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Study of Genetic Diversity in Sunflower (*Helianthus annuus* L.)

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A B S T R A C T

In the present investigation thirty two sunflower (*Helianthus annuus* L.) genotypes including two checks were evaluated to study genetic divergence. The experiment was laid out at Research Farm, Tirhut College of Agriculture, Dholi, Bihar during spring 2015-16. Data were recorded on eleven quantitative characters. The thirty two genotypes of sunflower were grouped into six cluster using Tocher method. The genotypes in cluster III and cluster IV, due to maximum inter cluster distance, exhibited high degree of genetic diversity and thus may be utilized under inter varietal hybridization programme (transgressive breeding) for getting high yielding recombinants. Similar inter varietal crosses may be attempted in cluster V and cluster VI and cluster III and cluster V. On the basis of cluster mean values, the genotypes present in cluster VI was found early in terms of days to fifty per cent flowering and having highest volume weight and oil content. Genotypes present in cluster V have maximum harvest index and 100 seed weight. Genotypes which are present in cluster III may be selected for minimum plant height and maximum biological yield while the genotypes present in cluster II was suitable for early in days to maturity. Based on cluster mean values for a given characters we can select highly divergent genotypes from the respective clusters and can be used in hybridization work.

Introduction

Sunflower (*Helianthus annuus* L.) emerged as an admirable crop for its quality oil in the oilseed scenario of India. The introduction of sunflower "a crop of all seasons" in India was taken up in view of its various advantages *viz.*, photo and thermo insensitivity, short duration, high yield and better quality of oil with low cholesterol content. Sunflower belongs to family Compositeae (Asteraceae). It is diploid with chromosome number 2n = 34 and protandrous in nature wherein pollen and stigma mature at different time, therefore it has been essentially categories as a cross pollinated crop. Studies on genetic divergence are important to guide breeding programme aiming to obtain hybrid cultivars so that crosses are made among genetically divergent lines that have contrasting and complementary traits. Therefore, the breeder would choose genetically distinct parents for hybridization since heterotic crosses expected to arise as a result of crosses between divergent parental

lines. Genetic diversity between parents of the crosses indicates differences in gene frequency, which can be exploited to improve inbreds or parental lines. The D^2 analysis has been successfully utilized in sunflower to classify genotypes and determine their inter relationships by many workers (Marinkovic *et al.*, 1992 and Teklewold *et al.*, 2000). In this context, an attempt was made to study the genetic diversity among thirty two genotypes.

Materials and Methods

The materials used for the present investigation consisted of thirty two genotypes of sunflower (*Helianthus annuu*s L.) including two checks which were maintained at AICRP (Sunflower) of the oil seed improvement project, Department of Plant Breeding and Genetics, Tirhut College of Agriculture, Dholi. All the thirty two genotypes have been shown in table 1. These genotypes along with checks were sown in RBD in three replications during spring 2016 at College Farm, Tirhut College of Agriculture, Dholi. Each genotype was sown in three rows of 4.5 m length with a spacing of 60 x 30 cm. Two to three seeds were sown per hill to facilitate better emergence and to provide uniform stand. Observations were recorded on three randomly selected plants from each row of eleven traits including days to fifty per cent flowering, plant height (cm), days to maturity, biological yield, head diameter (cm), harvest index, 100-seed weight (g), volume weight (g/100ml), oil content (%), seed yield per plant (g) and oil yield per plant (g). Observations were recorded for yield and yield attributing characters from these tagged plants for all the genotypes in each replication except for days to fifty per cent flowering and days to maturity. The data for these two characters were recorded based on plot means. The method of recording data for each trait is described below.

Days to 50 per cent flowering

The number of days from the date of sowing to the day on which flowers in fifty per cent of the plants open were recorded.

Plant height (cm)

The height from the scar of the cotyledonary leaves to the top of the peduncle of the capitulum was measured in centimeters at the time of harvest.

Days to maturity

The number of days from the date of sowing to the day on which the back of the capitulum in fifty per cent of plants in a line turned to lemon yellow colour was recorded.

Biological yield

Total dry weight of the plant of each genotype was recorded in gram.

Head diameter (cm)

The diameter of the mature head at its maximum width was measured in centimeters.

Harvest Index

Harvesting index is the ratio of economical yield to biological yield and it was calculated by using the following formula.

$$\text{Harvest index} = \frac{\text{Grain yield}}{\text{Total biological yield (grain yield + straw)}} \times 100$$

100-seed weight (g)

Total of 100 grains in each genotype was taken and weight was recorded in gram.

Volume weight (g/100ml)

The measuring cylinder was filled to 100 ml volume with seeds of each entry and was weighed in gram as volume weight/100 ml.

Oil content (%)

The seed oil content in per cent was determined directly with the help of Nuclear Magnetic Resonance (NMR) spectrometer installed at IIOR, Rajendranagar, Hyderabad.

Seed yield per plant (g)

The total weight of filled seeds per plant was recorded in grams.

Oil yield per plant (g)

Oil yield was calculated as per the formula given below

$$\text{Oil yield} = \frac{\text{Seed yield X Oil content}}{100}$$

Genetic divergence of thirty two genotypes including two checks of sunflower was assessed using the Mahalanobis D^2 statistics.

Results and Discussion

Selection of suitable parents for utilization in crop improvement programme is an important but rather difficult task for plant breeders. Genetic diversity is considered to be important for realizing heterotic response in F_1 and a broad spectrum of variability in segregating generations (Arunachalam, 1981). Diversity analysis helps in assessing the nature of diversity in order to identify genetically diverse genotypes for their use in breeding programmes. In heterosis breeding programme, the diversity of parents is always emphasized more diverse the parent within a reasonable range, better the chances of improving economic characters under consideration in the resulting offspring. Mahalnobis's D^2 statistic is an unique tool for classifying genetically diverse parents based on quantitative traits which could be appropriately utilized in hybridization programme.

All the genotypes were grouped into different clusters on the basis of genetic distance among the genotypes. The distribution pattern of genotypes, cluster mean for different clusters, intra and inter cluster divergence (D^2) value and contribution percentage of various traits towards genetic divergence were presented in the table 2, 3, 4 and 5 respectively.

Clustering pattern

In the present investigation, all the thirty two genotypes taken for genetic divergence analysis differed significantly with regard to the characters studied and displayed marked divergence. They were grouped into six clusters on the basis of Tocher's method of clustering utilizing D^2 values. Cluster I comprised fifteen genotypes namely IB-225-1, CMS-300B-1, CMS-20B-1, IB-103, TGP-4-07-2, GMU-654-1, GMU-456, Morden-B-1, DRSF-108-3, GMU-681, GMU-501-1, GMU-658-2, GMU-676-1, GMU-484 and IB-102-2. Cluster II comprised five genotypes namely HOLA-44, GP-6-329B-1, DRSF-108-2, R-13-3 and DRSF-113-1 white. Cluster III had five genotypes namely GMU-506-1, IB-101-1, Gene pool-1-6-1-2, GMU-479 and GMU-506. Cluster IV had five genotypes namely DRSF-113-1, DRSF-108(C), Morden-2, Morden-1 and DRSF-113(C). Two of the thirty two genotypes namely DRSF-113-2 and LSF-71-1-4-1 are fall into clusters V and VI, respectively. Mohan and Seetharam (2005) also observed similar clustering pattern of genotypes among cluster as some cluster were unique having only single genotypes.

Table.1 List of genotypes of Sunflower (*Helianthus annuus* L.) studied

Sl. No.	Genotypes	Source
1	IB- 225-1	IIOR, Hyderabad
2	HOLA – 44	IIOR, Hyderabad
3	G.P-6- 329- B1	IIOR, Hyderabad
4	CMS –20B	IIOR, Hyderabad
5	CMS-300B-2	IIOR, Hyderabad
6	GMU – 456	IIOR, Hyderabad
7	GMU – 479	IIOR, Hyderabad
8	GMU – 484	IIOR, Hyderabad
9	GMU – 501	IIOR, Hyderabad
10	GMU – 506	IIOR, Hyderabad
11	GMU– 506-1	IIOR, Hyderabad
12	GMU-654-1	IIOR, Hyderabad
13	GMU-658-2	IIOR, Hyderabad
14	GMU-676-1	IIOR, Hyderabad
15	GMU-681	IIOR, Hyderabad
16	Gene pool-1-6-1-2	IIOR, Hyderabad
17	LSF-71-1-4-1	IIOR, Hyderabad
18	DRSF-113-1 white	IIOR, Hyderabad
19	R-13-3	IIOR, Hyderabad
20	IB-101-1	IIOR, Hyderabad
21	IB-102-2	IIOR, Hyderabad
22	IB-103	IIOR, Hyderabad
23	TGP-4-07-2	IIOR, Hyderabad
24	Morden	IIOR, Hyderabad
25	Morden-B-1	IIOR, Hyderabad
26	Morden-2	IIOR, Hyderabad
27	DRSF-113-1	IIOR, Hyderabad
28	DRSF-113-2	IIOR, Hyderabad
29	DRSF-108-2	IIOR, Hyderabad
30	DRSF-108-3	IIOR, Hyderabad
31	DRSF-113(C)	IIOR, Hyderabad
32	DRSF-108(C)	IIOR, Hyderabad

Table.2 Distribution of thirty two genotypes of sunflower in different cluster

Cluster	No. of Genotypes within cluster	Genotypes in cluster
I	**15**	IB-225-1, CMS-300B-1, CMS-20B-1, IB-103, TGP-4-07-2, GMU-654-1, GMU-456, Morden-B-1, DRSF-108-3, GMU-681, GMU-501-1, GMU-658-2, GMU-676-1, GMU-484 and IB-102-2
II	**5**	HOLA-44, GP-6-329B-1, DRSF-108-2, R-13-3 and DRSF-113-1 white
III	**5**	GMU-506-1, IB-101-1, Gene pool-1-6-1-2, GMU-479 and GMU-506
IV	**5**	DRSF-113-2, DRSF-108(C), Morden-2, Morden-1 and DRSF-113(C)
V	**1**	DRSF-113-2
VI	**1**	LSF-71-1-4-1

Table.3 Cluster mean for characters in sunflower

	Days to 50% Flowering	Plant Height cm	Days to Maturity	Biological Yield(g)	Head Diameter cm	Harvest Index	100 Seed Weight gm	Volume Weight (g/100ml)	Oil Content (%)	Seed Yield/ Plant gm	Oil Yield (g/Plant)
Cluster I	63.13	69.92	88.24	171.00	8.43	8.97	4.30	38.46	33.12	16.21	5.40
Cluster II	58.86	71.11	85.93	50.53	7.27	17.00	3.95	33.36	29.81	8.60	2.52
Cluster III	65.80	69.78	88.66	273.86	7.80	3.56	4.13	36.87	29.46	10.22	2.97
Cluster IV	64.73	77.08	89.53	63.33	8.68	26.36	5.45	36.20	36.84	16.67	6.14
Cluster V	70.00	115.93	95.66	127.66	15.96	41.20	7.76	35.43	32.83	52.63	17.43
Cluster VI	63.00	71.33	99.66	237.00	11.43	3.13	3.83	47.26	38.13	7.50	2.83

Table.4 Intra and inter cluster distances in thirty two genotypes of sunflower

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI
Cluster I	**131.07**	246.87	247.71	310.91	347.13	251.26
Cluster II		**93.05**	417.69	355.65	442.35	587.31
Cluster III			**75.71**	700.42	606.25	428.65
Cluster IV				**153.67**	364.02	375.84
Cluster V					**0.00**	653.22
Cluster VI						**0.00**

Table.5 Independent character contribution towards divergence in eleven characters of sunflower

Source	Times Ranked 1st	Contribution %
1 Days to fifty per cent Flowering	35	7.06
2 Plant Height (cm)	20	4.03
3 Days to Maturity	0	0.00
4 Biological Yield (g)	197	39.72
5 Head Diameter (cm)	3	0.60
6 Harvest Index (%)	8	1.61
7 100 Seed Weight (g)	4	0.81
8 Volume Weight (g/100ml)	1	0.20
9 Oil Content (%)	178	35.89
10 Oil Yield (g/Plant)	1	0.20
11 Seed Yield (g/plant)	49	9.88

Genotypes grouped into the same cluster presumably diverge little from one another as the aggregate of characters measured. Theoretically crossing of genotypes belonging to the same cluster is not expected to yield superior hybrid or segregant. In general, larger the divergence between the genotypes, the higher will be the heterosis.

Cluster means for different characters

A comparison of the mean values of eleven traits for different clusters showed considerable differences among them. Cluster VI comprising genotype LSF-71-1-4-1 had the maximum mean value for days to maturity (99.66), volume weight (47.26) and oil content (38.13) whereas minimum mean values for harvest index (3.13), 100 seed weight (3.83), seed yield per plant (7.50) and days to fifty per cent flowering (63.00). Cluster V comprising genotype DRSF-113-2 had the maximum mean value for plant height (115.93), days to fifty per cent flowering (70.00), seed yield per plant in gram(52.63), harvest index(41.20), oil yield (17.43), head diameter (15.96) and 100 seed weight (7.76).

Cluster III had maximum mean value for biological yield (273.86) and minimum mean value for plant height (69.78) and oil content (29.46). Cluster II had minimum mean value for days to maturity (85.93), biological yield (50.53), volume weight (33.36), head diameter (7.27) and oil yield (2.5).

III. Average intra and inter cluster distances (D^2)

Maximum intra cluster distance was observed in cluster IV followed by cluster I and cluster II indicating differences in genotypes within cluster. Least intra cluster distance was found in cluster III indicating that close resemblance between the genotypes present in the cluster. The genotypes in cluster III and cluster IV, due to maximum inter cluster distance between them, exhibited high degree of

genetic diversity and thus may be utilized under inter varietal hybridization programme (transgressive breeding) for getting high yielding recombinants. Similar inter varietal crosses may be attempted in cluster V and cluster VI and cluster III and cluster V for getting high recombinants. The lowest inter cluster distance was observed between cluster I and II followed by between cluster I and III and cluster I and VI showing this cluster was relatively less divergent and crossing between them cannot produce vigorous offspring (F_1 progenies). Similar studied based on D^2 statistics was also performed by that of Shamshad *et al*, (2014) and Neelima *et al*, (2016).

Contribution percentage of each character towards divergence

The highest contribution in the manifestation of total genetic divergence was exhibited by biological yield (39.72) followed by oil content (35.89), seed yield (9.88), days to fifty per cent flowering (7.06), plant height (4.03) and head diameter (1.61). The contribution of remaining traits in manifestation of genetic divergence was low.

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