported by Khan *et al.* (2003) and Alam *et al.* (1987) for seed yield while Srinivasa (1982) observed moderate heritability for seed yield.

The present study focuses to identify the high yielding and medium to high oil content accessions with black colour through cluster analysis. Black coloured seeds are usually preferred by Indian farmers. Knowledge of diversity among the accessions will help the breeder to choose the appropriate material. Genetic divergence among the parental or inbred lines or in working germplasm was studied by Komaraiah *et al.* (2004), Srinivas *et al.* (2006) and Reddy *et al.* (2012). To visualize the expression and relatedness of each trait across the five environments heat map approach was used. Mean data across the five test sites were subjected to hierarchical clustering (HCA) and heat map analysis (**Fig. 1**). Days to 50 % flowering and maturity days fall under one group and showed a more or less similar type of pattern in the expression of the traits depicted by histogram. Earlier Dudhe *et al.* (2017) studied relatedness among the traits in sunflower by using a heat map approach which supports the results of the present study. Relatedness of genotypes was depicted through dendrogram and traits based on their Euclidean distances. Thirty-five genotypes were grouped into two major clusters. The high yielding and medium oil content check DRSF-113 and accession GMU 440 grouped under Ist cluster and thirty-three accessions grouped under IInd cluster which reflects that these two genotypes were diverse from the rest of the accessions. High yielding accessions GMU 355, GMU 296 and GMU 802 were grouped in the second cluster. Medium to high oil content accessions GMU 355, 296, GMU 802, HOHAL 30, Selection 2 and PSECO 177 were also grouped under the second cluster. All these accessions may serve as the base material to develop medium to high

Table 1. *Per se* performance and description of the accessions

S. No.	Name of accessions	Days to 50% flowering	Maturity days	Plant height (cm)	Head diameter (cm)	100 seed weight (g)	Yield/plant (g)	Oil content (%)	Specific attributes
1	PSMO 53	52.0	84.0	105.0	13.0	3.6	12.0	34.0	Pre-breed line
2	Selection 2	51.0	84.0	109.0	12.0	4.3	15.0	36.0	Inbred line
3	GP2 1227	54.0	87.0	109.0	11.0	5.6	15.0	32.0	Gene pool line
4	GMU 806	51.0	84.0	100.0	14.0	4.7	17.0	34.0	Germplasm
5	GMU 935	53.0	83.0	106.0	11.0	5.4	10.0	34.0	Germplasm
6	GP4 745	54.0	84.0	93.0	9.0	4.7	17.0	31.0	Gene pool line
7	PSCIM 181	49.0	81.5	101.0	10.0	4.3	13.0	32.0	Pre-breed line
8	PSCIMO 118	53.0	84.0	100.0	12.0	4.0	12.0	28.0	Pre-breed line
9	PSCEM 139	48.0	80.0	84.0	12.0	4.3	15.0	34.0	Pre-breed line
10	GP6 951	53.0	86.0	113.0	12.0	5.0	12.0	32.0	Gene pool line
11	PSCIM 199	46.0	75.0	80.0	13.0	4.3	15.0	32.0	Pre-bred line
12	GMU 635	46.0	78.0	101.0	14.0	4.4	18.0	32.0	Germplasm
13	HOHAL 23	50.0	79.0	94.0	13.0	3.3	11.0	32.0	Inbred line
14	GMU 896	51.0	82.0	96.0	13.0	4.9	13.0	35.0	Germplasm
15	HOHAL 30	49.0	79.0	88.0	8.0	4.2	14.0	37.0	Inbred line
16	PSECO 177	51.0	82.0	95.0	10.0	4.3	10.0	36.0	Pre-breed line
17	GMU 130	52.0	83.0	76.0	13.0	5.2	15.0	28.0	Germplasm
18	HOHAL 72	49.0	83.0	106.0	11.0	4.4	13.0	27.0	Germplasm
19	HOHAL 70	51.0	80.0	108.0	9.0	4.0	13.0	29.0	Germplasm
20	GMU 786	53.0	84.0	100.0	10.0	4.9	13.0	30.0	Germplasm
21	HOHAL 34	49.0	80.0	97.0	12.0	5.8	12.0	29.0	Inbred line
22	CSFI 99	55.0	84.0	92.0	12.0	4.3	12.0	30.0	Inbred line
23	GP2 745	53.0	85.0	105.0	14.0	4.8	12.0	30.0	Gene pool line
24	GMU 1119	52.0	84.0	121.0	12.0	4.3	14.0	29.0	Germplasm
25	GMU 477	54.0	87.0	106.0	12.0	4.0	15.0	31.0	Germplasm
26	GMU 440	55.0	88.0	122.0	14.0	4.5	14.0	34.0	Germplasm
27	GMU 804	53.0	86.0	90.0	13.0	4.7	17.0	34.0	Germplasm
28	GMU 355	56.0	88.0	101.0	12.0	3.9	16.0	30.0	Germplasm
29	GMU 296	53.0	84.0	102.0	12.0	5.7	19.0	31.0	Germplasm
30	GMU 806-1	52.0	82.0	100.0	9.0	4.5	13.0	31.0	Germplasm
31	GMU 802	55.0	84.0	89.0	9.0	3.8	17.0	36.0	Germplasm
32	GMU 579	53.0	83.0	86.0	11.0	4.5	11.0	32.0	Germplasm
33	GMU 700	53.0	84.0	108.0	12.0	4.6	12.0	33.0	Germplasm
34	GMU 211	53.0	86.0	96.0	10.0	4.9	11.0	30.0	Germplasm
35	DRSF 113 ©	54.0	88.0	143.0	13.0	4.3	18.0	31.0	National variety
	Minimum	46	75	76	8	3.6	10	27	
	Maximum	56	88	143	14	5.7	22	37	

Table 2. Combined analysis for seed yield and yield parameters

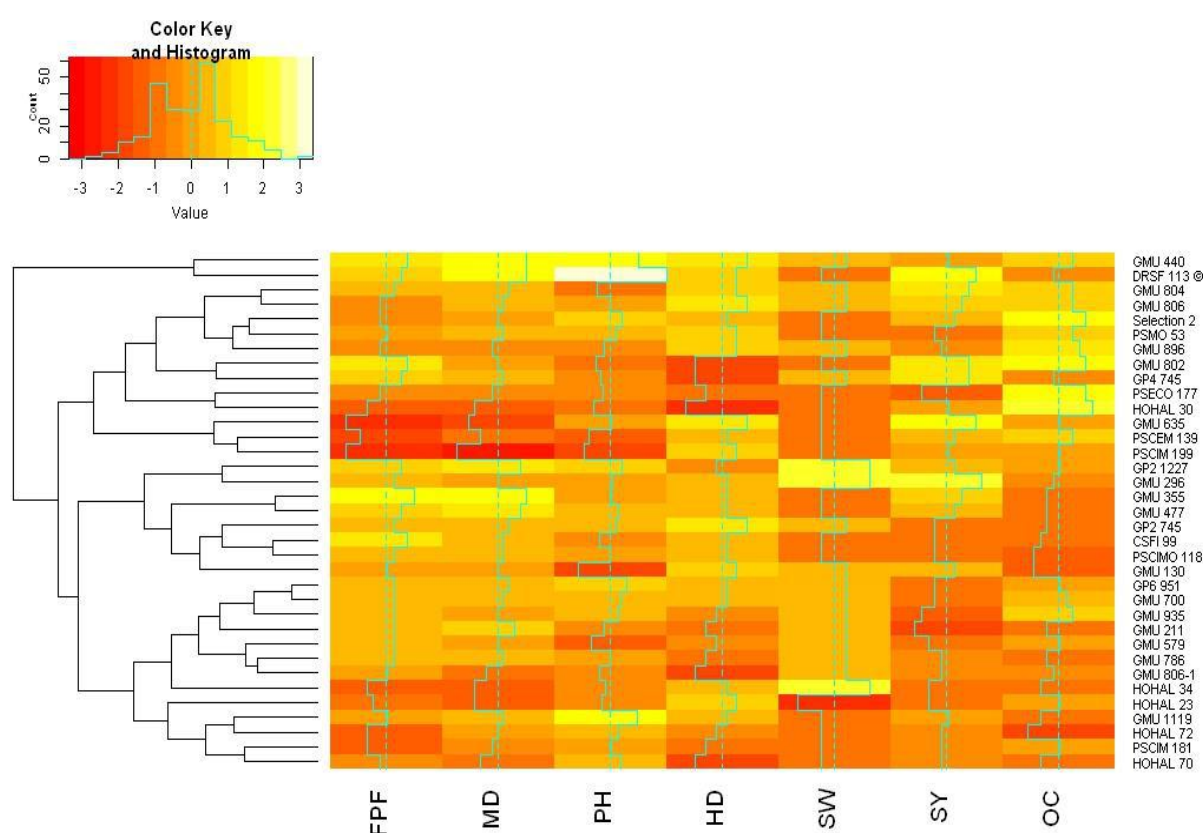
Source	Trait	DF	Mean Square	F value	Pr>F	Significant
FPF						
Environment (E)		4	385.5800	385.5800	<.0001	**
Location (Replication)		1	14.6844	14.6844	<.0001	**
Genotype (G)		34	2.7744	2.7744	<.0001	**
G x E		136	1.0994	1.0994	0.2781	NS
Error		170	1.0000			
MD						
Environment (E)		4	1224.2896	1224.290	<.0001	**
Location (Replication)		1	3.3033	3.3033	0.0071	**
Genotype (G)		34	3.5827	3.5827	<.0001	**
G x E		136	0.9473	0.9473	0.6277	NS
Error		170	1.0000			
PH						
Environment (E)		4	3871.6239	3871.624	<.0001	**
Location (Replication)		1	2.2546	2.2546	0.0512	NS
Genotype (G)		34	22.9052	22.9052	<.0001	**
G x E		136	14.5863	14.5863	<.0001	**
Error		170	1.0000			
HD						
Environment (E)		4	56.1129	56.1129	<.0001	**
Location (Replication)		1	8.4069	8.4069	<.0001	**
Genotype (G)		34	2.6319	2.6319	<.0001	**
G x E		136	1.8686	1.8686	<.0001	**
Error		170	1.0000			
SW						
Environment (E)		4	56.1129	171.2714	<.0001	**
Location (Replication)		1	8.4069	20.0866	<.0001	**
Genotype (G)		34	2.6319	3.9317	<.0001	**
G x E		136	1.8686	0.7519	0.9584	NS
Error		170	1.0000			
SY						
Environment (E)		4	97.3048	97.3048	<.0001	**
Location (Replication)		1	4.7209	4.7209	0.0005	**
Genotype (G)		34	6.7207	6.7207	<.0001	**
G x E		136	7.0968	7.0968	<.0001	**
Error		169	1.0000			
OC						
Environment (E)		4	99.6427	99.6427	<.0001	**
Location (Replication)		1	0.4835	0.4835	0.7882	NS
Genotype (G)		34	3.0274	3.0274	<.0001	**
GxE		136	1.3691	1.3691	0.0261	*
Error		170	1.0000			

** = Significant at 1 % probability level; * = Significant at 5 % probability level; NS = Non significant

Where, Seed yield (SY), days to 50% flowering (FPF), maturity days (MD), plant height (PH), head diameter (HD), 100-seed weight (SW) and oil content (OC)

Table 3. Estimates of genetic parameters for morphological traits

	$s^2 p$	$s^2 g$	PCV (%)	GCV (%)	H^2 (%)	GAM (%)	GA
Days to 50% flowering	7.69	3.71	5.34	3.71	48.28	5.31	2.75
Maturity days	8.75	6.36	3.56	3.03	72.73	5.33	4.43
Plant height	90.44	83.08	9.41	9.02	91.85	17.81	17.99
Head diameter	3.47	1.03	16.23	8.85	29.75	9.95	1.14
100 seed weight	0.37	0.29	13.16	11.64	78.29	21.22	0.98
Seed yield	7.16	4.65	19.74	15.91	64.95	26.41	3.58
Oil content	5.19	3.08	7.21	5.56	59.49	8.84	2.79

**Fig. 1. A hybrid representation of dendrogram and heatmap used to depict the diversity among 35 sunflower genotypes and traits with corresponding expression of genotype for each trait**

Where, FPF: Days to 50 % flowering, MD: Maturity days; PH: Plant height; HD: Head diameter; SW: 100-seed weight; SY: Seed yield/plant; OC: Oil content

oil gene pools and inbreds for semi-dryland conditions. Reddy *et al.* (2012) studied the diversity among the 62 exotic germplasm measured from seed yield and yield attributing traits and grouped the accessions into 9 clusters based on diversity.

Character association indicated that among the seven traits studied (Table 4), seed yield per plant had a significant

negative association with oil content which indicated an increase in one character would lead to a decrease in another character. Seed yield per plant had a highly significant positive association with days to maturity and head diameter. Hence, selection criteria based on these component traits along with seed yield will be more useful than simply based on seed yield. Earlier researchers (Rana *et al.*, 1991; Mogali and Virupakshappa, 1994 and

Narayana and Patel, 1998) reported the relationships among yield components and concluded that selection for grain yield in sunflower should largely be dependent on head diameter, stem diameter, 100-seed weight and plant height. Similarly, Dudhe *et al.* (2018) and Anandhan *et al.* (2010) reported improvement in seed yield along with other component traits in sunflowers.

The importance of traits towards the principal components can be realized from the corresponding eigenvalues are presented in **Table 5**. The principal component analysis (PCA) technique is utilized for genetic diversity and grouping of genotypes through biplot diagrams with practical application in the selection of superior genotypes for crop breeding (Tabrizi *et al.*, 2011 and Dudhe *et al.*, 2018). The results of PCA revealed that the first four components contributed about 79.31 per cent of total variability among all the genotypes for the seven traits (**Table 6**). The first principal component accounted for 33.19 per cent of the total variation in the population. Oil content contributed higher to the variation and had the highest loading in PC1 indicating the significant importance of the trait for this component. Five characters viz., 50% flowering, plant height, maturity days, head

diameter, 100 seed weight and seed yield contributed negative to the first component and showed a negative association which implies that genotypes with negative values of PC1 have reduced height, less seed yield, early flowering and maturity. The second principal component contributed 17.69 per cent of the total variation and except 50 % flowering and 100 seed weight contributed negatively in the second component which expresses negative associations among the traits. The third principal component accounted for 14.96 per cent of the total variation in the germplasm. Oil content contributed the highest (0.78) followed by seed yield (0.44). Dudhe *et al.* (2018) have assessed the variability of seven traits in sunflower and recorded similar observations, similarly Sasikala, *et al.* (2020) conducted PCA studies to study in the variability in the sunflower genotypes which supports our findings.

Fig. 2 showed that variables and genotypes are superimposed on the plot as vectors. The contribution of these variables in the variation of the genotypes is a representation of the distance of each variable with respect to PC1 and PC2. The biplot showed that seed yield and head diameter vectors are in overlapping to each other.

Table 4. Phenotypic correlation coefficients for seven traits in 35 sunflower accessions

Character	Days to 50% flowering	Plant height	Maturity days	Head diameter	100-seed weight	Seed yield/plant	Oil content
Days to 50% flowering	1.00	0.84**	0.31**	-0.07	0.26**	0.05	-0.10
Plant height		1.00	0.54**	0.14 **	0.23**	0.12**	-0.14
Days to maturity			1.00	0.22**	-0.01**	0.11	-0.09**
Head diameter				1.00	0.02	0.17**	-0.07*
100-seed weight					1.00	0.03**	-0.07*
Seed yield/plant						1.00	-0.09*
Oil content							1.00

** = Significant at 1 % probability level; * = Significant at 5 % probability level

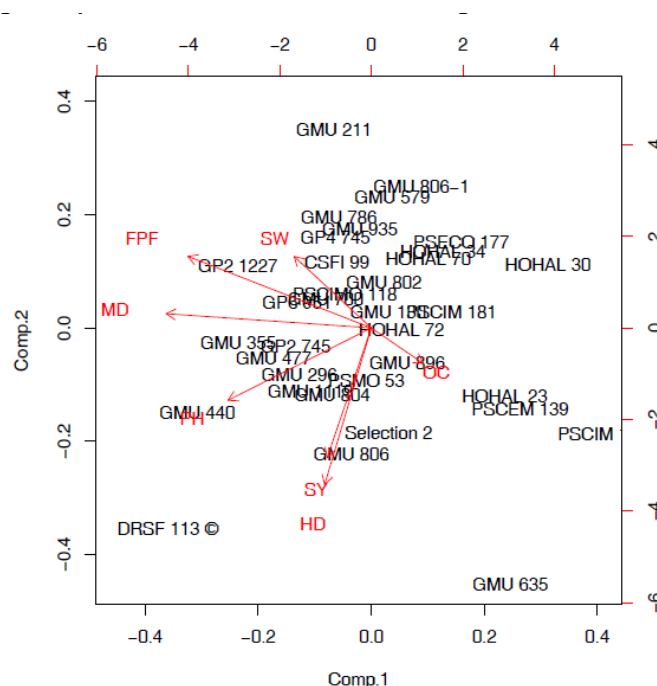
Table 5. Principal component analysis for quantitative traits in sunflower accessions – non rotated loadings

Character	PC1	PC2	PC3	PC4	PC5
FPF	-0.555	0.296	0.182	0.113	0.633
MD	-0.392	-0.621	0.124	-0.210	-0.739
PH	-0.434	-0.300	-0.151	0.365	0.136
HD	-0.141	-0.649	-0.315	-0.301	0.448
SW	-0.234	0.296	0.156	-0.795	0.251
SY	-0.134	-0.537	0.442	-0.261	-0.654
OC	0.157	-0.147	0.788	0.218	0.534

Where, FPF: Days to 50% flowering; MD: Maturity days; PH: Plant height; HD: Head diameter, SW: 100-seed weight, SY: Seed yield; OC: Oil content

Table 6. Principal components the eigenvalues, proportion of variation and total variation across axis

	Principal component axis						
	1	2	3	4	5	6	7
Eigenvalues	164.25	10.35	6.91	5.61	2.49	0.70	0.44
Proportion of variation (%)	33.19	17.69	14.96	13.88	10.98	0.07	0.01
Cumulative variation (%)	33.19	50.88	65.84	79.31	90.71	98.56	100.00

**Fig. 2. Biplot between PCs 1 and 2 showing contribution of various traits**

Seed yield, head diameter, plant height, maturity days, days to 50 % flowering and 100-seed weight contributed maximum towards variability in germplasm.

It was observed that genotypes were equally scattered around the vectors in the biplot diagram lead to distinct groups. For example, GMU 296, 355, 477, 635, 745, 804, 806, PSMO 53, Selection 2 and DRSF113, were scattered around the vectors of seed yield, head diameter, plant height and maturity days. Similarly, GP₆ 1227 and GP₂ 1227 were scattered around the days to 50% flowering and days to maturity vectors. GMU 896 and HOHAL 72 was round to oil content and nearer to seed yield. HOHAL 30 was towards the extreme of the vector. A better way to understand the nature of the genotypes is by comparing the mean values of these genotypes for seed yield and other attributes. Hence, genotypes GMU 806, GMU 635, GMU 296, GMU 802 and check DRSF113, can be considered as high yielding with medium oil content and medium maturity genotypes. Under semi-arid environment, medium duration genotypes are mostly preferred among the sunflower growing farmers. The

rest of the germplasm with average mean values was located far apart from the vectors in the biplot diagram. Therefore, selection for one of these traits should be accompanied by the associated traits, and this would provide the opportunity to exert multi-trait selections in sunflower breeding as indicated by Ghafari *et al.* 2004. Another consideration of the biplot diagram is the angles of vectors. Kroonenberg (1995) concluded that the angle of vectors shows correlations among the traits. In **Fig. 2**, vectors represent different traits. Plant height, days to 50% flowering, days to maturity and 100-seed weight and which had a small angle with each other indicates that they had positive associations. Similarly seed yield, head diameter had positive correlations. Therefore, the smaller angle among vectors indicates the greater positive association among related traits and *vice versa*. Tabrizi *et al.* (2011) also recorded similar types of observations while evaluating sunflower hybrids for germination and early seedling growth. Based on the biplot diagram, three distinct groups of the sunflower hybrids were formed and the best performing hybrids were identified. Earlier in sunflower, Tersac *et al.* (1993) used to represent

the structure of sunflower populations by the country of origin. De la Vega *et al.* (2001) also used PCA for revealing two-dimensional structures among genotypes and their environments based on their interactions. They have also reported the effectiveness of PCA for revealing environmental interactions.

The present study demonstrated that G x E interaction was significant for all traits except for days to 50% flowering, maturity days and 100-seed weight which means different genotypes respond differently to different environments. Under the semi-arid environments, identified promising four stable trait specific black coloured genotypes GMU 806, GMU 635, GMU 296, GMU 802 and check variety DRSF113 may prove worthy to be utilized for the development of high yielding, medium oil content and medium duration diverse gene pool, inbreds, populations and hybrids in sunflower.

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