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Research Article

Genetic divergence studies for yield and its attributes in sunflower (H*elianthus annuus* l.)

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Abstract

The present study was undertaken at Regional Agricultural Research Station, Nandyal during *rabi*, 2016-17. Seventy genotypes of sunflower were evaluated in a randomized complete block design replicated thrice for assessment of genetic diversity. Highly significant differences were observed for all the characters studied. The results of PCA revealed that the traits *viz.*, plant height, head diameter, 100 achene weight, number of achenes per head, volume weight, and leaf area index can be utilized as selection criterion for increasing variability which can be harnessed in hybridization programmes to generate transgressive segregants.

Key words : Genetic divergence – Sun flower – variability.

Introduction

Edible oil seeds occupy a prominent role in the Indian economy next to pulses. India is the third largest producer of edible oils after U.S.A and China. Among the edible oil seeds, sunflower ranks fourth in position after groundnut, soybean, rapeseed and mustard. Sunflower oil is premium oil due to its light colour, bland flavor, high smoke point, towering level of unsaturated fatty acids, good nutritional quality and lack of linolenic acid. Besides, the crop can be grown on a large area owing to its inherent traits *viz*., short duration, day neutrality and thus fits in any cropping season and can be cultivated throughout the year. Sunflower is a potential source for vegetable oil and protein. As the modern cultigens of sunflower have reached an yield plateau, there is an urgent need to screen genotypes for genetic divergence to utilize them in breeding programmes for harnessing higher yields.

Genetic variability is very crucial item in the breeding programs (Sujatha *et al*. 2002). Exploitation of genetic variability is the foremost important for further genetic upgradation of the crop as genetic variation is the base for effective plant improvement programme. The traits having major contribution to the total variation within a group of genotypes can be identified through principal component analysis. This helps in selection of traits which simultaneously results in increased variation that forms the basis for hybridization programme resulting in generation of transgressive segregants.

PCA, a sort of multivariate analysis that brings about the reduction of the original variables into a new set of uncorrelated variables by linear transformation known as principal components (Mohammadi, 2003). PCs are orthogonal and independent of each other, and each PC helps in interpretation of different properties of the original data independently. In this way, the total variation in the original data set may be broken down into components that are cumulative (Mohammadi, 2003). Principal component analysis (PCA) result in generation of a two or three dimensional scatter plot of individuals and characters, whose geometrical distances helps in identification of correlated traits and identification of sets of genetically similar individuals (Mohammadi, 2003).

The canonical root analysis for 70 genotypes of sunflower was carried out as per the procedure outlined by Rao (1952). Tabrizi *et al*., (2009) and Ghaffari *et al*., (2011) used this method for genetic diversity estimation of single cross hybrids based on agronomic traits. In Arshad *et al*., (2010) study, the principal components analysis could help for identification of the best sunflower hybrids. The study of Sankar *et al*., (2004) using principal components analysis indicated that plant traits stomatal conductance, photosynthesis, root length, stem nitrogen, leaf nitrogen, flower head diameter and flower head weight are dominant and consistent traits for sunflower growth in different seasons. In the present study principal components analysis was used for identification of traits having major contribution towards genetic divergence.

Materials and methods

The experimental material comprised of 70 genotypes in sunflower sown in a randomized complete block design replicated thrice at Regional Agricultural Research Station, Nandyal, Andhra Pradesh during *rabi*, 2016-17. Each genotype was raised in a single row of 3 m length with a spacing of 30 cm between the plants and 60 cm between the rows. Recommended agronomic practices were adopted to raise good crop. Data were recorded on five randomly selected plants in each entry per replication for 15 quantitative traits *viz*., days to 50 per cent flowering, days to maturity, plant height, number of leaves per plant, head diameter, 100 achene weight, number of achenes per head, autogamy per cent, volume weight, achene yield per plant, hull content, oil content, SPAD chlorophyll meter reading, specific leaf area and leaf area index.

Results and discussion

The results of PCA resulted in 7 components having eigen value of greater than 0.96 contributed about 76.29% of total variability in 70 genotypes involving all the 15 quantitative traits studied (Table 1). The contribution of traits towards the PC could be seen from the corresponding eigen values which are presented in Table 2. The first and second roots accounted for 22.57 and 14.60 per cent respectively to total variability. Five canonical roots *viz*., third, fourth, fifth, sixth and seventh contributed 9.44, 8.45, 8.15, 6.66 and 6.41 per cent respectively towards the total variability.

In the vector Z1, traits contributing towards total divergence were hull content (0.19), days to 50% flowering (0.08) and days to maturity. While the remaining characters displayed negative contribution to the total diversity. For the vector $Z_{2,}$ days to 50% flowering (0.48) contributed maximum to the genetic diversity followed by days to maturity (0.42), number of leaves per plant (0.38), SPAD chlorophyll meter reading (0.26), plant height (0.23), volume weight (0.19), 100 achene weight (0.15), hull content (0.15), specific leaf area (0.13), autogamy per cent (0.09) and achene yield (0.02). In the vector $Z_{3,}$ the traits *viz*., volume weight (0.42), achene yield (0.34), number of achenes per head (0.27), oil content (0.25), days to 50% flowering (0.16), autogamy per cent (0.15), plant height (0.06) and number of leaves per plant (0.04) had significant contribution to the diversity. Hull content (0.56) had maximum contribution to the diversity in vector Z_4 followed by autogamy per cent (0.30), head diameter (0.28), number of leaves per plant (0.22), number of achenes per head (0.20), days to 50% flowering (0.17), 100 achene weight (0.13) and leaf area index (0.07).In the vector $Z_{5,}$ leaf area index (0.32) exhibited maximum contribution for diversity followed by number of leaves per plant (0.28), plant height (0.26), days to 50% flowering (0.08) and oil content (0.04).The trait days to maturity (0.47) had shown maximum contribution to the diversity in the vector Z_6 followed by volume weight (0.37), head diameter (0.29), days to 50% flowering (0.28), oil content (0.15), 100 achene weight (0.07) and autogamy per cent (0.03). The trait oil content (0.51) had registered maximum contribution for diversity in the vector Z_7 followed by days to 50% flowering (0.42), SPAD chlorophyll meter reading (0.15), number of leaves per plant (0.13), 100 achene weight (0.13), leaf area index (0.11), achene yield (0.10), head diameter (0.08), autogamy per cent (0.02) and days to maturity (0.01).

The tri-dimensional spatial figuration shows 7 basic clusters of the characters studied (Figure 1).Based on the Figure 1, it was observed that selection for the traits *viz*., days to 50% flowering, days to maturity, plant height, number of leaves per plant, autogamy per cent, volume weight, and oil content will result in development of hybrids with increased yields. The traits, hull content and specific leaf area were in opposite direction indicating the negative contribution of these traits for achene yield.

The cluster I had 2 characters in a group (days to 50% flowering, days to maturity) and cluster II (SPAD chlorophyll meter reading, autogamy per cent, number of leaves per plant) III (leaf area index, plant height, number of achenes per head) and IV (head diameter, 100 achene weight, volume weight) had 3 characters each. Cluster V, VI, VII had hull content, specific leaf area and oil content respectively. Traits grouped in one cluster are closely associated compared to those grouped under different clusters. Achene yield in sunflower is mainly determined by head diameter, 100 achene weight, and number of seeds per head. From the figure it can be inferred that these traits are grouped under clusters III and IV which are in turn correlated with other traits. Hence, the traits under these clusters *viz*., plant height, head diameter, 100 achene weight, number of achenes per head, volume weight, and leaf area index could be used as selection criterion for increasing variability which will result in increased achene yield.

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Table 1. Canonical root values, per cent of variation and cumulative variation explained for 70 genotypes of sunflower

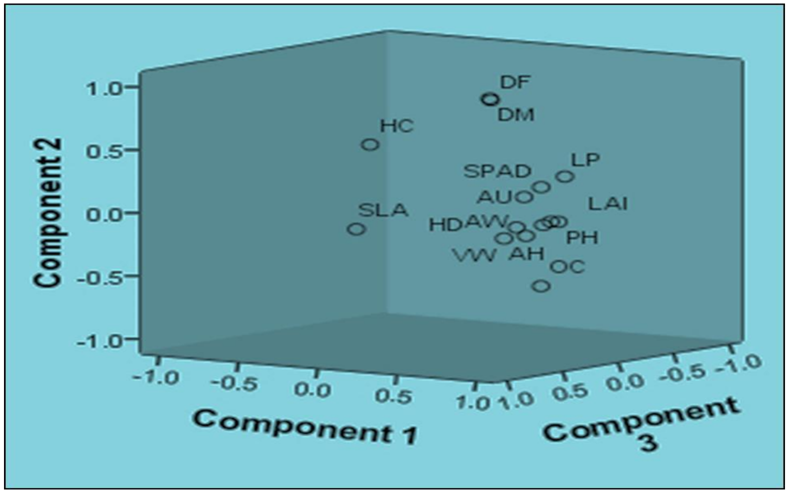
Canonical root	Value of canonical root	Percent of variation accounted for	Cumulative total variation accounted for
Z_1	3.39	22.57	22.57
Z_2	2.19	14.60	37.18
Z_3	1.42	9.44	46.62
Z_4	1.27	8.45	55.06
Z_5	1.22	8.15	63.22
Z_6	1.00	6.66	69.88
Z_7	0.96	6.41	76.29

Table 2. Canonical vectors for 15 characters in 70 genotypes of sunflower

SI.No	Character	Z_1	Z_2	Z_3	Z_4	Z_5	Z_6	Z_7
1.	Days to 50% flowering	0.08	0.48	0.16	0.17	0.08	0.28	0.42
2.	Days to maturity	0.05	0.42	-0.19	-0.04	-0.28	0.47	0.01
3.	Plant height	-0.40	0.23	0.06	-0.07	0.26	-0.07	-0.19
4.	Number of leaves per plant	-0.24	0.38	0.04	0.22	0.28	-0.31	0.13
5.	Head diameter	-0.18	-0.32	-0.29	0.28	-0.29	0.29	0.08
6.	100 achene weight	-0.25	0.15	-0.37	0.13	-0.27	0.07	0.13
7.	Number of achenes per head	-0.37	-0.23	0.27	0.20	-0.21	-0.05	-0.18
8.	Autogamy per cent	-0.44	0.09	0.15	0.30	-0.12	0.03	0.02
9.	Volume weight	-0.13	0.19	0.42	-0.17	-0.03	0.37	-0.53
10.	Achene yield	-0.05	0.02	0.34	-0.06	-0.60	-0.25	0.10

11.	Hull content	0.19	0.15	-0.03	0.56	-0.09	-0.26	-0.18
12.	Oil content	-0.27	-0.18	0.25	-0.31	0.04	0.15	0.51
13.	SPAD Chlorophyll meter reading (SCMR)	-0.11	0.26	-0.10	-0.37	-0.29	-0.45	0.15
14.	Specific leaf area	-0.25	0.13	-0.47	-0.32	-0.05	-0.06	-0.31
15.	Leaf area index	-0.39	-0.19	-0.17	0.07	0.32	0.05	0.11

Figure 1. Three-dimensional graph showing the grouping of the 15 traits studied.



Days to 50% flowering, DM-Days to maturity, PH-Plant height, LP-No. of leaves/ plant, HD-Head diameter, AW-100 Achene weight, AH-No. of achenes per head, AU-Autogamy per cent, VW-Volume weight, AY-Achene yield, HC-Hull content, OC-Oil content, SCMR-SPAD chlorophyll meter reading, SLA-Specific leaf area, LAI-Leaf area index.