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

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Abstract

The present investigation was carried out at the research fields of the oilseeds Section, Department of Plant Breeding and Genetics, Punjab Agricultural University, Ludhiana, India. The material for present study consisted of 31 germplasm lines. The material was raised in two rows with three replications each row of 4.5m length with 60 cm and 30 cm inter and intra row spacing respectively, in the randomized block design. All the agronomic practices recommended for the region were followed to raise a good crop. The data for agronomic and yield traits i.e. plant height, head diameter, volume weight, 100 seed weight, seed yield per plant was recorded. D^2 analysis assigned the test genotypes into six clusters indicating presence of enough genetic diversity in the material. All the 31 germplasm lines were grouped into six clusters. The critical examination of clusters indicated the presence of high level of genetic diversity in the material. Cluster I comprised of maximum number of lines (18) and cluster III (9), cluster II, IV, V and VI each consist one line respectively in normal environment. The genotypes included in the same cluster are considered genetically similar with respect to the aggregate effect of the characters examined; the hybridization attempted between these is not expected to yield desirable recombinants. Therefore, putative parents for crossing programme should belong to different clusters characterized by large inter-cluster distance. The intra cluster distances ranged from 0 (cluster II, IV, V and VI) to 417.294 (cluster I) indicating presence of only one line in cluster II, IV, V and VI whereas, genotypes in cluster I were more dissimilar in agronomic and yield traits than other clusters. The maximum inter-cluster distance was observed between the members of cluster II with cluster VI (12836.640) followed by cluster I with cluster VI (7084.305), cluster V with cluster VI (6600.998) and

cluster II with cluster IV (6498.283). The genotypes NC-41B (Morden), HOAL-38, P61R and TX-16R grouped in different clusters were identified as the most divers genotypes and should be used in hybridization program to realize high heterosis for these traits.

Keywords: Sunflower, genetic diversity and germplasm lines.

1. Introduction

Sunflower is important oilseed crop in the world and it is arousing the interest of farmers, agriculture professionals and companies, due to the possibility of using its oil as raw material for manufacturing biodiesel (Backes et al., 2008). In order to improve the crop production, researches in plant breeding and genetics are being held for obtaining and evaluation of genotypes contemplating important aspects in the production process (Messetti and Padovani, 2004). Improvement in sunflower emphasizes the urgency of generating a heterotic hybrid that is achieved by heterotic vigour available in the genetically diverse parental lines. Involvement of genetically divergent parents in hybridization will result in enhanced vigour or heterosis in the resultant hybrid. Several works that evaluated the genetic divergence in sunflower crop were conducted by using morphoagronomic characters (Arshad et al., 2007). The D^2 statistics enables to discriminate between different cultivars according to the diversity of parents (Mahalanobis, 1936). It is a powerful tool in quantifying the degree of genetic divergence among parents (Punitha *et al*., 2010). With this background, the present investigation was aimed to assess the genetic divergence and to identify promising parents among 31 genotypes of sunflower (*Helianthus annuus* L.) and quantify the magnitude of genetic divergence.

2. Materials and Methods

The material for present study consisted of 31 germplasm lines including cms A lines R lines and inbred lines. The material was raised in paired rows of 4.5m length with 60 cm and 30 cm inter and intra row spacing respectively, in the randomized block design with three replications. The present investigation was carried out in the research fields of the Oilseeds section, Department of Plant Breeding and Genetics, Punjab Agricultural University, Ludhiana, India during spring season 2013. All the agronomic practices recommended for the region were followed to raise a good crop. In each genotype, five plants were randomly selected and used for collection of data on yield and yield related characters like plant height, stem diameter, head diameter, 100 seed weight, seed yield per plant. The data were subjected to multivariate analysis using D^2 statistics (Rao, 1952). The genotypes were further grouped into different clusters based on Euclidean cluster analysis. The D^2 statistic for yield and yield attributes was computed using the INDOSTAT software program.

3. Results and Discussion

3.1. Distribution of genotypes into different clusters

D^2 analysis assigned the test genotypes into six clusters indicating presence of enough genetic diversity in the material. The 31 germplasm lines were grouped into six clusters. The critical examination of clusters indicated the presence of high level of genetic diversity in the material. Cluster I comprised of maximum number of lines (18) and cluster III (9), cluster II, IV, V and VI comprising of one genotype each (table 1). The genotypes included in the same cluster are considered genetically similar with respect to the aggregate effect of the characters examined; the hybridization attempted between these is not expected to yield desirable recombinants. Therefore, putative parents for crossing programme should belong to different clusters characterized by large inter-cluster distance. Mohan and Seetharam (2005) also observed similar clustering pattern of genotypes among clusters, as some clusters were unique having only single genotype.

3.2. Intra and Inter-cluster distances

Intra and inter-cluster distances as presented in table 2 reveals that the intra cluster distances ranged from 0 (cluster II, IV, V and VI) to 417.294 (cluster I) indicating presence of only one genotype in cluster II, IV, V and VI whereas, genotypes in cluster I were more dissimilar in agronomic and yield traits than other clusters. The maximum inter-cluster distance was observed between the members of cluster II with cluster VI (12836.640) followed by cluster I with cluster VI (7084.305), cluster V with cluster VI (6600.998) and cluster II with cluster IV (6498.283). The genotypes NC-41B, HOAL-38, P61R and TX-16R grouped in different clusters were identified as the most divers genotypes and should be used in hybridization program to realize high heterosis for these traits.

3.3. Cluster mean values

The cluster mean values for five different characters are presented in Table 3. It can be seen from the cluster means that each cluster has its own uniqueness that separated it from other clusters. Cluster I having dwarf plant type with moderate head diameter, volume weight, 100 seed weight and seed yield, while, highest seed yield (31.97), volume weight (35.5) with shorter plant height (87.0) were recorded in cluster V. Germplasm line belongs to cluster V may give high seed yield with dwarf type hybrids upon hybridization with member of cluster I. P 61R is a multi head, preferred restorer and can be used in hybrid breeding programme to develop high yielding hybrids with cluster I. Cluster III IV and VI had tall plant type. TX 16R the only member of cluster VI was characterized as unique genotype having maximum plant height (159), shortest head diameter (4.3) maximum volume weight (1.16) and minimum seed yield per plant (1.42). This was a disease free genotype and can be used in breeding programme for transferring disease resistance and other characters.

Table 1: Cluster composition of sunflower germplasm lines

Cluster No.	No. of Genotypes in Each Cluster	Name of Genotypes
Cluster I	18	RIL-45, RIL-11, RIL-15, RIL-10, HOAL-6, HOAL-11, P-69R, 10-B, DV 10X, CMS-XA, PUKZ-AP2, E OO2-91-A, E OO2-92-A, ARG-3 A, PRUN-29 A, PHIR-27 A, ARG-2 A, 11-B
Cluster II	1	NC-41 B
Cluster III	9	HO-28, HOAL-3, HOHAL-3,HOHAL-10, HOHAL-44, P-93 R, 234-B, ARG-6 A, 44-B
Cluster IV	1	HOHAL-38
Cluster V	1	P-61 R
Cluster VI	1	TX-16 R

Table 2: Inter Intra-cluster distances of sunflower germplasm

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI
Cluster I	**417.29**	1252.94	1327.61	2523.30	715.63	7084.31
Cluster II		**0.00**	4216.23	6498.28	2153.61	12836.64
Cluster III			**173.28**	375.24	1318.12	3208.71
Cluster IV				**0.00**	2058.76	2010.41
Cluster V					**0.00**	6601.00
Cluster VI						**0.00**

Table 3: Mean performance of cluster

Cluster no.	Plant height (cm)	Head diameter (cm)	volume weight (g/cm)	100 Seed weight (g)	Seed yield (g/ plant)
Cluster I	80.79	11.97	32.75	5.52	11.05
Cluster II	49.00	8.25	31.00	4.74	5.80
Cluster III	112.93	13.04	28.44	6.07	10.33
Cluster IV	128.50	15.45	31.00	6.31	16.92
Cluster V	87.00	6.30	35.50	3.81	31.97
Cluster VI	159.00	4.30	57.25	1.16	1.42

4. Conclusion

Diversity analysis indicates a lot of diversity between these germplasm lines which can be exploited in hybrids breeding program. The maximum genetic divergence was observed between cluster II and cluster VI which may give rise to very good cross combination and desirable recombinants could be selected upon in the segregated generation. P 61R and TX 16R the only member of cluster V and VI respectively can be used in hybridization with cms A lines present in cluster I to synthesize new high yielding hybrids.

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