Electronic Journal of Plant Breeding,
ISSN 0975-928X Vol 7 No 2 DOI: 10.5958/0975-928X.2016.00049.1

Genetic diversity study in interspecific inbreds of Sunflower

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(Received: December 2014, Accepted: July 2015)

Abstract

A field experiment was conducted by using fifty eight interspecific inbreds and two checks (PKVSF-9 and TAS-82) of sunflower in randomized block design in *kharif* 2013 at the field of Oilseeds Research Unit, Dr. PDKV, Akola to estimate the genetic diversity among genotypes. Mahalanobis D^2 statistics revealed presence of substantial genetic diversity among the genotypes. Among the ten characters studied, plant height (26.33%) followed by seed yield per plant (25.14%) and head diameter (18.87%) contributed maximum towards total genetic divergence while the characters seed filling percentage (0.34%) followed by harvest index (0.62%), 100 seed weight (2.32%) and oil content (2.99%) contributed least to the total genetic divergence. The genotypes were grouped in six clusters. Maximum inter cluster distance was observed between cluster II and VI (708.23) followed by cluster II and V (423.28) and cluster II and IV (363.57). Inter cluster distance was minimum between cluster III and IV (84.37). Cluster IV recorded highest intra cluster distance (91.71) followed by cluster I (77.47).

Key words: Genetic diversity, interspecific inbred, sunflower

Introduction

Sunflower (*Helianthus annuus* L.) has been emerged as a potential oilseeds crop in the world. In India it is harvested over an area of 7.20 lakh ha with the production of 5.81 lakh tones and productivity 806.94 kg/ha. (Anonymous, 2012). Sunflower is a photoinsensitive highly cross pollinated C_4 plant. Sunflower contains 38-42% edible oil which is rich in linoleic acid (55-60%) and poly unsaturated fatty acids (PUFA). For sunflower it is necessary to develop the varieties with high seed and oil yield potential to meet the need of edible oil for growing human population. Most of the present sunflower cultivars have reached a yield plateau due to the narrow genetic base. Therefore it is a primary need to widen genetic base by adding new genes from wild to cultivated species for improving seed and oil yield in sunflower. Presence of variability between the parents is of utmost importance to develop new varieties by the hybridization technique. Estimation of genetic diversity between the inbreds give an idea about existence of genetic variability among them.

Mahalanobis D^2 statistics is found to be an important tool to measure the extent of diversity among a set of genotypes. (Murty and Arunachalam, 1966). Bhatt (1970) highlighted the importance of D^2 statistics as an efficient method for choosing parents for hybridization in wheat. Thus in the present investigation interspecific inbreds derived from *H. occidentalis* Riddel and *H. maximiliani* Scharder were studied for estimation of genetic diversity.

Materials and Methods

The present study on genetic diversity comprised of 58 interspecific sunflower inbreds and two checks *viz.*, PKVSF-9 and TAS-82. Two checks were released varieties developed by Oilseeds Research Unit, Dr. PDKV, Akola. Total sixty genotypes were evaluated in randomized block design with three replications. Sowing was done in *kharif* season of 2013 with 60 cm spacing between rows and 30 cm between plants. The observations were recorded on ten biometrical characters *viz.*, days to 50% flowering (No.), days to maturity (No.), plant height (cm), head diameter (cm), hundred seed weight (gm), volume weight (gm/100 ml), seed filling percentage (%), seed yield per plant (gm), oil content (%) and harvest index (%). Oil content (%) in sunflower was determined by using NMR (Nuclear Magnetic Resonance) instrument available at Oilseeds Research Unit, Dr.PDKV, Akola. The data were recorded on five randomly selected plants from each plot. Genetic diversity was estimated by using D^2 analysis (Mahalanobis, 1928). The genotypes were grouped into various clusters by Tocher's method as described by Rao (1952).

Results and Discussion

The genotypes were grouped into six clusters. Grouping of genotypes in various clusters was presented in Table 1. Maximum number of genotypes were observed in cluster I (39 genotypes) followed by cluster II (12 genotypes) and cluster IV (6 genotypes). Cluster III, V and VI contained single genotype each. The contribution of each character towards total genetic divergence was presented in Table 2. The important characters contributing to the total divergence observed was plant height (26.33%). The traits like seed yield per plant (25.14%), head diameter (18.87%) and days to 50% flowering were next in the order. The characters viz., seed filling percentage (0.34%), harvest index (0.62%), volume weight (1.36%), 100 seed weight (2.32%) and oil content (2.99%) contributed least to the total divergence. The above results implied that in order to select genetically diverse parents, it is imperative to classify materials on the basis of traits like plant height, seed yield per plant, head diameter and days to 50% flowering. Punitha *et al.* (2010) and Manjula *et al* (2001) reported similar results for plant height and 100 seed weight. Average intra and inter cluster statistical distance was calculated by Tocher's method and was presented in Table 3. The intra cluster D^2 value ranged from 0 to 91.71. Cluster IV recorded highest intra cluster distance (91.71) followed by cluster I (77.47) and cluster II (73.24). The clusters III, V and VI did not show any intra cluster distance as these clusters contained only one genotype each. The average inter cluster distance was maximum between cluster II and VI (708.23) followed by cluster II and V (423.28), cluster II and IV (363.57), cluster V and VI (357.28), cluster I and VI (327.99), cluster IV and V (276.16), cluster III and VI (275.77), cluster III and V (246.12), cluster IV and VI (190.26) while it was lowest between cluster III and IV (84.37). Since these clusters had higher inter cluster distance among them, crossing between these clusters would result in increased heterosis. The inter cluster D^2 value was found to be minimum between clusters III and IV followed by clusters IV and VI, clusters III and V and clusters III and VI suggesting a close relationship between them and a low degree of diversity among genotypes and hence selection of lines from these clusters should be avoided. The cluster means of all the 10 characters for various clusters had been presented in Table 4. For days to 50% flowering highest cluster mean was recorded by cluster VI (57.67) followed by cluster V (57.33), cluster I (53.73) and cluster IV (52.78). For days to maturity highest cluster mean was found to be 77.0 in cluster VI followed by cluster IV (75.56), cluster I (72.96) and cluster III (71.67). For plant height cluster VI (157.0) showed highest cluster mean followed by cluster V (137.97), cluster IV (105.81) and cluster III (98.57). Lowest cluster mean for plant height was found in cluster II (56.98). Cluster VI (17.43) showed highest cluster mean for head diameter followed by cluster V (17.10), cluster IV (13.64) and cluster III (12.13). Maximum cluster mean for 100 seed weight was found in cluster V (4.73) followed by cluster IV (3.52) and cluster III (3.27). For volume weight cluster V (32.57) showed highest cluster mean followed by cluster III (27.8), cluster IV (27.01) and cluster II (25.13). For seed filling percentage cluster VI (80.93) showed highest cluster mean followed by cluster IV (76.77), cluster III (76.03) and cluster I (72.26). For seed yield per plant, cluster VI (22.13) showed highest cluster mean followed by cluster IV (19.93), cluster III (15.63) and cluster I (9.42). Maximum cluster mean for oil content was observed in cluster V (36.02) followed by cluster I (33.13), cluster II (33.04), cluster IV (32.81) and cluster III (32.28). Highest cluster mean for harvest index was recorded in cluster III (33.63) followed by cluster I (33.09), cluster II (32.62) and cluster V (32.40). Cluster means indicated appreciable variation among various clusters particularly for plant height, seed filling percentage and days to maturity. However, variations were low for hundred seed weight, head diameter and volume weight. It is always desirable to look for genotypes having more than one desirable traits but belonging to different clusters based on cluster mean values. Cluster V was grouped with genotypes showing good mean values for the characters of economic interest such as volume weight, seed filling percentage, seed yield per plant and oil content. From the estimates of genetic diversity, it was observed that the characters *viz.*, plant height, head diameter, seed yield per plant and days to 50% flowering showing maximum divergence would be useful in selection of genetically divergent parents for their exploitation in hybridization programme. Genotypes from the divergent clusters could be selected for hybridization by taking into account their desirable and complementary characters.

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Table 1: Grouping of genotypes into various clusters

Cluster	No. of genotypes	Name of genotypes
I	39	PSMO-52-3, PSMO-52-4, PSMO-53-1, PSMO-53-2-1, PSMO-53-3, PSMO-54-2, PSMO-54-3, PSMO-54-4, PSMO-55-1, PSMO-56, PSMO-57, PSMO-59, PSMO-60, PSMO-62, PSMO-63, PSECO-65, PSECO-69, PSECO-70, PSECO-75, PSECO-82, PSECO-84, PSECO-86, PSECO-88, PSECO-89, PSECO-90, PSECO-93, PSECO-97, PSECM-143,PSECM-168, PSECM-171, PSCIM-117, PSCIM-126, PSCIM-181-3, PSCIM-183-1, PSCIM-183-2, PSCIM-185, PSCIM-190, PSCIM-201, PKVSF-9
II	12	PSECO-64, PSECM-145, PSECM-146, PSECM-147, PSECM-148, PSECM-149, PSECM-154, PSECM-156, PSECM-157, PSECM-159, PSECM-161, PSCIM-123
III	1	PSCIM-195
IV	6	PSMO-53-4, PSMO-58, PSCIM-115, PSCIM-119, PSCIM-121, PSCIM-186
V	1	PSCIM-136
VI	1	TAS-82

Electronic Journal of Plant Breeding,
ISSN 0975-928X

Table 2 : Contribution of each character towards total divergence

Sl. No.	Character	Times ranked 1st	Contribution (%)
1	Days to 50% flowering	329	18.59
2	Days to maturity	61	3.45
3	Plant height (cm)	466	26.33
4	Head diameter (cm)	334	18.87
5	Hundred seed weight (gm)	41	2.32
6	Volume weight (gm/100 ml)	24	1.36
7	Seed filling percentage (%)	6	0.34
8	Seed yield per plant (gm)	445	25.14
9	Oil content (%)	53	2.99
10	Harvest Index (%)	11	0.62
	Total	1770	100

Table 3: Average intra and inter cluster distances ($D = \sqrt{D^2}$)

Clusters	I	II	III	IV	V	VI
I	**77.47**	187.39	103.1	171.08	166.01	327.99
II		**73.24**	175.42	363.57	423.28	708.23
III			**0.00**	84.37	246.12	275.77
IV				**91.71**	276.16	190.26
V					**0.00**	357.28
VI						**0.00**

$\overline{D}$=204.69

Note : The figures in diagonal indicate intra cluster distances

Table 4 : Cluster means for ten characters

Clusters	DFF	DM	PH	HD	HSW	VW	SFP	SYP	OC	HI
I	53.73	72.96	94.19	11.44	3.09	22.21	72.26	9.42	33.13	33.09
II	44.83	67.00	56.98	5.95	2.78	25.13	63.91	5.59	33.04	32.62
III	45.00	71.67	98.57	12.13	3.27	27.80	76.03	15.63	32.28	33.63
IV	52.78	75.56	105.81	13.64	3.52	27.01	76.77	19.93	32.81	32.18
V	57.33	71.00	137.97	17.10	4.73	32.57	68.27	5.52	36.02	32.4
VI	57.67	77.00	157.00	17.43	3.10	19.00	80.93	22.13	23.63	31.5
S.D.	5.74	3.55	35.17	4.24	0.69	4.70	6.19	7.24	4.22	0.74
Variance	32.90	12.60	1237.12	17.94	0.47	22.14	38.36	52.39	17.82	0.54

DFF : Days to 50% flowering (No.)
DM : Days to maturity (No.)
PH : Plant height (cm)
HD : Head diameter (cm)
HSW : Hundred seed weight (gm)
VW : Volume weight (gm/100 ml)
SFP : Seed filling percentage (%)
SYP : Seed yield per plant (gm)
OC : Oil content (%)
HI : Harvest Index (%)