



GENETIC EVALUATION AND IDENTIFICATION OF STABLE SUNFLOWER GENOTYPES UNDER SEMI-ARID DRYLAND CONDITIONS OF TELANGANA AND MAHARASHTRA STATE

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SUMMARY

The trial comprising of 32 sunflower germplasm accessions including three checks were evaluated at three semi-arid dryland locations of Telangana and Maharashtra states. In Telangana the location was Indian Institute of Oilseeds Research (IIOR), Hyderabad, and two locations at Maharashtra i.e. Zonal Agriculture Research Station (ZARS), Solapur and Agricultural Research Station (ARS), Savalvihir, MPKV, Rahuri. The objective of the study is to study the genetic variation among the germplasm and to identify the better performing accessions across the locations. The environment at IIOR, Hyderabad can be considered to be the most stable environment for seed yield and ZARS Solapur can be considered to be the most stable environment for maturity days because closer to the center of the site regression biplot. Based on site regression (SREG) model analysis and *per se* performance genotype GP₂-1217 for seed yield and maturity is an ideal genotype across environments. The magnitude of phenotypic coefficient of variation (PCV) values for all the traits were higher than the corresponding genotypic coefficient of variation (GCV) values indicating that all seven traits are under the influence of environmental effect. High heritability associated with high genetic advance as percent of mean were recorded for plant height, indicating less environmental influence on plant height and role of additive gene action. Two major clusters were identified based on heat map diversity approach. The high yielding and medium duration check genotypes DRSF-113 grouped under Ist cluster whereas check Morden which is dwarf and early duration genotype grouped under IInd cluster. The yield traits like 50% flowering and maturity days falls under one group and showed more or less similar type of pattern in the expression of traits. Based on diversity analysis genotypes identified into two major clusters that can be utilised for the development of high yielding and medium duration diverse gene pool in sunflower.

Key words: Sunflower, semi-arid, environment, stability, heritability

Key findings: Sunflower genotypes GMU-799 and GP₂-1217 for seed yield and for maturity days GP₆-951 are ideal genotypes across the environments. Based on SREG-Biplot and stability analysis and *per se* performance GP₂-1217 for seed yield and maturity days is an ideal genotype across environments. Consequently, the present study illustrated the existence of wide ranges of variations for most of the characters among the sunflower genotypes, which provides opportunity for genetic gain through selection or hybridization.

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INTRODUCTION

In India sunflower is the most important oilseed crop with the production of 0.415 million tonnes and productivity of 752 kg/ha during 2014-15 (GOI, 2015). The varieties and hybrids with early to medium maturity are mostly preferred by sunflower growers. 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. The variability present in the germplasm for 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. Study on genetic variability of germplasm collection was very important activity in identification different genotypes (Siddiqi *et al.*, 2012). Information on the nature and magnitude of variability and heritability in a population is one of the prerequisites for 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 mean (GAM) is more effective and reliable in predicting the resultant effect of selection (Patil *et al.*, 1996; Ramanjinappa *et al.*, 2011; Ramesh *et al.*, 2013). Genetic divergence among a set of germplasm provides background for selection and development of new genetically diverse inbred. Knowledge of genetic variation and genetic relationships between conserved germplasm is important for efficient germplasm preservation, characterisation and subsequent use by sunflower breeders. Earlier multivariate analysis has been used frequently for genetic diversity analysis in sunflower (Muppidathi *et al.*, 1995; Mohan and Seetharam 2005; Reddy *et al.*, 2012). In this study we have assessed diversity of sunflower germplasm by using heat map approach. Genotype x environment (G x E) analysis can be used to analyze the stability of

genotypes and the value of test locations. (G x E) can lead to differences in performance of genotypes over environment. Since it is impossible to test genotypes in all target environments, plant breeders do indirect selection using their own multiple-environment trials, or test environments. An important factor in plant breeding is the selection of suitable test locations, since it accounts for G x E and maximizes gain from selection (Yan *et al.*, 2011). G x E reduces the predictability of the performance of genotypes in target environments based on genotype performance in test environments. An efficient test location is discriminating, and is representative of the target environments for the cultivars to be released. The SREG (site regression) biplot is widely popular among agricultural researchers for genotype evaluation, mega environment delineation and representativeness (Yan *et al.*, 2007; Alwala *et al.*, 2010). Hence, by considering all above points this study was designed to quantify the level of phenotypic variation among sunflower germplasm accessions, to find stable performing medium maturing and high yielding 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

Experimental material, site and design

High yielding, early to medium duration genotypes identified from previous year field trial (2010-2013) at IIOR, Hyderabad were selected to constitute the germplasm trial. The trial comprising 32 sunflower genotypes including three checks (DRSF-113, Morden and Bhanu) were evaluated at three semi-arid dryland locations of Telangana and Maharashtra states during *kharif* 2013. In Telangana the location was IIOR, Hyderabad, and two locations at Maharashtra i.e. Zonal Agriculture Research Station (ZARS), Solapur and Agricultural Research Station (ARS), Savalvihiir, MPKV, Rahuri. The latitude, longitude and

annual rainfall of the locations are presented in Table 1. The experimental design used was randomized complete block design with two replications per location. The accessions were planted at 60 x 30 cm row on ridges and furrow bed. Hand-weeding and normal management practices were followed. The oil content parameter is excluded from the analysis due to non-receipt of the data from one of the centre under evaluation also volume weight is excluded from diversity study. Data collection was done

on randomly selected 5 plants and observations were recorded on days to 50% flowering (DFF); days to maturity (DM), plant height (PH), head diameter (HD), 100-seed weight (SW), seed yield/plant (SY) and volume weight (VW). The plant height and head diameter measured in cm and 100-seed weight, seed yield/plant and volume weight measured in (g). Seed yield/plant converted to yield /ha by using the formulae seed yield/ha = seed yield/plant x one hectare plant population with the spacing 60 x 30 cm.

Table 1. Details of trial conducted and annual rainfall.

No.	Centre name	Latitude	Longitude	Annual rainfall during evaluation year	Location
1.	Indian Institute of Oilseeds Research (IIOR), Hyderabad, Telangana	17° 22' 31" N	78° 28' 27" E	440 mm	Southern India
2.	Zonal Agriculture Research Station (ZARS), Solapur, Maharashtra	17.6599° N	75.9064° E	382 mm	Peninsular India
3.	Agril. Research Station (ARS), Savalvahir, Maharashtra	19.797736 N	74.469709 E	463 mm	Peninsular India

Statistical analysis

1. Analysis of variance

To determine the analysis of variance (ANOVA) and estimation of variance components the following model was used:

$$R_{ijr} = m + G_i + L_j + Br(L_j) + GL_{ij} + e_{ijr}$$

Where, R_{ijr} is yield response of the genotype i in the location j and block r , m = grand mean; the estimation of genotype (G_i) and location (L_j) main effects and GL interaction effects (GL_{ij}) and e_{ijr} = random error. All effects except the environment/location are assumed as fixed effect. Bartlett's test (Bartlett, 1937) was applied to see the homogeneity of means squares for individual block. If error variances are not same then transferred variables are used for combined analysis. Tukey's studentized range (HSD) test at 1% level used on raw mean data to find means that are significantly different from each other.

2. The site regression (SREG) model given by Crossa and Cornelius (1997) was used to

check the stability of the genotypes. A useful descriptive tool is to plot the first two components of the SREG and used in our study. This graph is called a biplot and depicts the relationships between environments, genotypes, and both combined; it allows breeders to observe patterns of response of genotypes across environments.

3. R version 3.1.3 package 'gplots' was used to draw heat map for diversity study. Hierarchical clustering and heatmap analysis were performed for mean-centered and standardized data in R. The 'hclust' function was used for hierarchical clustering. Heatmap.2 function used to draw 'heatmap' for given genotypes and traits analysed.
4. Phenotypic (PCV) and genotypic (GCV) coefficients of variation were calculated as the following formula proposed by Singh and Chaudhary (1985) was used:

$$PCV = (\sigma_p / \bar{x}) \times 100$$

$$GCV = (\sigma_g / \bar{x}) \times 100$$

Where, σ_p , σ_g , and \bar{x} are the phenotypic, genotypic standard deviation and grand mean of the traits respectively.

Heritability in the broad sense (h^2) was estimates on genotypic mean described by Allard (1999) as:

$$\text{Heritability } (h^2) = \sigma^2_g / \sigma^2_p$$

Expected genetic advance (GA) and percentage of GA calculated according to Shukla *et al.* (2006). Expected genetic advance (GA) = $i \sigma_{ph}^2$

$$\text{GA } (\%) = (\text{GA}/X) \times 100$$

Where, i is standardized selection differential, a constant (2.06), σ_p : phenotypic standard deviation.

RESULTS AND DISCUSSION

In India medium duration genotypes are mostly preferred among the sunflower growing farmers. The genotype which matures within the range of 85-100 days is considered as medium duration genotype. The *Helianthus annuus* L. germplasm collection in the Gene Bank at the Indian Institute of Oilseeds Research (IIOR) Rajendranagar, Hyderabad maintains 2322 accessions in the germplasm management unit (GMU) (Dudhe *et al.*, 2015). Identification of trait specific germplasm accessions after systematic evaluation over multilocation environments with genetically diverse background and agronomically desirable traits is of prime importance for sunflower breeding. Out of 2322 sunflower accessions high yielding, early to medium duration were used to constitute the germplasm trial. Bartlett Chi-Square test was performed (data not shown) to check the error variances ($P < 0.0001$) if the error variances are not same then transformed variable is used for combined analysis. The combined analysis of variance for 32 germplasm accessions tested at 3 locations indicated significant differences among the environments (E) and among the genotypes (G) suggesting the presence of variability among

genotypes and among environments (Table 2). From the results of combined analysis it is revealed that a highly significant variation among evaluated accessions for all investigated traits except head diameter. Genotype x Environment (G x E) interaction was significant for all traits under study which means different genotypes respond differently to different environments. Earlier Alem *et al.*, 2016 showed the significance of environmental variance compared to the genotype and GE interaction variance. They also reported significant variation for G x E interaction for seed yield among 11 sunflower genotypes tested at 6 environments. Similarly Mousavi *et al.* (2016) recorded significant effect of environment and genotype x environment interaction at four locations. They also reported significant effects of genotype x environment interaction of different genotypes.

Analysis of variance revealed significant treatment mean squares ($P < 0.0001$) for all the three environments for each character. Similarly, combined analysis of variance also depicted highly significant differences for Genotype x Environment ($P < 0.0001$), which means treatments do not perform equally well over all the locations and exhibited the presence of genotype and environmental crossovers and biplot model would be good to identify niches and to draw further inferences. The biplots of the first two principal components (PCs) showed 98.76% of total grain yield variance (Figure 1) and 99.57% for days to maturity (Figure 2). Figures 1 and 2 displays the main effects of genotypes (G) plus the G x E effect under three environments for two characters. The environments that contributed most to the G and G x E variability are located further apart in the biplot for seed yield were E3 (Solapur) and E2 (Savalvahir) followed by E1 (IIOR, Hyderabad). Hence, IIOR, Hyderabad can be considered as the most stable environment for seed yield because closer to the center of the biplot. Similarly for maturity days environments that contributed most to the G and G x E variability are located further apart in the biplot i.e. E2 (Savalvahir), E1 (IIOR, Hyderabad) followed by E3 (Solapur). Hence, ZARS Solapur can be

Table 2. Combined analysis for seed yield and yield parameters.

Source	Trait	DF	Mean square	F value	Pr > F	Significant
	SY					
Environment (E)		2	1943.026	1943.026	<.0001	**
Location (Replication)		1	6.291	6.291	0.0006	**
Genotype (G)		31	16.182	16.182	<.0001	**
G x E		62	5.950	5.950	<.0001	**
Error		93	1.0000	1.0000		
	FPF					
Environment (E)		2	3731.028	3731.028	<.0001	**
Location (Replication)		1	3.094	3.094	0.0307	*
Genotype (G)		31	4.402	4.402	<.0001	**
G x E		62	1.879	1.879	<.0001	**
Error		93	1.000	1.000	0.0029	
	MD					
Environment (E)		2	9290.021	9290.021	<.0001	**
Location (Replication)		1	26.327	26.327	<.0001	**
Genotype (G)		31	21.259	21.259	<.0001	**
G x E		62	1.529	1.529	0.0314	*
Error		93	1.0000	1.0000		
	PH					
Environment (E)		2	9290.022	9290.022	<.0001	**
Location (Replication)		1	26.327	26.327	<.0001	**
Genotype (G)		31	21.259	21.259	<.0001	**
G x E		62	1.529	1.529	0.0314	*
Error		93	1.000	1.000		
	HD					
Environment (E)		2	1275.257	1275.257	<.0001	**
Location (Replication)		1	2.416	2.416	0.0714	NS
Genotype (G)		31	8.791	8.791	<.0001	**
G x E		62	4.824	4.824	<.0001	**
Error		93	1.000	1.000		
	SW					
Environment (E)		2	410.022	410.022	<.0001	**
Location (Replication)		1	7.193	7.193	0.0002	**
Genotype (G)		31	5.562	5.562	<.0001	**
G x E		62	2.867	2.867	<.0001	**
Error		93	1.000	1.000		
	VW					
Environment (E)		2	4315.852	4315.852	<.0001	**
Location (Replication)		1	3.228	3.228	<0.0260	*
Genotype (G)		31	5.093	5.093	<.0001	**
G x E		62	3.608	3.608	<.0001	**
Error		93	1.000	1.000		

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

Seed yield (SY), 50% flowering (FPF), maturity days(MD), plant height (PH), head diameter (HD), 100-seed weight (SW) and volume weight (VW)

considered as most stable environment for maturity days because closer to the center of the biplot. Discriminating ability and representativeness of the environments are two important features of the biplot technique, which

enhances the efficiency of the programme (Yan, 2001).

The environments E1 (IIOR, Hyderabad) and E2 (Savalvihir) did not appear to be highly correlated with the other unstable

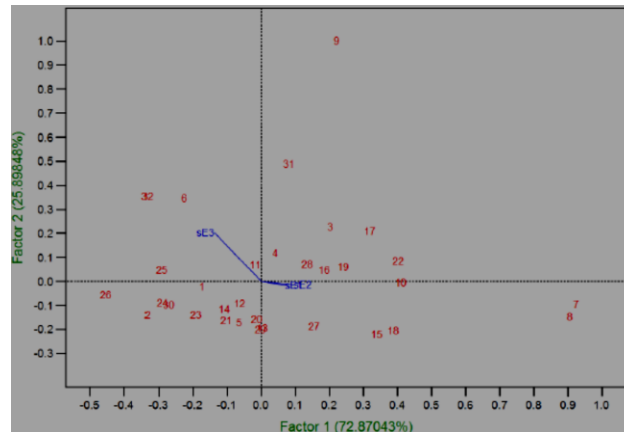


Figure 1. SREG Biplot for seed yield under different environments at IIOR, Hyderabad (E1), RARS, Savalvihir (E2) and ZARS, Solapur (E3).

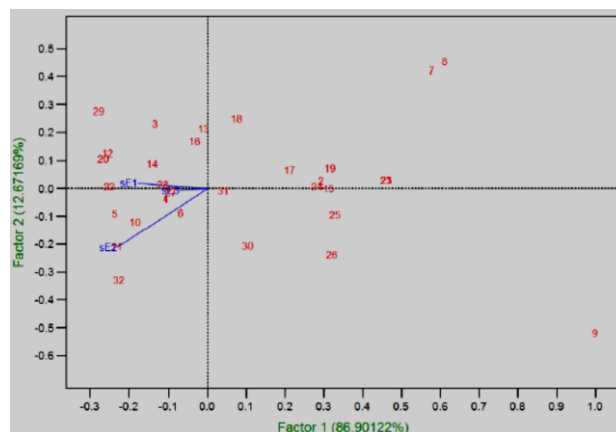


Figure 2. SREG Biplot for days to maturity under different environments at IIOR, Hyderabad (E1), RARS, Savalvihir (E2) and ZARS, Solapur (E3).

environments E3 (Solapur). For seed yield the environment Solapur was the discriminating, while the environments *viz.*, IIOR, Hyderabad and Savalvihir were found non-discriminating and similar to each other (Figure 1). Considering the fact that first component of the SREG analysis accounted for the non-crossover Gx \times E interaction variability and the second component is due to the crossover Gx \times E variance, the ideal genotype is one with the highest values for the first component and a value close to zero for the second component. Genotype 26 and 25 seems to be nearest to the definition of an ideal genotype for seed yield (Figure 1) and genotype 22 for maturity. Other genotypes that appeared

superior were 24, 30, 2 for seed yield and 5 and 10 for days to maturity. On the other hand, for seed yield genotypes located on the opposite quadrant, such as genotypes 31, 3 and 17 and 22 and for days to maturity were the 8, 17, and 18 were the worst performers in most of the environments (Figure 2).

Genotypes yield are sometimes expressed in each environment are considered as relative yields hence, it is important to analyse the stability of genotypes across environments. Ranks are allotted to the best performing genotypes across the environments. For maturity days late maturing genotypes ranked higher than early maturing genotype. Hence lower ranking

genotypes are more early than top ranking genotypes. Ranking of the genotypes based on seed yield and maturity days are calculated from the transformed means for each genotype. Genotype 13 (GMU-799) ranked first followed by 25 (GP₂-1217) across the environments for seed yield and for maturity days genotype 24 (GP₆-951) ranked first followed by 26 (GP₆-1227) (Table 3). The genotypes used in this

study are previously evaluated for seed yield and maturity days at IIOR, Hyderabad from 2010-2013. All the genotypes except GP₆-951 and GP₆-1227 matured slightly above medium duration across the environments i.e. 103 days where as all the genotypes matured in the range of 85 to 100 days. The ideal genotypes had the high *per se* and consistent performance in different environments (Yan *et al.*, 2000).

Table 3. Ranking of the genotypes based on seed yield and maturity duration.

No.	Treatment name	Seed yield			Maturity duration		
		Original mean values	Transformed mean values	Rank	Rank	Transformed mean values	Original mean values
1.	GMU-168	1419.00	7.10 ^{ABCDEFGH}	13	23	34.16 ^{EF}	89.00
2.	GMU-189	1862.67	9.12 ^{AB}	4	9	37.27 ^{ABC}	89.00
3.	GMU-229	1445.33	7.35 ^{ABCDEF}	11	18	34.67 ^{DEFG}	90.00
4.	GMU-258	922.67	4.73 ^{HJK}	29	13	35.72 ^{BCDE}	94.00
5.	GMU-440	1679.33	7.50 ^{ABCDEF}	10	12	35.78 ^{BCDE}	93.00
6.	GMU-601	1062.67	4.75 ^{HJK}	27	32	32.82 ^G	86.00
7.	GMU-616	1447.00	6.93 ^{BCDEFGH}	14	21	34.54 ^{DEFG}	90.00
8.	GMU-713	1162.67	6.10 ^{DEFGHI}	19	29	33.43 ^{EF}	87.00
9.	GMU-776	1203.00	5.49 ^{FGHIJK}	24	17	34.71 ^{DEFG}	91.00
10.	GMU-753	1453.00	7.20 ^{ABCDEF}	12	30	33.12 ^{FG}	87.00
11.	GMU-786	1247.00	5.76 ^{FGHIJK}	23	16	33.12 ^{FG}	91.00
12.	GMU-787	1091.00	5.49 ^{FGHIJK}	25	22	34.54 ^{DEFG}	90.00
13.	GMU-799	1879.67	9.61 ^A	1	26	33.73 ^{EF}	88.00
14.	GMU-798	1345.00	6.66 ^{BCDEFGHI}	15	31	33.08 ^G	87.00
15.	GMU-834	1200.33	6.01 ^{DEFGHIJK}	20	25	33.83 ^{EF}	87.00
16.	GMU-889	1240.33	6.54 ^{CDEFGHIJ}	16	11	35.96 ^{BCDE}	93.00
17.	GMU-897	1131.33	5.85 ^{EF}	21	19	34.59 ^{DEFG}	90.00
18.	GP ₆ -211	1677.67	8.85 ^{ABC}	5	4	37.94 ^{AB}	99.00
19.	GP ₆ -271	1600.67	7.82 ^{ABCDEF}	8	14	35.66 ^{BCDEF}	92.00
20.	GP ₆ -286	1749.67	9.19 ^{AB}	3	10	36.73 ^{ABCD}	95.00
21.	GP ₆ -571	1685.67	8.44 ^{ABCD}	6	3	38.16 ^{AB}	100.00
22.	GP ₆ -644	822.33	4.28 ^{JK}	31	5	37.86 ^{AB}	99.00
23.	GMU-797	1234.67	6.24 ^{DEFGHIJ}	18	27	33.66 ^{EF}	87.00
24.	GP ₆ -951	1116.00	5.84 ^{EF}	22	1	39.18 ^A	103.00
25.	GP ₂ -1217	1912.33	9.58 ^A	2	28	33.52 ^{EF}	87.00
26.	GP ₆ -1227	1006.33	5.13 ^{GHIJK}	26	2	39.18 ^A	103.00
27.	GP ₆ -1475	901.00	4.61 ^{LJK}	30	7	37.65 ^{AB}	99.00
28.	GP ₂ -1334-3	966.67	4.73 ^{HJK}	28	6	37.81 ^{AB}	99.00
29.	GP ₆ -714	698.67	3.51 ^K	32	8	37.37 ^{ABC}	99.00
30.	DRSF-113 ©	1546.67	7.63 ^{ABCDEF}	9	20	34.59 ^{DEFG}	90.00
31.	Morden ©	1232.67	6.50 ^{CDEFGHIJ}	17	24	33.97 ^{EF}	87.00
32.	Bhanu ©	1717.33	8.35 ^{ABCDE}	7	15	35.03 ^{CDEFG}	90.00
General mean			6.65			35.47	
p-value			< .0001			< .0001	
cv (%)			15.03			2.82	
SE(d)			0.577			0.577	
Tukey's HSD at 1%			2.2538			2.2538	

Hence, Genotype GMU-799 and GP₂ - 1217 for seed yield and for maturity days GP₆ 951 are ideal genotypes across the environments. Based on SREGBiplot and stability analysis and *per se* performance GP₂-1217 for seed yield and maturity days is an ideal genotype across environments. Mousavi *et al.* (2016) identified sunflower genotypes Terra, Vidoc and Alisson Cultivars for yield stability across environments through AMMI and GGE biplot analysis. Alem *et al.* (2016) identified Acc. 208768 with highest seed yield in 5 out of 6 environments. They also revealed that the ideal genotype i.e. Acc. 208768 was the closest genotype to the ideal cultivar through biplot analysis.

To compare the variation among various plant properties, phenotypic (PCV) and genotypic coefficient of variability (GCV), broad sense of heritability (H²) and genetic advance are calculated and given in Table 4. The magnitude of phenotypic coefficient of variation (PCV) values for all the traits were higher than the corresponding (GCV) values indicating that these characters may influenced by environmental effect. Phenotypic coefficients of variability ranged from 6.12 to 31.04% and the highest PCV obtained from seed yield/ha and the lowest from maturity days. Broad sense

heritability estimates was high for 50% flowering (80.55) plant height (76.91) and for maturity days (75.92). Genetic advance as percent of the mean (GAM) was highest for seed yield/ha (28.67%) followed by plant height (24.55%) and the remaining traits showed a moderate to very low amount of genetic advance. Higher heritability estimates for these traits indicate that environmental factors did not greatly affect phenotypic variation of such characters. Heritability values alone cannot provide any indication of the amount of progress that would result from selection because heritability in broad sense includes both additive and non-additive gene action. Therefore, high heritability estimates in broad sense would be a reliable tool for selection if accompanied by high genetic advance as percent of means (Ramesh *et al.*, 2013). High heritability associated with high genetic advance as percent of mean were recorded for plant height, indicating lesser environmental influence on plant height and a role of additive gene action. Similar observations for plant height were recorded by Ramesh *et al.* (2013) for head diameter and oil yield by Teklewold *et al.*, (1999), Ashok *et al.* (2000).

Table 4. Estimates of genetic parameters for morphological traits.

	$\sigma^2 p$	$\sigma^2 g$	PCV(%)	GCV(%)	H ²	GAM(%)	GA	S.E.	C.D.(%)	CV(%)
Seed yield/ha	168171.65	75396.39	31.04	20.79	44.83	28.67	378.74	175.85	492.42	23.06
50% flowering	38.38	30.92	10.33	9.27	80.55	17.14	10.28	1.57	4.41	4.55
Maturity days	32.16	24.42	6.12	5.33	75.92	9.58	8.87	1.60	4.49	3.00
Plant height	459.83	353.700	15.50	13.59	76.91	24.56	33.97	5.94	16.65	7.44
Head diameter	5.36	2.43	16.90	11.38	45.36	15.80	2.16	0.98	2.76	12.49
Seed weight	0.83	0.39	20.35	13.94	46.91	19.67	0.88	0.38	1.07	14.83
Volume weight	12.72	4.21	9.30	5.35	33.12	6.34	2.43	1.68	4.17	7.60

PCV: Phenotypic coefficient of variation, GCV: genotypic coefficient of variation,, H²: broad sense heritability, GA: genetic advance, GAM%: genetic advance as percent of mean. S.E: Standard error, C.D.: Critical difference and C.V: Coefficient of variation

Other objective of the present study was to identify the high yielding and medium duration genotypes through cluster analysis. Earlier in sunflower Komaraiah *et al.* (2004), Srinivas *et al.* (2006) and Ananda Kumar *et al.* (2007) studied genetic divergence either in parental or inbred lines or among working

germplasm. In this study 32 genotypes grown across the test sites were subjected to hierarchical clustering (HCA) and heat map analysis (Figure 3). Hierarchical clustering of genotypes based on the Euclidian distances for the eight traits is represented. Heat map approach gives an opportunity to visualize the

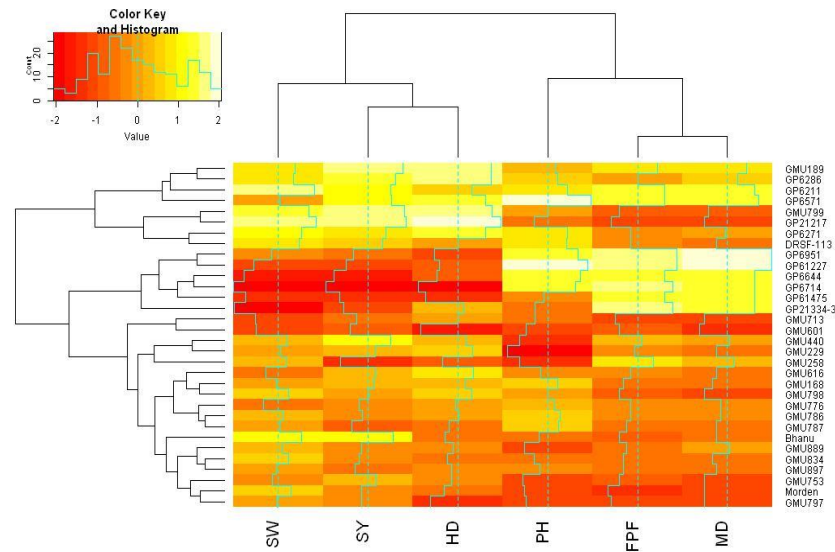


Figure 3. A hybrid representation of dendrogram and heatmap used to depict the diversity among 32 sunflower genotypes and traits with corresponding expression of genotype for each trait (Where, Seed yield (SY), 50% flowering (FPF), maturity days (MD), plant height (PH), head diameter(HD) and 100-seed weight (SW)).

expression of the each trait across the environments. Heat map and dendrogram displaying relatedness of genotypes and traits under study based on their Euclidean distances. Red and yellow correspond to low and high diversity for expressed traits. White colour represents median levels of expression. The color key indicates the correlation between diversity and colors. The histogram represents a distribution of each value under observation for particular trait. Based on the Ward's clusters analysis (Squared Euclidean distance) 32 genotypes and 7 morphological traits were considered for diversity study. The dendrogram of 32 genotypes is presented in Figure 3. Thirty two genotypes were grouped into two major clusters. Eight genotypes grouped under Ist cluster and twenty four genotypes grouped under IInd cluster. The high yielding and medium duration check genotypes DRSF-113 grouped under Ist cluster whereas check Morden dwarf and early duration genotype grouped under IInd cluster. Genotypes GMU-799, GP₂-1217, GP₆-951 and DRSF-113 top ranked for high yield and maturity duration. Hence, the genotypes in first cluster *viz.*, GMU-189, GP₆-286, GP₆-211, GP₆-571, GMU-799, GP₂-1217, GP₆-951 and

DRSF-113 can be considered diverse from the other cluster for high yield and medium duration which can be further utilized for the development of varieties or inbreds of medium duration coupled with yield. Similarly genotypes in second cluster can be considered diverse from the first cluster for early to medium duration. Genotypes grouped under these clusters can serve as the genetic base to develop medium maturing and high yielding varieties and inbreds for semi-dryland conditions. Reddy *et al.* (2012) reported diversity of the genotypes based on seed yield, total number of filled seeds, head diameter, 100-seed weight measured from Euclidean distances and Ward's minimum variance analysis in sunflower.

The first cluster created two sub-clusters; each of the 4 genotypes under each cluster. The second cluster comprised two sub-clusters; the first included the genotypes GP₆-951, GP₂-1334-3, GP₆-1475, GP₆-714, GP₆-644 and GP₆-1227 while the second sub-cluster included 18 genotypes. The yield traits 50% flowering and maturity days falls under one group and showed more or less similar type of pattern in the expression of the traits depicted by histogram. Check variety Morden and GMU-797

falls under one sub group. Check Morden is dwarf and early duration genotype the other genotypes which are near to check are GMU-834, 897 and 753. Use of diverse parents in hybridization programme can serve the purpose of combining desirable genes or to obtain recombination. Crosses between divergent parents usually produce greater heterosis than those between closely related ones (Moll and Stuber, 1971) hence, identified genotypes can be utilised for the development of high yielding and medium duration diverse gene pool in sunflower.

CONCLUSION

In summary we have demonstrated that genotype x environment (GxE) interaction was significant for all traits under study which means different genotypes respond differently to different environments. Genotype GMU-799 and GP₂-1217 for seed yield and for maturity days GP₆-951 are ideal genotypes across the environments. Based on SREG-Biplot and stability analysis and *per se* performance GP₂-1217 for seed yield and maturity days is an ideal genotype across environments. Consequently, the present study illustrated the existence of wide ranges of variations for most of the characters among the sunflower genotypes, which provides opportunities for genetic gain through selection or hybridization. The traits 50% flowering and maturity days falls under one group and showed more or less similar type of pattern in the expression of the traits by heat map approach. Based on diversity analysis identified genotypes from two major clusters can be utilised for the development of high yielding and medium duration diverse gene pool in sunflower.

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