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ASSESSMENT OF GENETIC DIVERSITY AMONG 51 INBRED SUNFLOWER LINES

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SUMMARY

Genetic divergence of 51 inbreds and 3 checks of sunflower was assessed using the Mahalanobis D^2 statistics. Fifty-one sunflower inbreds plus three checks, GAUSUF-15, TNASUF-7 and TNAU-1, of diverse geographical origin, were grouped into eight clusters which were not related to their geographic origin. Stem girth and seed yield per plant contributed the most to the total genetic divergence. Maximum inter-cluster distance was observed between the inbreds grouped in clusters I and V containing five and twelve inbreds, respectively, while the intra-cluster distance ranged from 0 to 2306.05. Based on mean performance, genetic divergence and clustering pattern, few inbreds namely CMS-234B, 7-1-B, CMS-597B, CMS-852B, ARM-250B, ARM-245B, HAM-69, ARM-284B, ARM-247B and HAM-174 were considered as potentially important for further breeding programs.

Key words: D^2 statistics, genetic divergence, multivariate analysis, sunflower

INTRODUCTION

Genetic diversity plays an important role in plant breeding because hybrids between lines of diverse origin generally display a greater heterosis than those between closely related parents. D^2 analysis is a powerful techniques for measuring genetic divergence. The choice of parents is of paramount importance in any breeding program. Assessment of a large number of inbreds for genetic diversity is of utmost importance. The D^2 statistics enables one to discriminate between different cultivars according to the diversity present (Mahalanobis, 1936). It provides a clearer idea about the diverse nature of populations. Clusters formed according to Tochers method (Rao, 1952) were used to determine the distance between and within clusters. Hail Kefence (1996) grouped 20 accessions of sunflower collected into eight clusters based on Mahalanobis D^2 statistics, while Manjula (1997) carried out Mahalanobis D^2 statistics and classified 46 germplasms of sunflower into 11

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clusters. Of the 14 characters studied, oil content and plant height contributed the most.

MATERIALS AND METHODS

Fifty-one inbreds along with three checks of sunflower of indigenous and exotic origins exhibiting a wide spectrum of variability were evaluated in a RCBD with 2 replications during summer 2000 under irrigated conditions at Regional Research Station, Hebbal, UAS, Bangalore. Each row was three meters long with an inter- and intra-row spacing of 60 and 30 cm, respectively. Observations were taken on five randomly selected plants from each row for 15 traits including plant height, number of leaves per plant, seed test weight, seed density, hull percentage, husk percentage, head diameter, percent autogamy, days to 50 percent flowering, 100-seed weight, percent seed set, seed yield per plant, oil content and oil yield. Genetic divergence of 51 inbreds and 3 checks of sunflower was assessed using the Mahalanobis D^2 statistics.

RESULTS AND DISCUSSION

The analysis of variance indicated the presence of significant differences among the inbreds for all characters. The magnitude of all possible D^2 values between any two inbreds ranged from 29.54 to 6486.32, indicating a high diversity in sunflower inbreds used in the study. All 51 inbreds and three checks were grouped into 8 clusters. Cluster VII had the maximum number of inbreds with 13 inbreds followed by cluster V (12), cluster IV (10), cluster VI (6), cluster I (15), cluster VIII (4), cluster II (3) and cluster III (1) (Table 1).

The inter-cluster D^2 values ranged from 458.86 to 7879.57 between cluster I and V and cluster II and VII, respectively (Table 2). The intra-cluster D^2 values also showed some variability ranging from 0 to 2306.05. The checks in the present study viz., GAUSUF-15, TNAUSUF-7 and KBSH-1 clustered into cluster VIII along with a single inbred ARM-247B.

The inbreds lines in cluster VII exhibited higher diversity with most of the other inbreds in different clusters. Cluster combination with very high inter-cluster D^2 values were combinations of cluster VII with cluster I, II, III, IV, V, VI and VII. Also combinations of cluster II with cluster IV and V had higher inter-cluster D^2 values. The other highly divergent combinations were combination of cluster I with IV, cluster II with VII and cluster III with IV. The other cluster combinations did not exhibit diversity between them and are considered as less divergent cluster combinations. The clusters which were closer to each other may not yield transgressive segregants or high heterosis.

Table 1: Clustering pattern of 51 sunflower inbreds along with checks

Cluster number	Number of entries	Entry number	Inbred line	Origin
I	5	43	RHA-587-II	USA
		13	ARM-246B	India
		16	MR-1	India
		19	HMA-9R	India
		28	RHA-278	France
II	3	15	ARM-243B	India
		18	CMS-351B	USA
		24	CMS-350B	USA
III	1	48	CMS-339B	USA
IV	10	14	CMS-353B	USA
		10	HAM-174B	India
		29	ARM-250B	France
		30	CMS-852B	USA
		31	7-1-B	India
		33	RHA-180	USA
		34	CMS-597	Canada
		42	RHA-272-I	USA
		50	338(C)-BF	USSR
		51	ARM-284B	India
V	12	1	RHA-348	USA
		3	RHA-801	USA
		7	RHA-274-I	USA
		25	RHA-274-II	Australia
		32	CMS-302B	USA
		36	RHA-R-R-I	USA
		37	CMS-234B-I	USA
		39	RHA-MR-I	USA
		40	$86B_3$	France
		41	CMS-851B	USA
		45	RHA-272-II	USA
		46	RR-I	USSR
VI	6	8	ARM-242B	India
		9	CMS-207B	USA
		2	CMS-234B	USA
		17	ARM-245B	India
		23	ARM-248B	India
		26	ARM-249B	India
VII	13	4	CMS-336B	USA
		6	CMS-343B	USA
		11	ARM-244B	India
		12	CMS-850B	USA
		21	CMS-300B	USA
		22	HAM-196	India
		27	CMS-843B	USA
		35	HAM-69	India
		38	CMS-89B	USA
		43	RHA-587-II	USA
		44	CMS-349B	USA
		49	CMS-62B	France
	4	20	ARM-247B	India
		52	GAUSUF-15(C)	India
		53	TNAUSUF-7(C)	India
		54	KBSH-1(C)	India

C-Check

Stem girth (35.85%) and seed yield per plant (29.21%) contributed the most to genetic divergence (Table 3). The contribution from other parameters viz., hull percentage (6.92%), seed test weight (6.22%), plant height (5.24%), percent seed set (3.56%) and husk percentage (3.07%) was considerably less. The contributions of other characters were very negligible (<1%). The contribution of number of leaves per plant, seed density, days to 5 percent flowering and oil yield towards divergence was essentially zero (Figure 1).

Table 2: Average intra- an inter-cluster D^2 values for eight clusters formed with 15 characters in sunflower

Clusters	I	II	III	IV	V	VI	VII	VIII
I	648.51 (26.16)	525.79 (22.93)	702.56 (26.51)	986.73 (31.41)	458.86 (21.42)	765.10 (24.66)	628.87 (26.13)	3025.21 (55.00)
II		375.63 (19.38)	728.68 (26.99)	1223.34 (34.98)	2748.18 (52.42)	698.67 (26.43)	817.40 (28.59)	7879.57 (88.77)
III			0.00 (0.00)	899.71 (30.00)	735.37 (27.12)	791.91 (28.14)	541.12 (23.26)	2277.67 (47.72)
IV				211.32 (14.54)	658.05 (25.65)	707.58 (26.60)	522.26 (22.85)	1343.22 (36.65)
V					1393.35 (37.33)	731.82 (27.05)	529.29 (23.01)	5582.30 (74.71)
VI						788.71 (28.08)	521.51 (22.84)	1723.85 (41.25)
VII							2306.05 (48.02)	1691.09 (41.12)
VIII								1520.52 (38.99)

Diagonal values indicate intra-cluster D^2 values
Above diagonal values indicate inter-cluster D^2 values
Figures in the parenthesis are square roots of D^2 values

Table 3: Degree of contribution of each character towards genetic divergence in sunflower inbreds

No.	Character	Percentage contribution	Rank
1	Plant height	5.24	06
2	No. of leaves per plant	0.00	-
3	Seed test weight	6.22	05
4	Seed density	0.00	-
5	Hull percentage	6.92	04
6	Husk percentage	3.07	07
7	Head diameter	0.14	10
8	Percent autogamy	0.56	09
9	Stem girth	35.85	01
10	Days to 50% flowering	0.00	-
11	100-seed weight	0.77	8
12	Percent seed set	11.88	03
13	Yield per plant	29.21	02
14	Oil content	0.14	11
15	Oil yield	0.00	-

The clusters contained sunflower inbreds of heterogeneous origin coming from different regions of the country. Even the exotic lines were grouped with indigenous materials. This indicated a lack of parallelism between genetic and geographical diversity. Murthy and Arunachalam (1966) showed that genetic drift and selection in different environments could cause greater diversity among the inbreds than their geographical distance. So, selection of parental material for hybridization simply based on geographic diversity may not be successful.

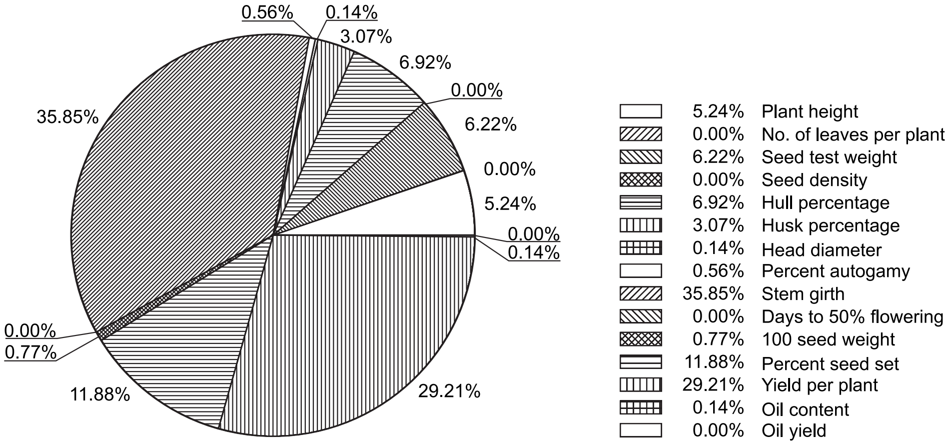

Figure 1: Degree of contribution of each character towards genetics divergence in sunflower inbreds

Intercrossing the inbreds from different clusters may generate large variability and it is expected to introduce high yield and transgressive segregants for population improvement programs. Selection of parents based on the extent of genetic divergence has been successfully done by earlier workers on others crops (Mishra *et al.*, 1987).

Any success through hybridization followed by selection depends primarily on the selection of parents having high genetic variability for different characters. While choosing the inbreds as parents for hybridization for heterosis breeding, the *per se* performance of inbreds with higher D^2 values should be taken into consideration in addition to maximum inter-cluster distance among the inbreds. If the mean *per se* performance of two inbreds is too low with less genetic divergence, such pair is not likely to produce very high yielding segregants or heterotic effects of an exceptionally high order to be of any practical value. Hence, the other method of identifying the ideal parental combinations could be to pick the inbreds with high yielding ability along with most desirable characters and observe all possible D^2 values among them and select the pair which has moderate to high D^2 value.

The inbreds CMS-234B, 7-1-B, CMS-597B, CMS-852B, ARM-245B, ARM-250B, HAM-69, ARM-284B, ARM-247B and HAM-174 are high yielding inbreds. In addition, they also had other desirable agronomic traits such as high seed test weight, medium thickness of the stem, high 100-seed weight, high percentage of seed set, and high percentage of oil content. Close look at the D^2 value combinations of these inbreds showed that combinations involving the inbreds ARM-245B with either

HAM-174 or CMS-852B, ARM-247B with CMS-234B, HAM-174 or CMS-852B, ARM-247B with CMS-234b, HAM-69 or 7-1-B, HAM-174 with 7-1-B or CMS-597B were the most divergent crosses.

The *per se* performance of the inbreds 7-1-B and CMS-597B in terms of yield was good which yielded about 49.90 and 47.76 g per plant, respectively. They also had other desirable traits like high percent autogamy, medium thickness of the stem, moderately high oil content. They also had certain undesirable traits like late flowering and medium percentage of hull. The diverse inbreds which can complement the lacunae of these inbreds, in addition to being moderately high yielder was the inbred HAM-174 which was early flowering and had the highest percentage of hull. The inbred HAM-69 could be advantageous in terms of larger head diameter, short duration and high percent seed set. ARM-284b had the highest seed test volume weight. Oil content was highest in the inbred ARM-245B, but it was very late in flowering. These desirable and divergent inbreds could be converted into CMS lines for future use in a heterosis breeding program.

CONCLUSION

The inbred lines CMS-234B, 7-1-B, CMS-597B, ARM-245B, ARM-250B, HAM-69, ARM-284B, ARM-247B and HAM-174 were high yielding. D^2 value combinations of these inbreds showed that the combinations involving the inbreds ARM-245B x HAM-174, ARM-245B x CMS-852B, ARM-247B x CMS-234B, ARM-247B x 7-1-B, HAM-174 x 7-1-B and HAM-174 x 597B were the most divergent crosses.

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EVALUACIÓN DE LAS DIVERGENCIAS GENÉTICAS DE LAS 51 LÍNEAS GONSANGUÍNEAS DE GIRASOL

RESUMEN

Mediante el método estadístico de Mahalanobis D^2, en el estudio se ha evaluado la divergencia genética de 51 consanguíneas y tres líneas control de girasol. Tres genotipos de control (GAUSUF-15, TNASUF-7 y TNAU-1) y 51 líneas consanguíneas de diferentes orígenes geográficos, se agruparon en ocho clusters, independientemente del origen. La mayor contribución a la total divergencia genética, han dado la circunferencia del tallo y el rendimiento de semilla por planta. La mayor distancia se ha notado entre los clusters I (cinco líneas) y V (12 líneas). La distancia entre clusters varía entre 0 y 2306,05. El rendimiento máximo obtenido, la divergencia genética y la fórmula de agrupamiento en clusters, han mostrado que varias líneas consanguíneas investigadas (CMS-234B, 7-1-B, CMS-597B, CMS-852B, ARM-250B, ARM-245B, HAM-69, ARM-284B, ARM-247B, y HAM-174) pueden considerarse potencialmente importantes para los futuros programas de mejoramiento genético.

ÉVALUATION DE LA DIVERSITÉ GÉNÉTIQUE DE 51 LIGNES INBRED DE TOURNESOL

RÉSUMÉ

La diversité génétique de 51 lignes *inbred* et de trois lignes de contrôle de tournesol a été évaluée par la méthode statistique Mahalanobis D^2. Cinquante et une lignes *inbred* et trois génotypes de contrôle (GAUSUF-15, TNASUF-7 et TNAU-1) d'origines géographiques différentes ont été groupées en huit *clusters* indépendamment de leur origine. La plus grande contribution à la diversité génétique a été donnée par la circonférence de la tige et le rendement en semences par plante. La plus grande diversité a été observée entre les lignes *inbred clusters* I (cinq lignes) et V (douze lignes). La distance entre les *clusters* variait entre 0 et 2306.05. Les performances moyennes obtenues, la diversité génétique et le mode de groupement *clusters* ont démontré que certaines lignes *inbred* (CMS-234B, 7-1-B, CMS-597-B, CMS-852B, ARM-250B, ARM-245B, HAM-69, ARM-284B, ARM-247B et HAM-174) pouvaient être considérées comme potentiellement importantes pour de futurs programmes de culture.