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GENETIC DIVERGENCE FOR SEED PARAMETERS IN SUNFLOWER (*Helianthus annuus* L.)

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SUMMARY

An investigation was taken up at the Directorate of Oilseeds Research, Hyderabad, India, to determine the extent of genetic divergence with respect to eleven characters in 85 sunflower genotypes consisting of 80 inbreds and five check cultivars. Univariate and multivariate analysis of variance revealed the presence of significant differences among the genotypes. Mahalanobis' D^2 statistic indicated the presence of substantial genetic diversity. The genotypes were grouped into fifteen clusters. Based on the intercluster distance and cluster mean for various characters, potential lines were identified from clusters III, IV, VI, VIII, XI, XII and XIV for crossing program. Among the investigated characteristics, the number of filled seeds per head, test weight, kernel to hull ratio and seed yield per plant exhibited high contribution towards genetic divergence. The present study indicates that the inclusion of GP-347, GP-1341, 300-B, ARM-244, ARM-248, HAR-5, 853-B, GP-913, GP-507 and GP-831 in future breeding programs could result in the development of superior sunflower cultivars.

Key words: **D^2, genetic divergence, inbreds, multivariate analysis, seed parameters, sunflower**

INTRODUCTION

Selection of parents based on genetic divergence is a prerequisite in a heterosis breeding program. The parents need to be selected from diverse groups so as to generate genetic variability. Since hybrid vigor essentially depends on genetic divergence of parents, it is necessary to identify diverse parents for hybridization. Multivariate analysis by means of Mahalanobis' D^2 statistic has been widely used for assessing the genetic divergence in several crops. It is a powerful tool in quantifying the degree of genetic divergence among parents (Joshi and Singh, 1979; Muppidathi *et al.*, 1995).

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Although this technique has been used frequently in many crop species, few reports are available regarding its application for seed parameters in sunflower. In addition, the studies conducted so far have been mainly based on yield and yield component characters while studies based on seed parameters and seed yield have been limited. Therefore, the present study was initiated to determine genetic divergence based on the seed parameters and seed yield in diverse sunflower genotypes.

MATERIALS AND METHODS

The material for the present investigation consisted of 80 inbred lines and five checks obtained from different sources. The experimental material was raised in randomized block design, replicated twice during summer 2000 at the Directorate of Oilseeds Research, Hyderabad, India. Each genotype was sown in two rows of 4 m length with row to row spacing of 60 cm and plant spacing within the row of 30 cm. The recommended package of practices was followed to raise a good crop. Ten random plants were tagged for recording the observations on characters viz., number of filled seeds per head, number of unfilled seeds per head, total number of seeds per head, test weight (100-seed weight), oil content, hull weight, kernel weight, hull content, kernel to hull ratio, kernel proportion in achene and seed yield per plant. Univariate analysis of variance following Cochran and Cox (1957) and simultaneous test of significance of differences between genotypes using Wilk's lambda criterion (Wilks, 1932) were performed. The genetic diversity existing between the genotypes with respect to the set of characters was estimated using Mahalanobis' D^2 statistic (Mahalanobis, 1936). Treating D^2 as a generalized statistical distance, the criterion used by Tocher (Rao, 1952) was applied for determining the group constellation. The character-wise rank totals have been used to calculate the percent contribution of each character to the total divergence. Average intra- and inter-cluster distances were determined following the method of Singh and Chaudhary (1977).

RESULTS AND DISCUSSION

Univariate analysis of variance showed highly significant differences among the genotypes. The simultaneous testing of significance of difference in mean value between genotypes based on Wilks' lambda criterion revealed highly significant differences (χ^2 = 4465.86 with 924 df) among the genotypes for the aggregate of the 11 characters considered. The 85 genotypes were grouped into 15 clusters (Table 1). The maximum number of genotypes was included in cluster I (43 genotypes) followed by cluster II (11), cluster IV (8), cluster III (7) and cluster VI (6). The other clusters each contained only one genotype. Cluster I included the genotypes from two sources which indicated that there was no association between clustering pattern and eco-geographical distribution of the genotypes. Murthy and Arunachalam

(1966) showed that genetic drift and selection in different environments could cause greater diversity among genotypes than their geographic distances. So, selection of parental material for hybridization simply based on geographic diversity may not be rewarding. Similar observations were reported by Muppidathi *et al.* (1995), Sankarapandian *et al.* (1996) and Teklewold *et al.* (2000) in sunflower.

Table 1: Distribution of 85 sunflower genotypes into different clusters

Cluster	No. of genotypes	Genotype
I	43	GP-371, DRM-13-1, GP-1313, GP-870, GP-999, GP-2154, GP-816, GP-534, GP-2169, GP-627, GP-229, GP-895, CO-4, GP-2200, GP-325, HAM-183, 234-B, GP-1345, GP-897, GP-1219, GP-1806, GP-851, IV-55-NB-4, 852-B, GP-46, X-15-NB-5, 88-8, R-83-R6, R-274, GP-1431, ARM-242, DRM-25-1, GP-2172, R-272-II, GP-961, IB-24, R-272-I, GP-543, ARM-243, GP-2184, DRM-7-2, GP-1053, GP-740
II	11	GP-970, V-55-NB-7, GP-1025, GP-2091, GP-1481, GP-992, GP-557, GP-1038, GP-2030, 1136-1, GP-2166
III	7	GP-1341, GP-2226, GP-400, Acc No-1156, Acc No-1147-1, GP-347, DSH-1
IV	8	GP-452, GP-688, GP-2158, GP-1162, ARM-248, 300-B, ARM-250, ARM-244
V	1	ARM-247
VI	6	HAR-5, Jwalamukhi, KBSH-1, CO-3, LIB-02M-12, GP-1098
VII	1	89-B
VIII	1	853-B
IX	1	GP-1159
X	1	GP-726
XI	1	GP-913
XII	1	GP-507
XIII	1	GP-1717
XIV	1	GP-831
XV	1	DRM-34-1

Though sunflower evolved as an economic crop in Russia, the present material was exclusively of Indian origin, from different sources like Hyderabad and Bangalore. It is likely that the genotypes from different places in the country have some common genes. Since sunflower is an introduced crop to India, the morphological grouping may be helpful for broad classification. The intra- and inter-cluster divergences among the studied genotypes were of varying magnitude (Table 2). The intra-cluster D^2 value was maximum in cluster I (733.33) followed by cluster II (718.24), cluster VI (643.64), cluster IV (579.36) and cluster III (548.94). Clusters V, VII, VIII, IX, X, XI, XII, XIII, XIV and XV had zero inter-cluster distance since they were represented by a single genotype. The maximum inter-cluster distance D^2 was observed between clusters XIII and XIV (12932.24) followed by XI and XIII (11642.41), IX and XIV (10547.29), VI and XIII (10500.10), IX and XI (10401.96), III and XIII (8311.97) and II and XIV (8197.50). Since these clusters have higher

Table 2: Intra= (diagonal) and inter-cluster average D and D^2 values (parenthesis) of 85 sunflower genotypes

Cluster no	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV	XV
I	27.08 (733.33)	38.42 (1476.10)	35.72 (1275.92)	39.26 (1541.35)	35.97 (1293.84)	44.48 (1978.47)	37.00 (1369.00)	46.72 (2182.76)	52.11 (2715.45)	44.33 (1965.15)	59.60 (3552.16)	40.04 (1603.20)	71.27 (5079.41)	65.77 (4325.70)	55.30 (3058.09)
II		26.80 (718.24)	51.32 (2633.74)	39.87 (1589.62)	53.10 (2819.61)	68.70 (4719.70)	41.40 (1713.96)	43.07 (1855.02)	31.97 (1022.08)	36.33 (1319.87)	83.61 (6990.63)	65.71 (4317.80)	54.96 (3020.60)	90.54 (8197.50)	61.66 (3801.96)
III			23.43 (548.94)	43.70 (1909.64)	43.00 (1849.00)	38.65 (1493.82)	57.95 (3358.20)	68.47 (4688.14)	65.37 (4273.24)	65.55 (4296.80)	50.56 (2556.31)	47.21 (2228.78)	91.17 (8311.97)	66.81 (4463.58)	62.78 (3943.84)
IV				24.07 (579.36)	38.39 (1473.80)	56.86 (3233.06)	49.63 (2463.14)	55.05 (3030.50)	40.12 (1609.61)	58.54 (3426.93)	81.65 (6666.72)	67.62 (4572.46)	82.26 (6766.71)	80.83 (6533.49)	72.02 (5186.88)
V					0.00 (0.00)	36.17 (1308.27)	36.01 (1296.72)	47.14 (2225.95)	60.34 (3640.92)	57.62 (3320.06)	61.11 (3734.43)	46.34 (217.40)	86.68 (7513.42)	46.49 (2161.32)	64.56 (4168.00)
VI						25.37 (643.64)	58.01 (3365.16)	71.28 (5080.84)	81.67 (6668.36)	73.47 (5397.84)	39.75 (1580.06)	34.78 (1209.65)	102.47 (10500.10)	40.26 (1620.87)	68.95 (4754.10)
VII							0.00 (0.00)	14.84 (220.23)	49.69 (2469.10)	26.62 (708.62)	73.14 (5349.46)	49.06 (2406.88)	55.22 (3050.35)	64.68 (4183.50)	57.02 (3251.28)
VIII								0.00 (0.00)	47.60 (2265.76)	26.55 (704.90)	86.69 (7515.16)	63.06 (3976.56)	49.64 (2464.13)	77.54 (6012.45)	63.45 (4025.90)
IX									0.00 (0.00)	44.60 (1988.27)	101.99 (10401.96)	82.11 (6742.05)	56.73 (3218.29)	102.70 (10547.29)	76.47 (5847.66)
X										0.00 (0.00)	82.59 (6821.11)	58.05 (3369.80)	30.72 (943.72)	85.38 (7289.74)	56.73 (3218.29)
XI											0.00 (0.00)	30.14 (908.42)	107.90 (11642.41)	45.81 (2098.56)	68.56 (4700.47)
XII												0.00 (0.00)	84.71 (7175.78)	41.90 (1754.77)	57.24 (3276.42)
XIII													0.00 (0.00)	113.72 (12932.24)	74.22 (5508.61)
XIV														0.00 (0.00)	80.05 (6408.00)
XV															0.00 (0.00)

Table 3: Cluster means for 11 characters in 85 sunflower genotypes

Character/ Cluster No.	Total no. of seeds per head	No. of filled seeds per head	No. of un-filled seeds per head	Test weight (g)	Oil percent	Hull weight (mg)	Kernel weight (mg)	Hull content (%)	Kernel to hull ratio	Kernel proportion in achene (%)	Seed yield per plant (g)
I	572.88	444.40	128.47	3.79	32.28	129.71	282.15	31.44	2.25	68.55	15.66
II	517.03	315.59	201.44	4.05	31.47	144.16	290.90	33.38	2.07	66.61	12.37
III	619.39	500.08	119.31	4.82	30.96	205.82	317.85	39.47	1.59	60.48	21.61
IV	395.06	311.15	86.05	5.39	37.84	146.42	427.65	25.48	2.98	74.58	15.72
V	565.62	494.11	71.51	4.15	38.54	90.32	346.53	20.65	3.84	49.35	16.43
VI	700.91	632.81	68.09	4.04	35.91	119.47	304.57	28.32	2.67	71.67	24.35
VII	656.14	469.36	186.77	2.47	38.15	69.44	236.70	22.68	3.40	77.32	11.71
VIII	498.29	338.28	160.01	2.15	40.12	52.49	189.40	21.70	3.61	78.30	7.79
IX	665.65	346.32	319.33	4.92	36.88	142.90	411.73	25.74	2.88	74.25	18.34
X	848.46	515.81	332.64	2.43	30.69	51.14	199.73	28.92	2.45	71.08	11.17
XI	1075.28	878.34	196.94	3.13	25.93	155.23	202.45	43.41	1.30	56.58	24.20
XII	1025.01	797.11	227.90	2.71	27.83	90.05	195.49	31.51	2.17	68.49	22.87
XIII	1032.10	531.76	500.34	2.06	23.29	73.46	154.71	32.22	2.10	67.77	8.51
XIV	948.52	846.92	101.60	2.76	39.50	65.79	260.96	20.13	3.97	79.87	23.43
XV	782.82	444.76	238.05	2.99	26.51	129.39	187.31	40.87	1.45	59.12	8.43

inter-cluster distance among them, crossing between these clusters will result in increased heterosis. The inter-cluster D^2 value was found to be minimum between clusters VII and VIII (220.23) suggesting a close relationship between them and a low degree of diversity among the lines. The magnitude of heterosis largely depends on the degree of genetic diversity among parents and hence selection of lines from these two clusters should be avoided.

The comparison of cluster means for characters under study marked considerable genetic differences between the clusters (Table 3). Cluster XI had higher values for the total number of seeds per head and number of filled seeds per head, cluster VI had the highest values for seed yield per plant and the lowest values for the number of unfilled seeds per head. Cluster IV had the highest values for test weight and kernel weight. Cluster VIII had the highest value for oil content and the lowest value for hull weight. Cluster XIV had the highest values for the kernel to hull ratio and kernel proportion in achene and the lowest value for hull content. Therefore, the contribution of various characters towards the expression of genetic divergence should be taken into account as a criterion for selection of parents for crossing program. The contribution towards genetic divergence indicated that the number of filled seeds per head (39.64%), test weight (31.46%), kernel to hull ratio (8.96%) and seed yield per plant (7.90%) contributed higher to the total genetic divergence in the genotypes of sunflower. For sunflower, Sankarapandian *et al.* (1996) reported that seed yield was an important character contributing to total genetic divergence, whereas Teklewold *et al.* (2000) considered duration of grain filling as the most important trait. It ensues from the present study that genotypes showing greater divergence may be considered for utilization in crossing program, irrespective of geographical considerations. It is worthy to note that in calculating cluster mean the superiority of a particular genotype with respect to a given character could get diluted by other genotypes that are grouped in the same cluster but are inferior or intermediate for the character in question. Hence, apart from selecting genotypes from the clusters which have an increased inter-cluster distance for hybridization, one can also think of selecting parents based on the extent of divergence with respect to a character of interest.

The present study indicates that the inclusion of GP-347, GP-1341 (cluster III), 300-B, ARM-244, aRM-248 (cluster IV), HAR-5 (cluster VI), 853-B (cluster VIII), GP-913 (cluster XI), GP-507 (cluster XII) and GP-831 (cluster XIV) in future breeding programs could result in the development of superior sunflower cultivars.

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DIVERGENCIA GENÉTICA DE PARÁMETROS DE SEMILLA EN GIRASOL (*Helianthus annuus* L.)

RESUMEN

En la Dirección de Investigación de los Cultivos Oleaginosos en Hyderabad (La India) se ha investigado el grado de divergencia genética de 11 propiedades en 85 genotipos de girasol (80 líneas inbred y cinco variedades de control). El análisis de univariación y de multivariación, han mostrado la presencia de las significantes diferencias entre los genotipos investigados. Por el método estadístico de Mahalanobis D^2 se ha determinado la presencia de una divergensidad genética significante. Los genotipos están agrupados en 15 clusters. A base de la distancia entre los clusters y valores medios de clusters para diferentes propiedades, en clusters III, IV, VI, VIII, XI, XII y XIV se han identificado las líneas potencialmente interesantes para los programas de cruzamiento. La mayor contribución a la divergencidad genética, han dado el número de las semillas vertidas por cabeza, masa hectolítrica, la relación entre la semilla descortezada y de la vaina y el rendimiento de semilla por planta. Los resultados de este trabajo, indican que los genotipos GP-347, GP-1341, 300-B, ARM-244, ARM-248, HAR-5, 853-B, GP-913, GP-507 y GP-831 tendrían que ser incluidos en los futuros programas de la mejora genética, con el motivo de creación de las variedades de girasol superiores.

DIVERGENCE GÉNÉTIQUE DES PARAMÈTRES SÉMINAUX DANS LE TOURNESOL

RÉSUMÉ

Le degré de divergence génétique de 11 propriétés dans 85 génotypes de tournesol (80 lignes inbred et cinq variétés de contrôle) a été étudié à la Direction pour la recherche des cultures oléagineuses à Hajderabad (Inde). Les analyses univariable et multivariable ont montré la présence d'importantes différences parmi les génotypes examinés. La méthode statistique Mahalanobis D^2 a établi la présence d'importantes divergences génétiques. Les génotypes étaient groupés en 15 groupes. Selon la distance entre les groupes et les valeurs moyennes des groupes pour différentes caractéristiques, des lignes potentiellement intéressantes pour les programmes de croisements ont été identifiées dans les groupes III, IV, VI, VIII, XI, XII et XIV. La plus grande contribution à la divergence génétique a été donnée par le nombre de graines versées par tête, la masse de 100 litres, le rapport entre les graines écaillées et les écailles et le rendement de graines par plante. Les résultats de ce travail indiquent que les génotypes GP-347, GP-1341, 300-B, ARM-244, ARM-248, HAR-5, 853-B, GP-913, GP-507 et GP-831 devraient être inclus dans les futurs programmes de culture d'espèces supérieures de tournesol.