Indian J. Plant Genet. Resour. 30(1): 66–71 (2017)
DOI 10.5958/0976-1926.2017.00008.0

Genetic Divergence Analysis among Sunflower (*Helianthus annuus* L.) Inbred Lines for Yield and Component Traits

Reena Rani*, RK Sheoran and Subhash Chander
Department of Genetics and Plant Breeding, CCS Haryana Agricultural University, Hisar-125004, Haryana, India

Received: 23 June 2016; Revised: 28 September 2016; Accepted: 11 November 2016)

Sunflower holds a great promise because of its short duration, wider adaptability and superior quality oil. Ninety sunflower inbred lines from different agro-ecological origins were evaluated to study the genetic divergence for seed yield and its components. Based on D^2 values, the 90 inbred lines were grouped into 8 clusters indicating considerable amount of genetic diversity. The character, seed filling percentage contributed maximum towards genetic divergence, followed by hull content and seed yield per plant. The genotype, AKSFI-54-3 exhibited the highest value of genotypic worth followed by EC-601957, RHA-3, RHA-859, AKSFI-33, EC-623015 and EC-601767. Mating among these genotypes shall be worthwhile to further expand genetic variability among populations and for selection of elite inbreds through convergent improvement for seed yield and its components for developing superior hybrids and/or elite populations through recurrent selection for composite varieties.

Key Words: Convergent, Divergence, Inbreds, Recurrent, Sunflower

Introduction

Sunflower (*Helianthus annuus* L.), belonging to the family '*Asteraceae*' (*Compositae*) is a diploid species (2n = 2x = 34) and native to southern parts of USA and Mexico. Sunflower is an important oilseed crop and is the preferred source of oil for domestic consumption and cooking worldwide (Hu *et al*., 2010).

In the oilseed scenario, sunflower competes with soyabean, groundnut and rapeseed mustard at global level. As an oilseed crop, sunflower holds a great promise because of its short duration, wider adaptability, photo-insensitivity, drought tolerance and higher amount of superior quality oil. Due to presence of polyunsaturated fatty acids, which are known to reduce the risk of cardiac related problems, higher oil yield is an ultimate objective of sunflower researchers (Monotti, 2004).

Genetic diversity is of major interest to plant breeders for developing cultivars with high grain yield and high oil yield potential in oilseeds. Sunflower being a highly cross-pollinated crop has a great scope for increasing productivity by diversification of hybrid base. The choice of suitable parents is of paramount importance for a planned hybridization programme. It is, therefore, imperative to identify the best parents with wide genetic base for characters of economic importance to obtain heterotic expression in F_1 with possibility of broad spectrum of variability in segregating generations. Genetic divergence estimation between different sunflower genotypes is studied with the aim to identify best parents for hybrids constitution among divergent genotypes with complementary characteristics (Amorim *et al*., 2007).

The Mahalanobis D^2 statistic being independent of size of sample gives better idea about the magnitude of divergence and provides the basis for selection of parental lines for further breeding programme. Varieties from different geographical locations are generally included in the hybridization programmes by assuming genetic diversity and more likelihood of recovering promising segregants. However, Murthy and Anand (1966) and Medimagh *et al*. (2016) noted that there is no parallelism between geographical and genetical diversity. The present study was designed to quantify the magnitude of genetic divergence and using them in further breeding to evolve potential transgressive segregants and to elucidate the kind of relationship that exists between heterosis and parental diversity in sunflower.

Material and Methods

The present study was carried out on 90 sunflower genotypes selected from sunflower germplasm maintained at the Oilseeds Section, Department of Genetics and Plant Breeding, CCS Haryana Agricultural University, Hisar.

**Author for Correspondence: Email- saharanreena23@gmail.com, sheoranrk@yahoo.com*

The experiment was conducted at the Research Farm of CCS HAU, Hisar during spring, 2013. The description of genotypes is given in Table 1. All the genotypes were grown in a randomized block design (RBD) with three replications in single row plots of 3 m length, keeping row to row distance of 45 cm and plant to plant distance of 30 cm for each genotype. Observations were recorded on the characteristics like days to 50% flowering, days to maturity, duration of reproductive phase, plant height at harvest (cm), stem girth (cm), head diameter (cm), 100-seed weight (g), seed filling percentage, hull content (%), protein content (%), oil content (%) and seed yield/plant (g). Mahalanobis D^2 statistics was applied to assess genetic diversity among the genotypes and genotypes were grouped on the basis of minimum genetic distance using Tocher's method as described by Rao (1952).

Results and Discussion

Based on the divergence, 90 sunflower genotypes involved in the present study were grouped into 8 clusters. Clustering pattern revealed the presence of considerable amount of genetic diversity in this material. In general, intercluster distances were relatively greater than intracluster distances showing that genotypes included in different clusters were genetically more diverse than the genotypes included within a cluster. Highest number of genotypes were grouped in clusters-I and IV each having 21genotypes, followed by cluster-II with 14, clusters III and VII each with 12, cluster-V with 8 and clusters VI and VIII each containing only 1 genotype as seen from Table 2. Genotypes from different sources were grouped in the same cluster thereby, indicating that geographical diversity does not necessarily represent genetic diversity and there was little association of genetic divergence with place of origin of genotypes. Murthy and Anand (1966), Reddy *et al*. (2012) and Kumari and Sheoran (2012) also reported the same. However, in some clusters like, clusters III and V, the genotypes related to their place of origin have shown their tendency to group together in the same cluster.

Intra cluster distance was maximum for cluster VII, followed by clusters IV, V, III and II and minimum for cluster I which indicates the existence of maximum variability within cluster VII. Inter cluster distance was maximum in case of Cluster IV and VIII and minimum in case of clusters I and II as shown in Table 3. The higher intercluster distances exhibited the presence of more diversity among the genotypes involved in these clusters. So, it is desirable to select accessions from the clusters having high inter-cluster distance in the recombination breeding programmes.

Table 1. List of 90 genotypes selected for the study

1	ACGIP-1436	31	EC-601801	61	GPB-07
2	AKSFI-33	32	EC-601806	62	GPB-18
3	AKSFI-52-4	33	EC-601820	63	GPB-50
4	AKSFI-54-3	34	EC-601871	64	GPB-61
5	AKSFI-58-3	35	EC-601875	65	GPB-67
6	AKSFI-71	36	EC-601885	66	GPB-07-1
7	AKSFI-78	37	EC-601889	67	GPN-145
8	AKSFI-186	38	EC-601896	68	GPN-215
9	AKSFI-190	39	EC-601906	69	LSF-902
10	AKSFI-197	40	EC-601926	70	MR-6
11	CGP-17	41	EC-601935	71	NDR-2
12	CGP-39-1	42	EC-601953	72	P35R-PAU
13	CGP-112	43	EC-601957	73	RCR-22-2
14	CSF1-5311	44	EC-601963	74	RCR-24-11
15	CSF1-5313	45	EC-601971	75	RCR-39
16	CSF1-5317	46	EC-601974	76	RCR-72
17	DRSF-106	47	EC-623009	77	RHA-271
18	DRSF-120	48	EC-623013	78	RHA-859
19	EC-512673	49	EC-623015	79	RHA-298
20	EC-512674	50	EC-623016	80	RHA-2
21	EC-512676	51	EC-623017	81	RHA-3
22	EC-512684	52	EC-623019	82	R-101
23	EC-512687	53	EC-623020	83	R-102
24	EC-601746	54	EC-623024	84	R-103
25	EC-601747	55	EC-623025	85	R-105
26	EC-601748	56	EC-623026	86	R-107
27	EC-601755	57	EC-623028	87	1-OH-07-8
28	EC-601758	58	EC-623031	88	1-OH-07-62
29	EC-601767	59	EC-623032	89	1-OH-07-65
30	EC-601769	60	GPB-02	90	1-OH-07-108

Table 2. Clustering of 90 genotypes of sunflower on the basis of D^2 statistics

Cluster	No. of genotype(s)	Name of genotype(s)
I	21	GPB-07-1, RCR-39, GPB-67, 1-OH-07-108, R-101, GPB-18, EC-601871, R-103, MR-6, GPN-145, R-102, EC-601885, EC-623031, RHA-271, AKSFI-197, GPB-61, R-105, EC-623009, R-107, EC-512684, EC-601758
II	14	1-OH-07-8, 1-OH-07-62, LSF-902, DRSF-106, RHA-3, AKSFI-58-3, AKSFI-54-3, ACGIP-1436, EC-623017, EC-623016, RHA-859, EC-623015, DRSF-120, CGP-112
III	12	EC-601889, EC-601896, EC-512673, EC-601748, EC-623028, EC-601926, EC-601906, EC-601820, EC-623013, EC-623024, EC-512676, EC-601935
IV	21	RCR-22-2, RHA-2, AKSFI-78, AKSFI-33, CSF1-5317, 1-OH-07-65, AKSFI-52-4, CGP-17, CSF1-5311, CGP-39-1, AKSFI-186, RCR-24-11, AKSFI-71, CSF1-5313, GPB-07, RCR-72, GPB-50, GPB-02, GPN-215, AKSFI-190, EC-623019
V	8	EC-512687, EC-601746, EC-623020, EC-623026, EC-601974, EC-601769, EC-601806, EC-601963
VI	1	EC-601957
VII	12	EC-601755, EC-623025, EC-601801, EC-601747, RHA298, EC-601971, EC-601953, NDR-2, EC-601875, EC-623032, EC-512674, P35R-PAU
VIII	1	EC-601767

Table 3. Average intra (diagonal) and inter (above diagonal) cluster D^2 values in 90 genotypes of sunflower

Cluster	I	II	III	IV	V	VI	VII	VIII
I	10.45	13.67	14.77	21.26	16.14	20.97	16.55	18.14
II		12.13	19.77	20.53	20.56	17.66	16.88	24.16
III			13.51	24.34	17.26	24.80	20.37	16.17
IV				14.96	25.58	22.26	24.17	32.66
V					13.94	30.14	24.43	21.10
VI						0.00	16.73	28.55
VII							16.68	22.16
VIII								0.00

To get more heterotic F_1's and large number of desirable transgressive segergants, selection of parents for hybridization should be properly based on genetic diversity rather than geographic diversity. An effective hybridization programme may be initiated involving the genotypes belonging to diverse clusters with high mean for almost all component characters. The cluster means for seed yield and its component characters revealed considerable differences among all the clusters for most of the characters studied.

In the present study, days to 50% flowering had the highest mean value in cluster III and lowest mean value in cluster IV as shown in Table 4. For days to maturity, cluster VIII exhibited the highest mean value and cluster II showed the lowest mean value. Cluster III revealed the highest mean value for plant height, whereas cluster VI had the lowest mean value. For stem girth, cluster VIII had the highest mean value, while cluster V had the lowest mean value. Cluster VI showed the maximum mean value for head diameter and cluster III showed the lowest mean value. For 100-seed weight, the highest mean value was possessed by cluster VI and the lowest was possessed by cluster VIII. Seed filling percentage was the highest in cluster VIII and the lowest in cluster IV. Cluster V recorded the highest mean value of hull content, while cluster VI recorded the lowest. Protein content exhibited its highest and lowest mean values in cluster VIII and cluster V, respectively. Cluster II

Table 4. Mean values of different clusters for 12 characters in sunflower

Cluster	Days to 50% flowering	Days to maturity	Duration of reproductive phase (days)	Plant height (cm)	Stem girth (cm)	Head diameter (cm)	100-seed wt (g)	Seed filling per cent	Hull content (%)	Protein content (%)	Oil content (%)	Seed yield / plant (g)
I	60.95	94.44	32.97	127.39	5.61	11.85	3.74	66.49	31.29	22.23	38.56	19.67
II	59.52	91.86	32.07	123.38	5.66	13.50	5.63	68.03	30.03	21.95	38.95	34.67
III	67.64	102.44	32.53	142.22	6.11	10.87	3.71	61.50	32.96	24.27	38.18	12.24
IV	57.89	92.40	32.87	132.44	5.90	12.06	4.14	32.28	31.13	21.83	37.85	22.56
V	62.92	98.29	33.21	140.02	5.41	11.05	3.71	64.53	37.40	17.81	37.83	14.94
VI	67.00	98.00	31.00	121.57	5.93	15.87	5.73	56.42	21.05	24.31	38.33	37.07
VII	62.44	95.08	31.83	135.66	6.03	11.79	4.49	66.99	24.73	23.51	37.76	21.99
VIII	62.33	104.33	30.67	129.77	6.88	12.73	1.90	79.67	30.35	24.93	37.52	5.42
GM	62.59	97.11	32.14	131.56	5.94	12.47	4.13	61.99	29.87	22.61	38.12	21.07

revealed the highest mean value for oil content, whereas cluster VIII had the lowest mean value. The highest seed yield per plant was recorded in cluster VI and the lowest in cluster VIII for mean values.

Comparative evaluation of cluster means suggested that for improving specific characters, select the genotypes from the cluster having high mean value for that character. This comparison indicates that clusters II, IV, VI and VIII had better cluster means for most of the characters, therefore, these clusters might be considered better for selecting genotypes.

From Table 5, it was observed that out of 12 characters studied, the contribution of seed filling percentage was maximum (33.61%) towards genetic divergence, followed by hull content (25.24%), seed yield per plant (15.66%) and days to maturity (11.69%) whereas the remaining characters like, days to 50% flowering (0.12%), duration of reproductive phase (0.40%), plant height (2.75%), stem girth (0.07%), head diameter (0.42%), 100-seed weight (1.30%), protein content (7.37%) and oil content (1.37%) contributed very little for divergence. Similar results for one or more characters have been reported by Pandya *et al*. (2014), Manivannan *et al*. (2003) and Ravi *et al*. (2006).

Table 5. Contribution of different characters towards divergence

S.No.	Character	Times ranked 1st	Contribution towards divergence (%)
1.	Days to 50 % flowering	5	0.12
2.	Days to maturity	468	11.69
3.	Duration of reproductive phase (days)	16	0.40
4.	Plant height (cm)	110	2.75
5.	Stem girth (cm)	3	0.07
6.	Head diameter (cm)	17	0.42
7.	100-seed weight (g)	52	1.30
8.	Seed filling per cent	1346	33.61
9.	Hull content (%)	1011	25.24
10.	Protein content (%)	295	7.37
11.	Oil content (%)	55	1.37
12.	Seed yield plant-1 (g)	627	15.66

Table 6 shows diverse and promising genotypes namely, AKSFI-33, AKSFI-54-3, EC-601767, EC-601957, EC-623015, RHA-3 and RHA-859 which were selected on the basis of D^2 (intercluster distance) values and cluster means from different clusters including clusters II, IV, VI and VIII along with the list of characters for which they attributed superior performance, so these clusters may be used for selecting parents in future breeding programmes. Genotypic worth was then calculated for these genotypes on the basis of range of all the characters. AKSFI-71 has highest value of seed yield/ plant (g), *i.e*., 39.0g, ACGIP-1436 has highest value of oil content (%), 42.10% and EC-601935 has highest value of protein content (%), 29.64%. The genotype, AKSFI-54-3 exhibited the highest value of genotypic worth (17), and therefore, was adjudged the most superior, followed by EC-601957 (16), RHA-3 (15), RHA-859 (14), AKSFI-33 (14), EC-623015 (12) and EC-601767 (11).

These genotypes figured important to be included in crossing programme to further expand genetic variability among populations, to effect selection of elite inbreds for hybridization programme and/or elite populations for composite varieties.

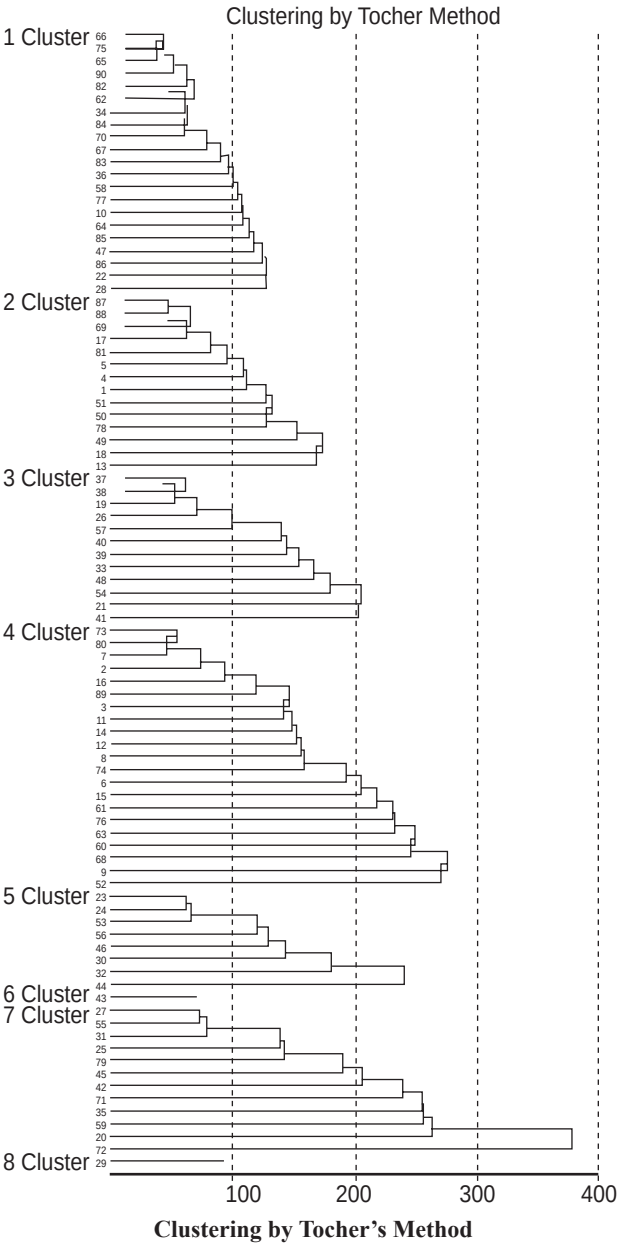
Table 7 shows the distribution of genotypes based on their values for individual traits. With the help of convergent improvement of these inbreds for a particular trait, the performance of these inbreds can be improved. Good general combiner inbreds can be utilized for development of synthetic varieties. The so developed synthetic varieties can be used as source populations for isolation of inbreds which are superior for several traits or show heterosis for several traits. As a result of this, the genetic variability will be further widened.

Table 6. Diverse and promising genotypes selected from different clusters in sunflower

Genotype	Cluster	Characters	Genotypic worth
AKSFI-33	IV	Days to 50% flowering, days to maturity, duration of reproductive phase, plant height, seed yield plant-1	3+3+3+2+3=14
AKSFI-54-3	II	Days to 50% flowering, days to maturity, plant height, seed filling percentage, oil content, seed yield plant-1	3+3+2+3+3+3=17
EC-601767	VIII	Plant height, seed filling percentage, stem girth, protein content	2+3+3+3=11
EC-601957	VI	Plant height, stem girth, head diameter, 100-seed weight, hull content, seed yield plant-1	2+2+3+3+3+3=16
EC-623015	II	Duration of reproductive phase, plant height, seed filling percentage, oil content, head diameter	2+2+3+3+2=12
RHA-3	II	Days to 50% flowering, days to maturity, seed filling percentage, oil content, seed yield plant-1	3+3+3+3+3=15
RHA-859	II	Duration of reproductive phase, plant height, seed filling percentage, head diameter, seed yield plant-1	3+2+3+3+3=14

Table 7. Distribution of genotypes based on value for each trait in sunflower

Characters	Number of genotypes			
	Low	Medium	High	Total
Days to 50% flowering	36	35	19	90
Days to maturity	19	44	27	90
Duration of reproductive phase (days)	34	20	36	90
Plant height (cm)	18	47	25	90
Stem girth (cm)	26	50	14	90
Head diameter (cm)	27	49	14	90
100 seed wt (g)	20	43	27	90
Seed filling percent	11	26	53	90
Hull content (%)	17	49	24	90
Protein content (%)	15	63	12	90
Oil content (%)	11	55	24	90
Seed yield (g/plant)	26	37	27	90



Conclusion

The present study has led to improve the understanding of many interrelated processes involved in the genetic control of variation in the seed yield. Based on genetic divergence and *per se* performance/genotypic worth for various traits some sort of inter-mating among diverse and promising genotypes namely, AKSFI-33, AKSFI-54-3, EC-601767, EC-601957, EC-623015, RHA-3 and RHA-859 figured important to further expand genetic variation for important yield attributing traits to build either improved populations or draw improved inbred lines for developing heterotic hybrids. Also the improved sunflower populations must combine high seed yield with high percentage of good quality oil for human health. For that matter, selection in segregating populations as evident from present studies, can be based on 100-seed weight, seed filling per cent, head diameter and oil per cent along with seed yield.

The results, thus, obtained in the present study would provide some guidelines in selection of parents and in the prediction of possible merits for genetic recombination and would also be of value in formulating model plant type for selection in segregating generations.

References

Amorim EP, NP Ramos, MRG Ungaro and AMT Kiihl (2007) Genetic divergence in sunflower genotypes. *Sci. Agrotechnologia* **31**: 1637-1644.

Hu J, G Seiler and C Kole (2010) Genetics, genomics and breeding of sunflower. *Routledge*, USA, 342 p.

Kumari S and RK Sheoran (2012) Genetic divergence in sunflower (*Helianthus annuus* L). Crop science and technology for food security, bioenergy and sustainability. AGROBIOS (INTERNATIONAL) Publication, Jodhpur, India. pp 219-223.

Manivannan N, V Muralidharan and B Subbalakshmi (2003) Genetic divergence in sunflower. *Agric. Sci. Digest* **23**: 125-127.

Medimagh S, M Mastouri, B Bargaoui, HB Salah and IBE Ali (2016) Agro-morphological diversity of tunisian sunflower (*Helianthus annuus* L.). 19th International sunflower conference, 29th April-3rd May. Edirne, Turkey, 614 p.

Monotti M (2004) Growing non-food sunflower in dry land conditions. *Italian J. Agronomy* **8**: 3-8.

Murthy BR and IJ Anand (1966) Combining ability and genetic diversity in some varieties of *Linum usitatissimum*. *Indian J. Genet.* **26:** 21-26.

Pandya MM, PB Patel, AV Narwade and GB Vaidya (2014) Genetic divergence studies in sunflower [*Helianthus annuus* (L.)]. *Trends Biosci.* **7**: 167-169.

Rao CR (1952) Advanced statistical methods in biometrical research. John Wiley and Sons, New York, 389 p.

Ravi E, M Bharathi, AV Reddy and K Madhvilatha (2006) Analysis of genetic divergence in sunflower (*Helianthus annuus* L.). *J. Oilseeds Res.* **23**: 165-167.

Reddy SM, TD Reddy and MY Dudhe (2012) Analysis of genetic diversity in germplasm accessions of sunflower (*Helianthus annuus* L.). *Madras Agric. J.* **99**: 457-460.