Original Research Article

Genetic Divergence Analysis in Sunflower (*Helianthus annuus* L.) Restorer Lines

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A B S T R A C T

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Genetic divergence using Mahalanobis D^2 statistic was worked out in 116 sunflower (*Helianthus annuus* L.) restorers including three checks. The 116 restorers were grouped into twenty three clusters using Touchers method. Cluster I had a large number of 35 genotypes. While twenty nine genotypes were included in cluster III, whereas II cluster included twenty two genotypes, cluster VIII and X with six genotypes each and cluster IV, V, VI, VII, IX, XI, XII, XIII, XIV, XV, XVI, XVII, XVIII, XIX, XX, XXI and XXIII were solitary. Characters like seed filling percentage, oil content, days to 50% flowering, seed yield per plant, head diameter, hull content, leaf lamina width, leaf lamina length, volume weight and test weight contributed more to the total divergence. The pattern of distribution of genotypes into various clusters revealed that there was no relationship between geographical distribution and genetic diversity. Greater genetic divergence was found between X and XXIII clusters and X and XXI clusters, thus suggesting that the genotypes of these clusters may be exploited to explore the fullest range of variability for the character (s) and to realize good recombinant lines.

Introduction

Oilseed plays an important role and occupy pride place in Indian economy. The requirement of edible oil in India is increasing day by day due to increase in population and demand of oil for domestic and industrial purpose. The exploitation of sunflower as a source of edible oil in India with the help of sunflower introduction from USSR sunflower emerged as an admirable crop for its quality oil in oilseeds scenario of India. For yield improvement, it is essential to have knowledge on variability of various traits. Genetic diversity is one of the criteria of parent selection for hybridization programme. The availability of transgressive

segregants in any breeding programme depends on the diversity between the parents involved. The quantification of genetic diversity through Mahalnobis D^2 statistics has made it possible to choose genetically diverse parents. The use of stable germplasm with restorer behavior in heterosis breeding programme and those with maintainer behavior to the good combiner CMS sources assembled should receive priority for hybrid synthesis. The new restorer identified will help in exploiting new CMS sources in hybrid development by ensuring better heterosis and diversity of cytoplasm in sunflower.

Restorer may be exploited in hybrid development or may be in the development of new restore lines. Keeping the above aspects an attempt was made to estimate genetic divergence in 116 restorer lines of sunflower.

Materials and Methods

A field experiment consists of 116 restorer lines including three checks were sown in randomized block design with two replications during the *kharif* season of 2014 at Oilseed Research Station, Latur. Each genotype was sown in two rows of 3.0 m length adopting a spacing of 60 cm x 30 cm. Two to three seeds were sown per hill to facilitate better emergence and to maintain uniform stand. Thining was done at second week to retain one seedling/hill. Recommended agronomic practices were followed to grow a healthy crop. Observations were recorded on five randomly selected plants for each genotype in each replication. The characters studied were days to 50% flowering, days to maturity, plant height, head diameter, leaf lamina length, leaf lamina width, seed filling%, hull content%, 100 seed weight, oil content%, volume weight and seed yield per plant. The mean values over replications were subjected to analysis of variance and then to Mahalanobis D^2 statistic to measure genetic divergence as suggested by Rao (1952). The genotypes were grouped into various clusters following Toucher's method described by Rao (1952).

Results and Discussion

The analysis of variance revealed significant differences among the 116 genotypes for all the 12 traits, indicating the existence of genetic variability. On the basis of relative magnitude of D^2 statistics, the 116 genotypes were grouped into twenty three clusters (Table 1) using Toucher's method (Singh and Chaudhary, 1977). Cluster I had a large number of 35 genotypes. Twenty nine genotypes were included in cluster III, whereas II cluster twenty two genotypes, cluster VIII and X with six genotypes each and cluster IV, V, VI, VII, IX, XI, XII, XIII, XIV, XV, XVI, XVII, XVIII, XIX, XX, XXI, XXII and XXIII were solitary. Thus, the pattern of distribution of genotypes from different geographical regions into different clusters was random, indicating that there is no correlation between clustering pattern and eco-geographical distribution of genotypes.

Tendency of genotypes occurring in clusters across the geographical boundaries demonstrates that the geographical isolation is not the only factor causing genetic diversity in sunflower. Similarly, the forces other than geographical origin such as genetic drift, natural and artificial selection, exchange of breeding material might have played an important role in the fixation of diversity among the genotypes.

Variation in the environment could also be responsible for this diversity. The success and usefulness of Mahalonobis's analysis in qualifying the genetic divergence has been followed in sunflower (Thirumala Rao, 2002 and Srinivas, 2006). The average intra and inter cluster D and D^2 values among twenty three clusters were presented in table 2 and 3 respectively. Most of the intra clusters are closely related and intra-cluster average cluster D^2 values ranged from 106.5 (Cluster I) to 223.2 (Cluster X), while the maximum D^2 value was found between the cluster X and cluster XXIII (1336.60) indicating the more genetic diversity between these two groups, while the minimum inter-cluster D^2 values was observed between cluster VI and XI (59.70), suggesting close genetic relationship and similarity for most of the traits between the clusters indicates the less genetic diversity between the genotypes.

Table.1 Composition 116 restorer lines including three checks of sunflower into different clusters by Tocher's method

Sr. No.	Cluster	No. of strains	Genotypes
1.	Cluster I	35	EC-601825, EC-601879, EC-601810, EC-601935, EC-601875, EC-601695, EC-601800, EC-601813, EC-601724, NSH-312-1, EC-601807, EC-601747, R-271, EC-601916, EC-601906, EC-601812, EC-512674, EC-601961, PAC-3739-4, EC-623072, RCR-1296, LR-6-12, EC-601958, EC-601878, 99RT, EC-601932, R-273, EC-601766, EC-601966, EC-623025, P-141-R, EC-601953, EC-601967, EC-601874, EC-601846.
2.	Cluster II	22	EC-601937, P-146-R, EC-623008, EC-601957, EC-512682, R-271-1, EC-601612, EC-623016, P-144R, EC-601713, R-64NB, R-16, PAC-3794WP, EC-601901, RHA-138-2, EC-623030, EC-623011, EC-601746, EC-601764, EC-601768, LR-6-3, EC-601729.
3.	Cluster III	29	R-274, MRHA-2, RHA-1-1, EC-601767, DOR-R-3, IR-1-1, NO.1147-4-2, R-272, NSH-312, EC-601751MR-234B, AK-345-2, PAC-3793,R-856, EC-601971, LTRR-341, EC-601820, EC-601900, EC-601974, EC-623031, EC-601836, EC602060, EC-601938,EC-601755, DS-3900,EC-623017, EC-623022,EC-601955,EC-601769.
4.	Cluster IV	1	P-148R
5.	Cluster V	1	EC-601939
6.	Cluster VI	1	EC-623024
7.	Cluster VII	1	EC-601821
8.	Cluster VIII	6	EC-601871, EC-623028, NDR-1, LSF-8, EC-601951, EC-623026.
9.	Cluster IX	1	AK-345
10.	Cluster X	6	RHA-418, 83R6, 6-D-1R, EC-623027, MORDEN, EC-6230223.
11.	Cluster XI	1	EC-601817
12.	Cluster XII	1	EC-601889
13	Cluster XIII	1	EC-601945
14.	Cluster XIV	1	EC-512687
15.	Cluster XV	1	DOR-R-2
16.	Cluster XVI	1	EC-601801
17.	Cluster XVII	1	EC-623015
18.	Cluster XVIII	1	EC-623020
19.	Cluster XIX	1	EC-601970
20.	Cluster XX	1	EC-623013
21.	Cluster XXI	1	EC-601888
22.	Cluster XXII	1	SS-2038
23.	Cluster XXIII	1	P-127

Table.2 Inter and intra cluster D values for twelve characters studied in sunflower

	C1	C2	C3	C4	C5	C6	C7	C8	C9	C10	C11	C12	C13	C14	C15	C16	C17	C18	C19	C20	C21	C22	C23
C1	10.32	15.45	14.24	12.80	14.69	12.13	12.32	20.56	13.00	22.12	12.81	18.19	18.99	17.97	16.70	15.58	17.35	15.91	17.45	16.07	18.83	14.48	21.74
C2		11.27	21.95	17.35	15.29	13.27	17.74	15.97	17.82	30.66	15.91	26.57	25.36	13.70	19.31	22.65	19.30	16.53	22.18	15.67	14.79	15.65	15.71
C3			13.10	15.17	19.66	16.02	14.89	25.46	15.45	17.71	16.83	15.59	16.35	24.36	17.63	15.50	18.51	20.28	16.67	20.72	25.30	16.88	28.59
C4				0.00	12.42	13.53	10.65	22.08	16.34	20.61	13.87	18.94	16.78	19.33	19.24	19.27	16.17	12.86	21.37	11.60	22.69	16.72	21.71
C5					0.00	18.17	15.33	21.55	15.33	25.98	20.59	25.39	24.18	11.83	24.51	21.32	21.84	18.64	25.39	12.17	18.28	19.75	23.29
C6						0.00	13.68	14.66	17.71	24.75	7.73	19.58	16.63	19.01	8.62	19.29	10.86	12.26	13.85	15.20	19.03	10.62	17.64
C7							0.00	21.19	15.72	20.78	11.75	13.40	14.15	22.11	19.18	20.59	17.76	19.37	20.73	14.10	18.08	17.61	21.26
C8								13.55	25.17	33.52	19.02	28.41	24.30	20.28	17.93	29.52	17.02	19.72	21.36	19.47	17.26	19.38	17.98
C9									0.00	21.25	18.49	20.84	23.65	18.66	21.36	10.93	22.56	21.28	20.79	19.28	20.24	14.53	25.71
C10										14.94	24.86	18.89	19.91	32.65	24.81	21.20	23.41	27.54	23.57	25.46	33.79	24.34	36.56
C11											0.00	17.53	17.51	22.50	13.17	19.76	15.05	14.20	17.88	16.58	20.35	13.66	16.74
C12												0.00	11.03	32.08	21.13	21.60	20.99	25.89	18.46	25.39	26.41	22.80	29.83
C13													0.00	30.39	17.00	25.03	15.24	22.72	16.04	22.75	27.06	21.67	29.05
C14														0.00	24.35	23.82	24.41	19.21	26.44	17.07	18.16	18.79	22.59
C15															0.00	21.42	10.21	16.13	9.31	21.13	24.33	13.34	23.60
C16																0.00	24.87	21.77	20.52	24.76	27.74	16.06	30.72
C17																	0.00	14.67	13.43	16.99	24.13	16.50	21.61
C18																		0.00	20.20	16.13	24.54	16.77	18.40
C19																			0.00	25.29	25.00	16.81	27.79
C20																				0.00	20.02	19.41	18.83
C21																					0.00	21.96	17.04
C22																						0.00	22.29
C23																							0.00

Table.3 Inter and intra cluster D^2 values for twelve characters studied in sunflower

	C1	C2	C3	C4	C5	C6	C7	C8	C9	C10	C11	C12	C13	C14	C15	C16	C17	C18	C19	C20	C21	C22	C23
C1	106.5	238.7	202.8	163.8	215.8	147.1	151.8	422.7	169.0	489.3	164.0	330.8	360.6	322.9	246.5	242.7	301.0	253.1	304.5	258.2	354.6	209.7	472.6
C2		127.0	481.8	301.0	233.8	176.0	314.7	255.0	317.5	940.0	253.1	705.9	643.1	187.7	372.9	513.0	372.5	273.2	491.9	245.5	218.7	244.9	246.8
C3			171.6	230.1	386.5	256.6	221.7	648.2	238.7	313.6	283.2	243.0	267.3	593.4	310.8	240.2	342.6	411.3	277.9	429.3	640.1	284.9	817.3
C4				0.00	154.2	183.0	113.4	487.5	266.9	424.8	192.4	358.7	281.6	373.6	370.2	371.3	261.5	165.4	456.7	134.6	514.8	279.6	471.3
C5					0.00	330.1	235.0	464.4	235.0	674.9	423.9	644.6	584.7	139.9	600.7	454.5	476.9	347.5	644.6	148.1	334.2	390.1	542.4
C6						0.00	187.1	214.9	313.6	612.5	59.7	383.4	276.6	361.4	74.3	372.1	117.9	150.3	191.8	231.0	362.1	112.8	311.1
C7							0.00	449.0	247.1	431.8	138.1	179.6	200.2	488.8	367.9	423.9	315.4	375.2	429.8	198.8	326.9	310.1	451.9
C8								183.6	633.5	1123.6	361.8	807.1	590.4	411.3	321.5	871.4	289.6	388.9	456.2	379.1	297.9	375.6	323.2
C9									0.00	451.6	341.9	434.3	559.3	348.2	456.3	119.5	508.9	452.8	432.2	371.7	409.6	211.1	661.0
C10										223.2	618.0	356.8	396.4	1066.0	615.5	449.4	548.0	758.4	555.5	648.2	1141.7	592.4	1336.6
C11											0.00	307.3	306.6	506.2	173.4	390.5	226.5	201.6	319.7	274.9	414.1	186.6	280.2
C12												0.00	121.6	1029.1	446.5	466.5	440.6	670.3	340.8	644.6	697.5	519.8	889.8
C13													0.00	935.7	289.0	626.5	232.3	516.2	257.3	517.6	732.2	469.6	843.9
C14														0.00	592.9	567.4	595.8	369.0	699.1	291.4	329.8	353.1	510.3
C15															0.00	458.8	104.2	260.2	86.7	446.5	591.9	177.9	556.9
C16																0.00	618.5	473.9	421.1	613.1	769.5	257.9	943.7
C17																	0.00	215.2	180.4	288.7	582.2	272.2	466.9
C18																		0.00	408.0	260.2	602.2	281.2	338.5
C19																			0.00	639.6	625.0	282.6	772.2
C20																				0.00	400.8	376.7	354.5
C21																					0.00	482.2	290.3
C22																						0.00	496.8
C23																							0.00

Table.4 Cluster mean for the twelve characters studied in sunflower

Characters / clusters	Days to 50% flowering	Days to maturity	Plant height (cm)	Head diameter (cm)	Seed filling (%)	Hull content (%)	Oil content (%)	Test weight (g)	Volume weight (g/ml)	Leaf length (cm)	Leaf width (cm)	Yield /plant (g)
Cluster I	44.81	97.16	140.34	13.21	74.03	36.78	33.99	4.53	31.93	21.21	17.85	20.62
Cluster II	47.32	100.86	157.56	16.16	87.35	31.46	33.89	6.24	38.61	22.56	20.39	34.97
Cluster III	48.0	97.21	140.84	11.29	62.80	42.21	33.49	4.15	24.43	21.33	18.80	14.64
Cluster IV	41.50	98.50	154.0	15.00	72.50	44.0	25.75	4.50	25.00	22.93	18.73	23.25
Cluster V	40.50	105.00	163.0	14.25	79.56	33.78	26.25	5.28	38.50	27.06	23.74	30.39
Cluster VI	54.50	100.50	150.0	15.54	79.12	40.94	34.25	4.73	31.00	21.60	19.07	24.99
Cluster VII	42.50	89.50	112.0	11.50	71.92	48.07	30.65	5.03	35.50	20.40	14.60	26.05
Cluster VIII	60.08	103.50	166.17	14.35	87.82	30.97	31.58	5.64	38.40	22.76	18.06	33.89
Cluster IX	40.50	97.50	138.0	13.00	62.74	34.51	37.95	7.45	31.50	23.06	20.40	27.00
Cluster X	49.42	92.50	129.33	11.58	34.67	45.81	29.68	4.06	23.30	20.82	18.59	12.38
Cluster XI	47.50	89.50	122.0	16.00	77.18	45.70	35.55	4.71	33.01	18.40	14.40	21.34
Cluster XII	46.50	88.50	73.33	6.50	64.70	46.32	31.85	4.05	24.50	13.93	11.93	7.48
Cluster XIII	54.50	101.0	131.0	7.50	67.71	51.64	27.15	4.05	23.00	18.60	13.60	9.60
Cluster XIV	42.50	104.50	228.0	16.00	89.50	29.67	33.35	5.46	38.77	26.73	24.40	39.02
Cluster XV	61.50	105.0	178.0	13.88	69.50	41.79	37.54	4.25	25.50	19.60	16.27	21.96
Cluster XVI	43.50	99.50	121.0	15.00	64.67	36.01	40.25	5.62	22.50	26.40	24.40	11.11
Cluster XVII	61.50	104.0	169.0	14.67	60.84	34.95	27.55	4.50	29.50	17.00	15.73	20.55
Cluster XVIII	47.50	106.0	181.0	18.50	79.23	33.30	28.45	4.06	21.50	22.83	16.26	17.68
Cluster XIX	60.50	108.50	172.0	8.50	68.95	32.84	36.65	4.00	19.50	15.50	15.07	12.76
Cluster XX	45.50	101.50	151.0	18.50	68.39	42.64	26.65	4.43	43.00	22.73	20.40	43.95
Cluster XXI	44.50	94.50	122.0	9.63	93.40	26.91	36.05	6.13	41.74	18.06	14.26	48.95
Cluster XXII	55.00	87.00	176.0	17.00	67.0	36.50	37.80	7.15	27.50	25.00	23.00	23.24
Cluster XXIII	44.50	92.00	117.0	18.50	91.0	28.78	31.45	6.75	39.84	14.60	11.73	40.90

Table.5 Percent contribution of different characters towards genetic divergence for twelve characters for 116 genotypes

Sr. No.	Source	Times Ranked 1st	Contribution (%)
1	Days to 50% flowering	788	11.81%
2	Days to maturity	42	0.63
3	Plant height	161	2.41%
4	Head diameter	578	8.67%
5	Seed filling %	1727	25.89%
6	Hull content (%)	507	7.60%
7	Oil content (%)	945	14.17%
8	Test weight	223	3.34%
9	Volume weight	273	4.09%
10	Leaf length	322	4.83%
11	Leaf width	392	5.88%
12	Grain yield/plant	712	10.67%
	Total	6,670	

Variation in environment was also responsible for this diversity. Similar conclusions were also drawn by other researchers (Komuraiah, 2002; Reddy and Devasenamma, 2004 and Mohan and Seetharam, 2005).

The characters contributing maximum divergence needs greater emphasis for deciding on the clusters for the purpose of selection of parents in the respective cluster for hybridization. The number of times each of the yield component character appeared in first rank and its respective per cent of contribution towards genetic divergence were presented in table 5. The results showed that seed filling per cent contributed highest towards genetic divergence (25.89%) by taking 1727 times ranking first, followed by oil content per cent (14.17%) by 945 times, days to 50% flowering (11.81%) by 788 times, seed yield/plant (10.67%) by 712 times, head diameter (8.67%) by 578 times, hull content per cent (7.60%) by 507 times, leaf lamina width (5.88%) by 392 times, leaf lamina length (4.83%) by 322 times, volume weight (4.09%) by 273 times and plant height (2.41%) by 161 times.

Cluster mean of genotypes for various characters in sunflower (Table 4) revealed that cluster I and cluster XVII represented genotypes with highest mean for days to 50% flowering, whereas plant height, leaf lamina length and leaf lamina width were included in cluster XIV. High genotypic means for seed filling% and seed yield/plant were present in cluster XXI and cluster XX had genotypes with high means for head diameter and volume weight.

Cluster XIII had genotypes with high mean for hull content% and cluster XV included genotypes with high mean for oil content%, whereas test weight was included in cluster IX. These clusters can be preferred in selecting the genotypes for the respective traits as they recorded good means.

The genetic divergence analysis revealed presence of substantial amount of genetic variability among the genotypes.

The pattern of distribution of genotypes into various clusters is random, showing that geographical diversity and genetic diversity are not related to each other.

Greater genetic divergence was found between X and XXIII cluster and X and XXI cluster indicating that superior hybrids or recombinants can be realized by mating between the lines of these clusters in a definite fashion.

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