Electronic Journal of Plant Breeding, 5(3): 577-580 (Sep 2014)
ISSN 0975-928X

Research Note

Genetic diversity among sunflower genotypes

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(Received: 27 April 2014; Accepted:21 Jul 2014)

Abstract

Genetic divergence of 38 sunflower genotypes was assessed using Mahalanobis D^2 statistics. These genotypes were grouped into 13 clusters, among which the cluster IX with 9 genotypes was the largest. This was followed by cluster X with 5 genotypes. Maximum inter cluster distance was recorded between cluster XII and XIII (39.58) followed by clusters II and XII (38.18). Hence hybridizing between these divergent groups may lead to higher variation in segregating population. Based on cluster means, the genotypes *viz.,* GMU 463, GMU 475, GMU 498, GMU 1075 and GMU 1131-1 in the cluster X recorded highest seed yield per plant with high head diameter. The study revealed that the characters *viz.*, 50% flowering followed by seed yield (35.00%) contributed more to the total genetic divergence in the genotypes. In this study, the genotypes *viz.,* GMU 322, COSF3B and COSF4B in the cluster II, the genotypes *viz.,* GMU 503, GMU 1074, GMU 1108 in the cluster XII and the genotype COSF1B in the cluster XIII are widely divergent and crosses may be effected among the genotypes of these clusters to get more heterosis among the hybrids.

Key words:
Sunflower, D2 statistics, genetic divergence.

Sunflower is the second major oilseed crop having a potential source for vegetable oil and protein. Sunflower (*Helianthus annuus* L.) has become an important oil crop in the world with annual production of 20 to 25 million hectares worldwide in present decade (Machikowa and Saetang, 2008). 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 investigations that evaluated the genetic divergence in sunflower crop were conducted by using morphoagronomic characters (Arshad *et al*., 2007).

The choice of suitable parents is of paramount importance for a planned hybridization programme. Hence, it is imperative to identify the best parents with wide genetic divergence for characters of economic importance, so that they can be utilized in breeding programmes to produce desirable recombinants. Genetic diversity is of major interest to plant breeders, more diverse the parents, greater are the chances of obtaining heterotic expression in F_1 with possibility of broad spectrum of variability in segregating generations. D^2statistics is one of the potent techniques to study the genetic divergence in breeding materials. Hence, the present study aimed to assess the genetic divergence among 38 genotypes of sunflower.

The materials used in the present study consisted of 38 genotypes in sunflower (*Helianthus annuus* L.) maintained in the Department of Oilseeds, Tamil Nadu Agricultural University, Coimbatore. The experiment was conducted during *Rabi*/Summer 2012-13. Each genotype was sown in two rows of 5m length with spacing of 60 cm between rows and 45 cm between plants. The experiment was laid out in a Randomized Block Design with two replications. In each genotype, five plants were randomly selected and used for collection of data on six characters *viz.*, days to 50% flowering, days to maturity, plant height (cm), head diameter (cm), 100 seed weight (g) and seed yield per plant (g). The data were subjected to statistical analysis using Mahalanobis D^2 statistic (Mahalanobis, 1936) and Toucher's method as described by Rao (1952) for determining group constellation.

All the 38 genotypes were grouped into 13 clusters (Table 1.) Among the clusters, cluster IX was the largest comprised of 9 genotypes followed by cluster X which had 5 genotypes. The cluster I, II and XII possessed 3 genotypes each and the clusters III, IV, V, VI, VII, VIII and XI comprised of 2 genotypes each. The cluster II possessed two maintainer lines *viz.*, COSF 3B and COSF 4B and the cluster XI possessed only one maintainer line *viz.,* COSF 2B. The cluster XIII had only one genotype which was a maintainer line *viz.,* COSF 1B. Therefore, 38 genotypes falling as many as 13 clusters is an indication of prevalence of good extent of diversity in the materials.

The genotypes grouped within a cluster exhibit a narrow range of genetic variability, whereas in different clusters indicate wider variability. The average inter and intra cluster distances are presented in the Table 2. Maximum intra cluster distance was noticed among the genotypes of cluster XII (21.59) indicating higher genetic divergence among them. The least intra cluster distance was noticed among the genotypes belonging to cluster III (3.60) indicating that they are genetically similar. Such type of narrow range of genetic variability among the genotypes within the clusters was also reported by many authors (Ramasubrhamanyam *et al*., 2003 and Srinivas *et al*., 2006). Maximum inter cluster distances was noticed between clusters XII and XIII (39.58) followed by clusters II and XII (38.18) suggesting that hybridization between these divergent groups may lead to higher magnitude of heterosis and more variability in segregating populations. The above findings involving parents from divergent clusters to obtain superior heterosis is in accordance with the reports of Asish *et al*., 2007 and Anandakumar *et al*., 2008.

Different characters revealed by cluster means are presented in the Table 3. It is always desirable to look for genotypes having more than one desirable trait but belonging to different clusters based on cluster mean values. The contrasting genotypes for days to flowering were grouped in XIII, II and XII, for plant height in III and VIII, for head diameter in XIII and X, for 100 seed weight in II and IV and for seed yield in XIII and X. The genotypes *viz.*, GMU 463, GMU 475, GMU 498, GMU 1075 and GMU 1131-1 in the cluster X recorded highest seed yield per plant with high head diameter. The genotypes of this cluster can be used in crossing programmes for producing heterotic hybrids and for generating variability.

To get early maturing hybrids, the genotypes *viz.*, GMU 322, GMU COSF 3B and COSF 4B in the cluster II and COSF1B in the cluster XIII can be involved and for developing late maturing hybrids, the genotypes *viz.*, GMU 503, GMU 1074 and GMU 1108 in the cluster XII can be used. The contribution towards genetic divergence indicated that the 50% flowering (36.27%) followed by seed yield (34.99%) contributed higher to the total genetic divergence in the genotypes (Table 3). Mohan and Seetharam (2005), Loganathan *et al*. (2006) and Punitha *et al.* (2010) also reported that seed yield contributed maximum towards genetic divergence in sunflower.

The present study revealed that the selection of parents should be on the basis of wider inter cluster distance and superior mean performance for yield and yield components. In this study, the genotypes *viz.*, GMU 322, COSF3B and COSF4B in the cluster II, the genotypes *viz.*, GMU 503, GMU 1074, GMU 1108 in the cluster XII and the genotype COSF1B in the cluster XIII were widely divergent and crosses may be effected among the genotypes of these clusters to get more heterosis among the hybrids. The characters *viz.*, days to 50% flowering and seed yield were found to be important contributors for genetic divergence.

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Table 1. Clusters with parental lines in sunflower (*Helianthus annuus* L.)

Cluster	Number of genotypes clustered	Parental lines
I	3	GMU321, GMU591, GMU1032
II	3	GMU322, COSF3B, COSF4B
III	2	GMU409, GMU597
IV	2	GMU438, GMU458
V	2	GMU528, GMU557
VI	2	GMU389, GMU455
VII	2	GMU411, GMU450
VIII	2	GMU392, GMU466
IX	9	GMU329, GMU 336, GMU 342, GMU 360, GMU 410, GMU 415, GMU 457, GMU 477, GMU 729
X	5	GMU463, GMU 475, GMU 498, GMU 1075, GMU 1131-1
XI	2	COSF2B, COSF5B
XII	3	GMU503, GMU 1074, GMU 1108
XIII	1	COSF1B

Table 2. Average inter and intra cluster distances grouped with parental lines in sunflower (*Helianthus annuus* L.)

	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII
I	11.66	28.79	13.25	11.99	9.86	10.16	10.62	11.04	15.92	26.56	21.35	17.84	28.97
II		19.44	33.30	21.40	27.26	28.78	23.26	30.53	34.60	27.88	15.25	38.18	15.34
III			3.60	17.39	8.70	11.34	18.14	18.22	14.46	25.47	25.77	13.78	35.65
IV				3.65	10.32	12.79	6.38	13.38	19.42	22.62	14.15	22.79	20.63
V					4.18	10.75	11.80	15.03	15.16	21.09	18.88	16.84	29.33
VI						4.28	12.01	10.68	14.86	28.79	22.54	16.63	28.04
VII							6.07	10.10	18.99	25.61	16.39	22.24	21.76
VIII								6.25	17.85	32.14	24.17	20.31	27.94
IX									19.44	30.13	27.78	18.65	35.41
X										20.19	21.24	31.87	33.26
XI											10.93	31.28	17.17
XII												21.59	39.58
XIII													0.00

Note: The figures in diagonal indicate intra cluster distances

Table 3. Cluster means for six characters in sunflower (*Helianthus annuus* L.)

Cluster	Days to 50% flowering	Days to maturity	Plant height (cm)	Head diameter (cm)	100 seed weight (g)	Seed yield per plant (g)
I	85.83	117.00	175.93	13.22	5.20	40.45
II	63.00	93.50	146.47	10.05	3.60	20.90
III	88.75	119.25	133.53	13.25	5.33	35.33
IV	78.50	110.75	155.68	11.93	7.68	37.05
V	83.25	115.00	153.20	13.85	6.03	39.75
VI	86.50	117.75	151.48	11.48	5.38	26.13
VII	81.00	112.50	176.85	11.80	5.85	40.00
VIII	88.00	118.75	195.45	12.98	6.88	38.90
IX	89.39	120.33	157.40	13.26	5.65	37.22
X	71.30	105.10	130.58	14.29	5.10	46.14
XI	67.50	98.00	171.88	14.03	4.43	30.30
XII	93.00	122.33	149.73	13.20	5.00	39.32
XIII	64.00	95.00	155.20	8.50	6.10	14.40
Contribution towards D2 (%)	36.27	0.28	3.56	9.96	14.94	34.99