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Research Article

Assessment of genetic diversity among the maintainer and restorer inbreds of sunflower (*Helianthus annuus* L.)

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Abstract
Sunflower (*Helianthus annuus* L.) is one of the most important oilseed crops grown worldwide because of its supreme oil quality and commercial importance. Assessment of diversity among inbreds is a vital prerequisite to select parents for a hybridization programme. Hence, in the present investigation, the genetic divergence of 29 genotypes consisting of both maintainer and restorer inbreds was studied using Mahalanobis (D^2) analysis. Genotypes were grouped into eight clusters, in which cluster I was the largest with 13 genotypes. Clusters IV, VI, VII and VIII were the smallest, with one genotype each. The maximum intracluster distance was observed in cluster I followed by II. Maximum inter cluster distance was recorded between clusters II and V followed by clusters II and VII. Days to 50% flowering had the maximum contribution (32.76%) for genetic divergence. Superior mean performance for head diameter, 100 - seed weight, seed yield per plant and oil content was observed in cluster VI whereas earliness in terms of days to 50% flowering and days to maturity was observed in cluster II. Cluster VIII recorded superior mean performance for volume weight and the lowest mean plant height was observed in cluster VII. Hence, hybridization between cluster II (CMS 10B, HA 89B, RHA-1-1) and cluster V (CMS 519B, HA 430B) could create more variability in the segregating generations.

Key words: Sunflower, genetic diversity, inbreds, maintainer, restorer.

INTRODUCTION

Sunflower (*Helianthus annuus* (L.) belonging to the family Asteraceae is native to North America. It is a wide spectrum adaptable crop, grown in all three seasons but typically requiring subtropical climate. It has various advantages *viz*., photo and thermo insensitivity, short duration, high yield and better quality of oil (36 - 45 %), oleic acid (20%), linoleic acid (70%), palmitic acid (4.6 %) and stearic acid (2.3%) (Radanovic *et al.,* 2018). India's cultivable area of sunflower is about 0.25 million hectares with the production and productivity of 0.23 million metric tonnes and 891 kg/ha, respectively (Directorate of Economics & Statistics, DAC&FW, 2020). Genetic diversity is one of the critical tools to assess the variation in the germplasm. Immense efforts are being made to develop hybrids with higher economic value and wider adaptation with desirable characteristics. Understanding the genetic nature of parental lines is one of the prerequisites for hybridization in any heterosis breeding program. Hence, it is major culpability for a plant breeder to evaluate the prevailing genetic variability among parental lines before using them in a hybridization programme. The D^2 analysis has been successfully utilized in sunflower to classify genotypes and determine theirs inter relationships (Dhillon *et al*., 2017; Naik *et al.,* 2018). Therefore, an attempt has been made to study the genetic diversity among the set of sunflower germplasm comprising maintainer and restorer inbred lines for further use in a hybridization programme.

MATERIALS AND METHODS

The experimental material comprised of 29 sunflower inbreds containing 24 maintainers and five restorer lines. These genotypes were raised in experimental plots of the Department of Oilseeds, Tamil Nadu Agricultural University, Coimbatore in January 2021. All genotypes were raised in Randomized Complete Block Design (RCBD) with three replications. Each genotype was sown in a single 4m row with a spacing of 60 cm between rows and 30 cm between plants. Recommended agronomic practices for Tamil Nadu (Crop Production Guide, 2020) were followed throughout the crop growth period. Eight traits *viz*., days to 50% flowering, days to maturity, plant height (cm), head diameter (cm), volume weight (g/100 ml), 100-seed weight (g), seed yield per plant (g) and oil content (%) were recorded on five randomly selected plants of each genotype in all the three replications. Analysis of variance (ANOVA) for Randomized Complete Block Design was performed using the TNAUSTAT program (Manivannan, 2014). The recorded data were subjected to statistical analysis using Mahalanobis D^2 statistic (Mahalanobis, 1936) and Tocher's method (Rao, 1952) for determining group constellation. The D^2 statistics were also computed using the TNAUSTAT software program.

RESULTS AND DISCUSSION

The analysis of variance (ANOVA) revealed that the genotypes differed significantly for all characters under investigation. The V-statistics also showed significance, and hence the data were subjected to genetic divergence analysis. The Mahalanobis D^2 analysis grouped 29 genotypes into eight clusters based on Tocher's cut off value (**Table 1**). Among the eight clusters, cluster I was the largest with 13 genotypes, followed by cluster III, which consisted of seven genotypes. Cluster II and V possessed three and two genotypes, respectively. Clusters IV, VI, VII and VIII were the smallest and solitary ones. The genotypes grouped within the same cluster showed narrow genetic divergence and would be almost genetically similar, and the genotypes in different clusters exhibited a wider range of genetic variability. The average intra and inter cluster distances of these clusters are presented in **Table 2.** The intra cluster distance ranged from 24.21 (cluster I) to 12.03 (cluster V). Hence, the genotypes in cluster I was more dissimilar among them followed by cluster II (23.39) and cluster III (22.66). Maximum inter cluster distance was recorded between clusters II and V (264.54) followed by clusters II and VII (256.77). Many researchers reported a similar wider

Table 1. Distribution of genotypes into clusters

Cluster number	Number of genotypes	Name of the genotypes
I	13	COSF 13B, COSF 15B, COSF 7B, CMS 207B, COSF 11B, HA 300B, COSF 1B, 852-B-1, COSF 10B, CMS 302B, RCR CMS 38B, COSF 12B, COSF 17B
II	3	CMS 10B, HA 89B, RHA-1-1
III	7	CSFI 17006, LTRR 341, 234 B, RCR CMS 105B, COSF 6B, CMS 104B, ARM 248B
IV	1	CMS 112B
V	2	CMS 519B, HA 430B
VI	1	COSF 16B
VII	1	CSFI 1862
VIII	1	IR6

Table 2. Intra (diagonal) and inter cluster distance of sunflower genotypes

Cluster number	I	II	III	IV	V	VI	VII	VIII
I	**24.21**	40.45	36.12	34.22	178.06	54.98	175.94	87.89
II		**23.39**	71.28	45.92	264.54	114.70	256.77	170.09
III			**22.66**	38.48	186.55	34.87	158.94	66.91
IV				**0.00**	170.21	77.77	166.72	84.15
V					**12.03**	189.64	40.07	88.26
VI						**0.00**	183.64	78.22
VII							**0.00**	66.54
VIII								**0.00**

divergence (Shamshad *et al*., 2014; Deshmukh *et al*., 2016; Naik *et al.,* 2018). The closest proximity was found between clusters I and IV (34.22). Such a narrow range of genetic variability among the lines within the clusters had also been reported by different sunflower workers (Subrahmanyam *et al*., 2003, Srinivas *et al*., 2006). Hence, the genotypes in the diverse clusters could be utilized in the hybridization programme to realize heterotic hybrids and more variability in the segregating generations.

Based on the cluster means (**Table 3**), it was observed that genotypes in cluster II showed earliness in flowering (55.56 days) and maturity (85.11 days) followed by cluster IV (59 and 89 days) and cluster I (59.56 and 90.44 days). The genotypes in cluster VI had the highest head diameter (15.14 cm), 100 - seed weight (4.75 g), seed yield per plant (48.61 g) and oil content (39.57 %) followed by cluster II with a head diameter of 12.97 cm and seed yield of 26.77 g. The highest volume weight was observed in cluster VIII (37.18 g/100ml). Cluster VII had the least plant height (92.82 cm), followed by cluster II (96.80cm). It is always preferable to look for genotypes belonging to different clusters with many desired traits. Contrasting genotypes for days to 50% flowering and maturity were grouped in clusters II and V, for plant height in VII and IV, for head diameter clusters VIII and VI, for volume weight in IV and VIII, for oil content in II and VI, 100-seed weight and seed yield per plant in VIII and VI. Based on the cluster means, the inbred lines in cluster II (CMS 10B, HA 89B, RHA-1-1) could be promising donors to develop inbred lines for earliness. Likewise, inbred of cluster VII (CSFI 1862) for dwarf plant height, cluster VI (COSF 16 B) for head diameter, 100-seed weight, seed yield and oil content and cluster VIII (IR 6) could be used as a donor for trait based improvement.

The major contributing characters to genetic divergence were days to 50% flowering (32.76%) followed by oil content (25.62%) (**Table 4**) The present findings were in agreement with the results of Chandirakala and Manivannan (2014) and Naik *et al.* (2018) for days to 50% flowering and Punitha *et al.* (2010) and Neelima *et al.* (2016) for 100-seed weight and oil content.

To conclude, the genotypes in cluster II (CMS 10B, HA 89B, RHA-1-1) and cluster V (CMS 519B, HA 430B) showed wider divergence, and crosses could be effected among them to obtain more variability in the segregating populations. The male sterile lines of maintainer inbreds and restorer inbreds *viz*., CMS lines (CMS 10B, HA 89B) vs restorer line CSFI 1862 and CMS lines (CMS 519A, HA 430) vs restorer line RHA 1-1 can be intercrossed to realize heterotic hybrids. Among characters, days to 50% flowering had more variability, which performed as a major contributor to genetic divergence.

Table 3. Cluster mean for different quantitative traits in sunflower

Cluster	Days to 50% flowering	Days to maturity	Plant height (cm)	Head diameter (cm)	Volume weight (g/100 ml)	100 seed weight (g)	Seed yield/plant (g)	Oil content (%)
I	59.56	90.44	104.63	11.42	31.96	4.16	20.32	34.72
II	55.56	85.11	96.80	10.32	27.99	4.37	19.09	32.50
III	59.57	90.52	131.98	11.44	35.19	4.06	26.36	38.58
IV	59.00	89.00	140.93	11.19	26.14	3.32	18.93	33.44
V	78.33	102.00	110.92	12.97	31.77	4.26	26.77	33.92
VI	61.33	94.00	132.33	15.14	31.69	4.75	48.61	39.57
VII	76.00	98.67	92.82	8.72	33.51	2.09	7.57	38.69
VIII	66.67	97.67	113.92	7.05	37.18	1.64	7.52	37.00

Table 4. Contribution of different quantitative characters towards genetic divergence

S. No.	Character	Times ranked 1st	Contribution (%)
1.	Days to 50% Flowering	133	32.76
2.	Days to maturity	42	10.34
3.	Plant height	57	14.04
4.	Head diameter	34	8.37
5.	Volume weight	11	2.71
6.	100 seed weight	13	3.20
7.	Seed yield/plant	12	2.96
8.	Oil content	104	25.62

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