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GENETIC DIVERSITY IN NON-OILSEED SUNFLOWER (*Helianthus annuus* L.) GENOTYPES

K. Manjula, H.L. Nadaf and K. Giriraj*

Oilseeds Project, University of Agricultural Sciences, Dharwad 580 005, India

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SUMMARY

Genetic diversity was assessed in 46 non-oilseed sunflower genotypes for 14 characters by adopting D^2 analysis. Oil content and plant height exhibited maximum contributions towards genetic divergence. The genotypes were grouped into 11 clusters. The inter-cluster D^2 values ranged from 288.17 to 3972.34. The contribution of oil content towards genetic divergence in the 46 genotypes was confirmed when D^2 analysis was performed for seed characteristics such as test weight, volume weight, hull content, kernel recovery, oil and protein content.

Key words: **genetic diversity, non-oilseed sunflower, sunflower (*Helianthus annuus* L.), D^2 analysis**

INTRODUCTION

Sunflower has been established as a potential oilseed crop of economic importance. Presently, oil type cultivars with average oil content of 38 to 40% are grown. Sunflower utility for confectionery purpose and also for export has been realized recently. Exhaustive literature relating to genetic diversity, character association, heterosis and combining ability has been generated for oilseed sunflower (Fick *et al.*, 1974; Škorić, 1974; Seetharam *et al.*, 1977; Kovačik and Škaloud, 1978; Giriraj *et al.*, 1979; Giriraj *et al.*, 1986; Muppidathi *et al.*, 1995; Alvarez *et al.*, 1996; Chungui *et al.*, 1996; Joshi *et al.*, 1997). In contrast, non-oilseed sunflower has received scant attention in the past and research efforts in this direction are rather meagre. The present study involved a total of 46 non-oilseed genotypes. These were assessed for genetic divergence using D^2 analysis with the goal of isolating diverse genotypes of economic importance for use in breeding programs.

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* Corresponding author

MATERIALS AND METHODS

The experimental material comprised of 46 genotypes including three checks viz., MSFH-17, Surya and Morden. The non-oilseed sunflower germplasm lines were received from Project Coordinating Unit (Sunflower), Bangalore, and National Bureau of Plant Genetic Resources, New Delhi, India. The experimental material was sown on 6 January 1997. Each genotype was sown in a single row of 4.2 m length by adopting a spacing of 60 x 30 cm in a randomized complete block design in three replicates. All recommended agronomic practices were followed to raise a successful crop. The genotypes were evaluated for 14 characters viz., stem girth at 30 DAS, days to initiation of flowering, days to 50% flowering, days to maturity, leaf area index (LAI), plant height at maturity, head diameter, 100-seed weight, yield per plant, volume weight, hull content, kernel yield per plant, oil content and protein content. Oil estimation was carried out on dry seed weight basis using nuclear magnetic resonance. Protein content was estimated by following the procedure outlined by Jackson (1967). The genetic divergence of the 46 sunflower genotypes was estimated by using Mahalanobis' D^2 statistics (1936). The D^2 values for "K" characters between i^{th} and j^{th} genotypes was computed as

$D^2 = (y_{it} - y_{jt})^2$

The significance of D^2 values was tested by treating them as Chi-square (χ^2) values at "t" degrees of freedom at 0.05 level of significance, where "t" is the number of variables or characters considered. The genotypes were grouped into a number of clusters, D^2 being treated as the square of the generalized distance, according to the Tocher's method described by Rao (1952).

In all combinations, each character was ranked on the basis of $d_i = y_I - y_{ki}$ values. Rank one was given to the highest mean difference. The ranks were totaled for each D^2 component over all combinations and the rank totals were obtained. Percentage contribution of each character was computed by using the formula "X" = N (x) 100/1035

where,

N (x) = number of genotypic combinations which were ranked first for character

"X" out of total genotypic combinations of 1035 (all possible combinations between the 46 genotypes).

RESULTS AND DISCUSSION

Genotypes were grouped into 11 clusters and they exhibited a high range of inter-cluster D^2 values ranging from 288.173 to 3792.34, between clusters I & V and V & VII, respectively (Table 1). The intra-cluster distance also showed variability ranging from 0 to 271.07.

Table 1: Inter- and intra-cluster distance values for 11 clusters formed with 14 characters in sunflower

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X	XI
I	204.51	458.02	558.89	442.56	288.17	302.66	2639.79	518.94	769.21	1048.57	1602.85
II		185.38	562.21	446.21	935.46	623.93	1354.07	320.77	471.83	483.80	690.22
III			153.79	1194.54	756.26	298.37	2699.25	331.47	360.57	503.05	1346.89
IV				190.04	725.15	844.64	1866.94	1203.01	1090.01	1293.77	1298.14
V					0.00	358.63	3792.34	952.98	1211.98	1557.14	2405.47
VI						0.00	3126.54	536.20	598.28	1011.25	1788.82
VII							151.60	2639.70	1755.53	1279.47	558.07
VIII								0.00	394.00	525.85	1062.28
IX									0.00	322.22	0860.82
X										0.00	467.74
XI											271.07

Diagonal values indicate intra-cluster distance.
Above diagonal values indicate inter-cluster distance.

The analysis for estimating the contribution of various characters towards the expression of genetic divergence indicated that oil content (43.48%) and plant height at maturity (37.87%) were the major contributors towards divergence (Table 2). The contribution of the other characters was comparatively lower. Muppidathi *et al.* (1995) reported that seed yield and head diameter were the major contributors towards divergence. In another contradicting report, Alvarez (1996) noticed that days to flowering, days to maturity, number of leaves, plant height, total number of achenes, grain yield, 1000-achene weight and protein percentage had best discriminatory powers. The present result regarding the contribution of oil content towards diversity are in accordance with the results of Chungui *et al.* (1996) who showed that linear regression model fits the relationship between seed content and genetic divergence. Contradictory reports on the contribution of different characters towards divergence could be due to different kinds of material used in these studies.

Table 2: Degree of contribution of each character to divergence

Sl. No.	Character	Percentage contribution	Rank
1	Stem girth at 30 DAS	0.19	11
2	Days to initiation of flowering	1.64	7
3	Days to 50% flowering	0.77	8
4	Days to maturity	0.39	10
5	Leaf area index	1.84	6
6	Plant height at maturity	37.87	2
7	Head diameter	0.19	11
8	100-seed weight	2.03	5
9	Yield per plant	0.39	10
10	Volume weight	9.68	9
11	Hull percentage	3.38	4
12	Kernel yield per plant	0.77	8
13	Oil content	43.48	1
14	Protein content	6.38	3

The clusters which were close to each other may not yield transgressive segregants or high heterosis. The superior clusters with respect to seed yield were grouped in cluster VII followed by cluster X (Table 3). Genotypes of cluster VII, in addition to being high yielders, also exhibited other desirable traits such as high stem girth (13.18 mm), high leaf area index (3.92), wide head (18.88 cm), high test weight (8.76 g), high volume weight (4.2 g/10 ml), high kernel yield per plant (54.86 g) and also high protein content (20.17%). On the other hand, they also had some undesirable traits such as late flowering (62.16 days), late maturity (90 days) and high plant height (209.8 cm). Genotypes of cluster X showed a lower yield (62.66 g/ plant) than genotypes of cluster VII (98.16 g) but compared with the check it was significantly high yielding, and had some complementing desirable characters in comparison to cluster VII, *i.e.*, early flowering (55 DAS), short stature (154 cm) and

Table 3: Cluster mean values for 14 different characters in sunflower

Cluster	SG	DF	DFF	DM	LAI	PH	HD	TW	YP	VW	HP	KY	OC	PC
I	10.27	50.85	56.75	84.12	2.29	128.18	13.53	5.72	37.76	3.71	31.12	26.36	34.55	16.48
II	9.94	54.92	58.71	87.33	2.69	156.78	13.96	6.26	44.17	3.91	30.32	33.28	33.05	19.97
III	9.09	55.09	58.14	86.43	2.22	127.65	13.65	5.68	36.27	3.69	37.96	20.85	26.76	18.85
IV	10.35	53.67	58.67	87.83	3.41	148.62	14.62	5.30	39.30	3.77	25.32	29.43	41.78	20.03
V	10.80	48.67	54.33	84.33	2.47	104.43	15.43	4.93	40.00	3.57	31.17	32.43	37.33	13.90
VI	9.73	55.67	58.67	82.33	1.85	122.77	13.67	3.67	18.10	3.06	42.20	11.03	33.70	19.37
VII	13.18	62.17	67.17	90.17	3.92	209.83	18.88	8.77	98.17	4.20	40.48	54.87	33.06	20.18
VIII	7.66	54.33	59.33	87.00	2.05	153.67	13.33	6.20	44.33	3.80	24.73	33.47	26.87	11.03
IX	8.33	65.67	69.00	81.67	3.63	144.33	14.00	6.30	47.67	3.67	35.93	28.87	27.70	23.13
X	12.50	55.00	60.83	89.33	3.20	154.00	18.40	8.77	62.67	3.77	38.20	38.33	25.43	20.93
XI	15.77	59.83	62.50	90.83	3.93	185.78	18.94	6.72	59.32	4.92	40.73	32.40	29.63	18.51

SG = Stem girth (mm) at 30 DAS
LAI = Leaf area index (LAI)
PH = Plant height at maturity (cm)
KY = Kernel yield per plant (g)
DF = Days to initiation of flowering
DFF = Days to 50% flowering
HD = Head diameter (cm)
YP = Yield per plant (g)
PC = Protein content (%)
VW = Volume weight (g/10 ml)
DM = Days to maturity
HP = Hull percentage (%)
OC = Oil content (%)
TW = 100 seed weight (g)

also low oil content of 25.43% which is very much desirable when selecting genotypes for confectionery purpose. Intercrossing genotypes from these two clusters may generate wider variability and it is expected to produce high-yielding transgressive segregants in population improvement programs.

While choosing genotypes as parents for hybridization, the *per se* performance of genotypes with high D^2 value should be taken into consideration in addition to maximum inter-cluster distance among the genotypes. If the mean *per se* performance of two genotypes is too low, with low genetic divergence, such a pair is not likely to produce high-yielding segregants or a heterotic effect of an exceptionally high order to be of any practical value. Hence other methods of identifying ideal parental combinations should be used to identify genotypes possessing high yielding ability along with most desirable characters, observe all possible D^2 values among them and select the pair which has a moderate to high D^2 value.

The accessions EC 376211 and EC 376218 included in cluster VII, EC 376240 of cluster X, EC 376151 of cluster XI and ACC 1149 of cluster II were high-yielding. In addition, they had other desirable traits such as high protein content, high kernel yield per plant, high volume weight and high test weight. A keen perusal of the D^2 value combinations of these genotypes showed that the combinations involving the genotypes ACC 1149 with either EC 376211 or 376218 and EC 376240 with either EC 376211 or EC 376218 were the most divergent crosses. The *per se* performance of EC 376211 and EC 376218 in terms of yield was exceptionally good, 99.7 and 96.7 g/plant, respectively. They also had other desirable traits such as thick stem, high leaf area index and broad head with achences recording very high test weight and volume weight and high seed protein content with moderate oil content. These combinations also had certain undesirable traits such as late maturity and very tall plant stature. The diverse genotypes which can complement the lacunae of these genotypes in addition to being moderately high yielders, were genotypes ACC 1149 which was early in flowering, early in maturing and had a comparatively short stature, while genotype EC 376240 could be advantageous in terms of low oil content in seed. These desirable and divergent genotypes could be converted into CMS lines for further use in heterosis breeding programs.

Table 4: Degree of contribution of each character to divergence (D^2) analysis considering 6 seed characteristics

Sl. No.	Character	Contribution (%)	Rank
1	100-seed weight	4.73	5
2	Volume weight	3.19	6
3	Hull percentage	9.95	3
4	Kernel recovery per plant	11.792	2
5	Oil content	60.68	1
6	Protein content	9.66	4

The D^2 value for confectionery parameters was estimated on the basis of multiple measurements wherein importance was attached to all 14 characters. Some of these characters may have substantial contribution to quality parameters of yield, while some may have lower contribution. Breeding sunflowers for confectionery purposes concentrates on the improvement of seed characteristics and its components such as oil and protein contents. Hence, D^2 analysis was performed using only seed characteristics to establish the extent of diversity existing in the genotypes analyzed for confectionery characters. viz., test weight, volume weight, hull percentage, kernel recovery per plant, oil and protein content. A total of 15 clusters were formed, indicating wide genetic diversity of the genotypes for these parameters also. Even when only seed parameters were used for D^2 analysis, oil content had the maximum contribution towards divergence (60.68%) (Table 4). Based on the results of D^2 analysis, the relationship between seed oil content and genetic divergence has been confirmed.

CONCLUSIONS

In conclusion, the study has resulted in identifying four genotypes with desirable traits conforming to non-oilseed characteristics. Two characters viz., oil content and plant height, contributed most towards assessing genetic divergence of these genotypes.

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DIVERSIDAD GENETICA DE GENOTIPOS NO OLEAGINOSOS DEL GIRASOL (*Helianthus annuus* L.)

RESUMEN

La diversidad genetica ha sido evaluada por el analisis D^2 de 14 caracteristicas en 46 tipos no oleaginosos del girasol. El contenido de aceite y la alteza de planta han contribuido maximamente a la diversidad genetica. Los genotipos investigados fueron divididos en 11 grupos. Los valores D^2 de estos grupos variaban de 288,17 a 3972,34. La contribucion del contenido de aceite a la diversidad de 46 genotipos fue confirmado por el analisis D^2 de caracteristicas de semillas como son el peso/hectolitro, peso de volumen, cortenido de cascara, porcentaje de pipa, contenido de aceite y proteinas.

DIVERSITÉ GÉNÉTIQUE DANS LES GÉNOTYPES DE TOURNESOL NON-OLÉAGINEUX (*Helianthus annuus* L.)

RÉSUMÉ

La diversité génétique de 46 types non-oléagineux de tournesol a été évalué par l'analyse D^2 de 14 caractéristiques. Ce sont le contenu en huile et la taille de la plante qui ont contribué pour une plus grande part à la diversité génétique. Les génotypes observés avaient été partagés en 11 groupes. Les valeurs D^2 de ces groupes variaient de 288,17 à 3972,34. La contribution du contenu en huile à la diversité génétique de 46 génotypes a été confirmé par l'analyse D^2 de caractéristiques séminales comme le poids de l'hectolitre, le poids de la masse, le contenu de l'écale, le pourcentage du noyau, le contenu en huile et en protéines.