Received: 15 May 2020 | Revised:08 Dec 2020 | Accepted: 10 Dec 2020

Electronic Journal of Plant Breeding

Research Article

Multivariate analysis in sunflower genotypes for yield associated traits

R. Sasikala[1*], G. Raiza Christina[1], P. Sahithi Reddy[1], PL. Viswanathan[1] and S. Manonmani[2]

[1] Department of Oilseeds,
[2] Department of Plant Genetic Resources, Centre for Plant Breeding and Genetics, TNAU, Coimbatore-641 003, Tamil Nadu, India.
***E-Mail:** sasikalacpbg@gmail.com

Abstract
Development and evaluation of genetics resources are an essential part of sunflower breeding. To evolve the potential heterotic hybrids in sunflower, plant breeding studies are being carried out for the selection of promising parental inbreds for various yield attributed traits. Ninety -one sunflower germplasm accessions were evaluated for seven quantitative traits during *Rabi* 2018-19 and data were subjected to biometric analysis for correlation and Principal Component Analysis. PCA analysis revealed that, out of 7 PCs, only 3 PCs exhibited more than 1.0 Eigenvalue and showed 71.45% variability for 91 genotypes. PC1 reported for highest variability in traits like days to 50% flowering and days to maturity. PC3 showed the positive load on yield attributing traits like hundred seed weight and single plant yield. PC1 and PC3 allowed for simultaneous selection of yield related traits. Maximum PC value found in genotypes TSG 349, GP6-313, CPI 1, CPI 12, CMS PET89B, NDI11, PM155, PM81, DRSF113, GP6 1075, TSG 331 and SCG 103 would be of practical value in sunflower breeding for identifying genotypes with specific traits for utilization in the breeding programme.

Keywords
Sunflower, germplasm, quantitative traits, PCA

INTRODUCTION

Sunflower is an important oilseed crop cultivated for its edible oil. It has high vitamin E content and low saturated fatty acids which help to prevent heart problems. Importance of sunflower oil is increasing among farmers and industrialists, due to the probability of use of oil as a raw material in biodiesel production (Srinivas *et al*, 2006 and Divya *et a*l., 2019). To advance the crop improvement studies, research is being carried out for identification and evaluation of genotypes considering important aspects in the production process (Chandirakala and Manivannan, 2014). The concept of hybrid development is the most important aspect in sunflower breeding. Hybrids with high heterotic vigour are possible by the use of genetically diverse parents in the crossing programme. Several studies have been carried out for genetic diversity of inbreds by employing agronomic traits in sunflower. Principal Component Analysis is a well-known method of reduction of large number variables present in the data set as well as resulted data set which contains almost all the information from a large set. Therefore, the present investigation aimed to evaluate and rank promising inbreds based on PCA analysis for further utilization of inbreds in hybridization programme.

MATERIALS AND METHODS

The experimental material consists of ninety -one sunflower germplasm accession received from IIOR, Hyderabad and maintained at Department of Oilseeds, Centre for Plant Breeding and Genetics, Tamil Nadu Agricultural University, Coimbatore. The experiment was

laid out in Augmented Block Design during *Rabi* 2018-19. The 91 sunflower lines which include 7 checks were evaluated in 3 blocks and checks were placed throughout the experimental bocks randomly. Each line were raised in a single row of four meter length with a spacing of 60 x 30 cm. All the recommended agronomical practices were followed to raise a good and healthy crop throughout the experimental period.

Observations were recorded for quantitative characters on five randomly selected plants from each genotype. Quantitative characters *viz.,* plant height, days to 50% flowering, days to maturity, head diameter, hundred seed weight, volume weight and single plant yield. Data were analysed for Principal Component Analysis (PCA) by using statistical package STAR (Statistical Tool for Agricultural Research) - IRRI Plant Breeding software.

RESULTS AND DISCUSSION

Principal Component Analysis is a non-parametric method which used mainly for extraction of useful information from the confusing data sets. Sultana and Ghafoor (2009) reported PCA as a powerful technique for reduction of large variables in the dataset that removes interrelationships among components and this technique has been considered effective for a selection of desirable clusters of promising genotypes by Muhammad *et al*., (2009). Ninety -one sunflower germplasm accessions were studied for seven quantitative traits such as plant height, days to 50% flowering, days to maturity, head diameter, hundred seed weight, volume weight and single plant yield. Data were subjected to biometric analysis for correlation and PCA and the results obtained are presented below.

The descriptive statistics of 91 sunflower germplasm is summarized in **Table 1**. Plant height had the largest variance and the minimum and maximum plant height are ranged between 48 and 196 cm. Days to maturity ranged from 84 (TSG349) and 118 (EC-601780) days and single plant yield ranged from 15 (TSG349) to 28.10g (GP6-313). The trait volume weight has the largest variance next to plant height, with the values ranging from 27g to 75g.

Table 1. Descriptive statistics for seven quantitative traits of 91 sunflower genotypes

Sl.No.	Variable	Minimum	Maximum	Mean	Std Dev.
1	Plant height	48.00	196.00	127.08	24.39
2	Days to 50% flowering	53.00	87.00	61.05	5.12
3	Days to maturity	84.00	118.00	92.04	5.13
4	Head diameter	4.70	14.80	10.08	2.06
5	100 seed weight	2.40	8.20	3.22	1.47
6	Volume weight	27.00	75.00	32.02	10.20
7	Single plant yield	15.00	28.10	20.33	2.16

Table 2. Phenotypic correlation for various quantitative traits of sunflower

Variables	PH	D50%F	DM	HD	HSW	VW	SPY
PH	1.00						
D50%F	0.01	1.00					
DM	0.02	0.99**	1.00				
HD	0.51**	-0.05	-0.04	1.00			
HSW	0.06	0.01	0.01	0.35**	1.00		
VW	0.25**	0.02	0.02	0.13	-0.01	1.00	
SPY	0.07	-0.03	-0.03	0.13	0.28**	0.03	1.00

** significant at 0.05

Note: PH-Plant Height; DFF- Days to 50% flowering; DM- Days to Maturity; HD- Head Diameter; HSW- Hundred Seed Weight; VW- Volume Weight; SPY-Single Plant Yield.
(Include in correlation coefficient paragraph)

Significant and high order correlation was observed between days to 50% flowering and maturity (0.99**). Positive correlations for both the traits were previously reported by (Komuraiah *et al.,* 2004). As well as significant positive correlation was observed for traits such as Plant height and head diameter (0.51**); plant height and volume weight (0.25**); head diameter and hundred seed weight (0.35**) and hundred seed weight and single plant yield (0.28**) (**Table 2**). Manivannan *et al*., (2005) also reported that plant height had a significantly positive association

with head diameter. Hence, the trait high hundred seed weight genotypes can be used for hybridization purpose to get the best heterosis which is having some positive correlation with two traits head diameter and single plant yield. Loganathan and Gopalan (2006) suggested that independent improvement of characters in sunflower without affecting each other could be made in sunflower breeding programme.

Principal component analysis was performed for seven quantitative traits of sunflower. Out of 7 PCs, only 3 PCs exhibited more than 1.0 Eigenvalue and showed 71.45% variability for 91 genotypes (**Table 3**). PC1 accounted for 28.67% variability which includes days to 50% flowering and days to maturity. Whereas, PC2 accounted for 25.74% variability which includes negative load on all the traits. PC1 and PC2 accounted for more than 50% of the total variability. PC3 showed the positive load on yield attributing traits like hundred seed weight and single plant yield. Hence, PC1 and PC3 can be allowed for simultaneous selection of yield related traits. Earlier studies confirmed that high value PC scores can be selected for further utilization in a breeding programme (Arshad *et al*., 2010).

Principal Component 1 (PC1) loaded positively for days to 50% flowering (0.701) and days to maturity (0.700). Third principal component accounted for positive significance on traits viz., hundred seed weight (0.554) and single plant yield (0.527) (**Table 3**). Hence, entries which are having positive loading in these PCs can be selected for crop improvement programmes.

Table 3. PC values for various quantitative traits of sunflower genotypes

Statistics	PC1	PC2	PC3	PC4	PC5	PC6	PC7
Eigen Values	2.01	1.80	1.19	0.89	0.71	0.40	0.0005
Variability %	28.67	25.74	17.04	12.66	10.19	05.69	00.01
Cumulative %	28.67	54.41	71.45	84.11	94.30	99.99	100.00
Traits							
Plant height	-0.036	-0.532	-0.407	0.185	0.413	0.587	-0.006
Days to 50% flowering	0.701	-0.082	0.035	0.002	0.015	-0.026	-0.707
Days to Maturity	0.700	-0.088	0.028	0.011	0.018	-0.027	0.707
Head diameter	-0.100	-0.604	-0.056	0.380	-0.031	-0.690	-0.005
Hundred seed weight	-0.047	-0.413	0.554	0.087	-0.596	0.398	0.002
Volume weight	0.001	-0.281	-0.495	-0.701	-0.422	-0.081	0.001
Single plant yield	-0.071	-0.296	0.527	-0.568	0.543	-0.110	0.004

Table 4. PCA scores of sunflower genotypes having positive >1 values in each PCs

PC1	CMS PET 89B(7.24), CMS850B(1.35), CMS819B(1.72), NDI 11(2.53), PM 155(2.1), PM81(3.17), TSG349(5.96), EC 601772(2.12), GP6-389(1.58), GP6-1047(1.17), GP4-2902(1.76), LTRR 341(1.62), ARM243B(1.51)
PC2	TSG349(3.67), CPI 12(1.08), R272(1.64), R 630(1.76), R3(1.3), HA124B(1.49), TSG103(2.86), TSG208(2.89), TSG331(1.12),RHA6D-1(1.2), CMS17B(1.48)
PC3	DRSF113(2.82), TSG349(2.01), GP6 1075(2.26), TSG331(2.0), HA124B(1.95),GP6-313(3.12), SCG103(2.37), NDI 11(2.24), CPI 12(1.12), NDI 7(1.49), CPI 12(2.98),

(Include in principal component analysis paragraph)

Maximum PC values were found in genotypes such as TSG 349, GP6-313, CPI 1, CPI 12, CMS PET89B, NDI11, PM155, PM81, DRSF113, GP6 1075, TSG 331 and SCG 103. Genotype TSG349 found common in PC1, PC2 and PC3, NDI 11 found in PC1 and PC3 and CPI12, TSG331, HA124B found common in PC2 and PC3 (**Table 4**). TSG 349 scores for different PCs PC1 (5.96), PC2 (3.67) and PC3 (2.01) showed that presence of the fair amount of genetic diversity and these entries can be effectively utilized for further breeding programmes.

The genotypes found in more than 1 PCs would be of top practical value in sunflower breeding for identifying genotypes with specific traits for utilization in a breeding programme. Previous studies of various authors also reported that high value PC scores can be selected for further utilization in plant breeding programmes and findings are confirmation with Ghanffari (2004), Arsad *et al*., (2010) and Renuka and Anita (2017).

ACKNOWLEDGEMENT

The authors would like to thank Dr A.Vishnuvardhan Reddy, Director, IIOR, Hyderabad and Dr M.Sujatha,

Principal Scientist and Head, (PI-AICRP Sunflower-Crop improvement) for providing plant genetic resources through AICRP on Sunflower.

REFERENCES

Arshad, M., Ayub Khan, M., Jadoon, S.A. and Mohmand, A.S. 2010. Factor analysis in sunflower (*Helianthus annuus* L.) to investigate desirable hybrids. *Pakistan Journal of Botany*, **42**(6): 4393-4402.

Chandirakala, R. and Manivannan, N. 2014.Genetic diversity among sunflower genotypes. *Electronic Journal of Plant Breeding,* **5**(3): 577-580.

Divya, S., Kalaimagal, T., Manonmani, S. and Rajendran, L. 2019. Genetic analysis of variability, heritability and genetic advance in F3 populations of sunflower *(Helianthus annuus* L.). *Electronic Journal of Plant Breeding*, **10** (2): 761-765. [Cross Ref]

Ghanffari, M. 2004. Use of Principal component analysis method for selection of superior three way cross hybrids in sunflower. *Seed and Plant*, **19**(4): 513-527.

Komuraiah, K., Reddy, S.S., Ranganatha, A.R.G. and Ganesh, M. 2004.Genetic divergence in the inbred lines of sunflower (*Helianthus annuus* L.). *Journal of Oilseeds Research*, **21**(1): 154-155.

Loganathan, P. and Gopalan A. 2006. Association analysis in sunflower (*Helianthus annuus* L.). *Research on Crop*, **7**(1): 202-203.

Manivannan, N., Muralidharan, V. and Subbalakashmi, B. 2005. Correlation analysis in sunflower. *Legume Research*, **28**(1): 71-73.

Muhammad, S., Bacha, S., Arshad, M., Din, R. and Ghafoor, A. 2009. Genetic diversity for determining yield potential and selection criteria in *Pisum sativum* (L.) genetic resources. *Pakistan Journal of Botany*, **41**: 2987-2993.

Renuka, S. and Anita, B. 2017. Principal Component Analysis of Chickpea (*Cicer arietinum* L.) Germplasm. *Int.J.Curr.Microbiol.App.Sci.,* **6**(10): 166-173. [Cross Ref]

Srinivas, B., Kuldeep, S.D., Laxmi Prayaga and Sudheer Kumar, S. 2006. Genetic divergence studies in Sunflower (*Helianthus annuus* L) germplasm lines. *J. Oilseeds Res*., **23**(1): 49- 51.

Sultana, T. and Ghafoor, A. 2008. Genetic diversity in *ex-situ* conserved *Lens culinaris* for Botanical Descriptors, Biochemical and Molecular Markers and Identification of Landraces from Indigenous genetic Resources of Pakistan. *Journal of Integrative Plant Biology*, **50**(4): 484-490. [Cross Ref]