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EVALUATION OF SUNFLOWER GENOTYPES FOR CONFECTIONERY PURPOSE

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SUMMARY

Fifty-two germplasm accessions of sunflower were evaluated for use as confectionery types. Analysis of variance revealed significant differences among the genotypes for all the characters. The estimates of genotypic and phenotypic coefficients of variability were high for seed yield per plant, percent husk, head diameter and number of filled seeds per plant. High heritability estimates were observed for days to 50 percent flowering, number of leaves per plant, percent husk and seed oil content. Genetic advance was high for number of filled seeds per plant, seed filling percent and percent husk. The accessions SG-1142, SG-1262, SG-1266, SG-1419, SG-1501, SG-1505, SG-1601, SG-433, SG-354 and SG-914 have been identified as promising confectionery type sunflower based on the attributes such as low seed oil content, low husk percent, high 100-seed weight, high 100-kernel weight and high seed yield.

Key words: Sunflower, evaluation, confectionery type

INTRODUCTION

Confectionery type of sunflower is largely grown in North America, South Dakota, California, Texas and Canadian Provinces (Lofgren, 1978). It has been established that sunflower oil containing 83 percent monounsaturated fatty acids and 7 percent polyunsaturated fatty acids is five times more resistant to oxidation than sunflower oil containing 18 percent monounsaturated fatty acids and 69 percent polyunsaturated fatty acids. Confectionery sunflowers are dehulled, roasted and sold as peanut substitutes to be consumed as snack item. Salted kernels with or without roasting are used in a variety of bakery products, salads, candies and some dishes. Such low oilseed types are supposed to be large in size with easily separable thin husk and low in fat content. Endeavors to evolve such cultivars primarily depends on the extent of variability for such traits. Hence, the present study was undertaken.

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MATERIALS AND METHODS

The material used for the present study consisting of 52 diverse sunflower genotypes was procured from Italy, Hungary, Zambia, Yugoslavia, USSR, Ethiopia, Turkey, USA, Bulgaria and Urugway. The list of the genotypes is furnished in Table 3. Each genotype was grown in three rows each of three metres length by dibbling two seeds per hill to maintain a spacing of 60 cm between rows and 30 cm between the plants. After the germination only one healthy seedling was retained per hill. The experiment was laid out in a randomized block design with three replications during kharif 1996 at Gandhi Krishi Vignana Kendra, University of Agricultural Sciences, Bangalore. The experiment site is located at the latitude and longitude of 12° 58' N and 77° 35' E, respectively, and has an altitude of 930 m above the mean sea level. The soil is of laterite type. Observations were recorded on five randomly selected competing plants of each genotype for days to 50 percent flowering, plant height (cm), number of leaves per plant, head diameter, number of filled seeds per plant, seed filling percent, seed yield per plant (g), husk percent, 100-seed weight (g), 100-kernel weight (g) and seed oil content.

Mean values of five randomly by selected plants was used for statistical analysis. Analysis of variance was carried out as suggested by Panse and Sukhatme (1985). The components of variance namely, phenotypic (σp^2) and genotypic (σg^2) variance, were used to estimate phenotypic and genotypic coefficient of variation as per the method suggested by Burton and Devane (1953).

$$\text{Genotypic coefficient of variation (PCV)} = \frac{\sigma g^2}{\bar{X}} \times 100$$

$$\text{Phenotypic coefficient of variation (PCV)} = \frac{\sigma p^2}{\bar{X}} \times 100$$

where X = population mean.

Heritability was estimated using the following formula,

$$h^2 = \frac{\sigma g^2}{\sigma p^2} \times 100$$

Genetic advance was estimated as per the formula suggested by Johnson *et al.* (1955).

$$\text{Genetic advance} = h^2 \cdot K \cdot \sigma p$$

where h^2 = heritability, K = constant, σp = standard phenotypic deviation.

RESULTS AND DISCUSSION

Analysis of variance (Table 1) indicated significant differences among the genotypes tested for all the traits. This has also been reflected on the range (Table 2) of the mean performance of the genotypes for all the characters. Thus there is substantial variability in the germplasm which could be utilized in selection of geno-

Table 1: Analysis of variance for 11 quantitative traits in sunflower

Source of d.f. variation	d.f.	Plant height	Days to 50% flowering	No. of leaves/ plant	Head diameter	Seed yield/ plant	No. of filled seeds/plant	Seed filling percent	100-seed weight	100-kernel weight	Percent husk	Seed oil content
Genotype	51	629.8235**	30.7813**	55.4825**	10.8608**	114.9216**	56411.76**	107.919**	1.248**	0.6253**	199.3623**	29.4347**
Replication	2	377.625	3.1563	216.4063	2.2725	69.123	6163.00	1.9375	0.8864	0.1819	37.4141	1.4688
Error	102	128.0882	0.8857	8.0836	3.2323	24.8872*	10294.12	33.9216	0.3348	0.1598	19.4506	2.0715
C.V. %		12.4487	1.6528	55.4825	16.6500	25.0889	23.50	6.6221	13.1232	12.3080	17.1370	4.8078

Note = ** Significant at 1 percent

Table 2: Range, mean, genotypic and phenotypic coefficient of variability, heritability, genetic advance for eleven characters in 52 genotypes of sunflower

Character	Range		Mean	Coefficient of variability		Heritability (broad sense)	Genetic advance as % mean
	Maximum	Minimum		Phenotypic	Genotypic		
Plant height (cm)	62.10	124.00	90.90	18.90	14.22	56.62	17.72
Days to 50 percent flowering	49.00	62.00	56.94	5.78	5.54	91.83	17.28
Number of leaves/plant	17.01	34.33	24.51	19.93	16.21	66.15	18.74
Head diameter (cm)	14.70	16.63	10.79	22.25	14.76	44.03	27.33
Seed yield per plant (g)	7.13	40.26	19.88	37.26	27.55	54.66	22.04
Number of filled seeds per plant	163.66	818.01	431.67	37.11	28.72	59.89	45.79
Seed filling (%)	58.55	95.24	87.95	8.70	5.64	42.10	41.95
100-seed weight (g)	2.93	5.76	4.40	18.13	12.51	47.63	7.53
100-kernel weight (g)	2.52	4.16	3.24	17.27	12.12	49.25	20.11
Percent husk (%)	8.31	43.28	25.73	34.62	30.09	75.50	53.86
Seed oil content (%)	22.05	36.75	29.93	11.17	10.08	81.49	10.94

types for confectionery types. The partitioning of the total variability into genotypic and environmental variance revealed major contribution of genotypic variability to the total variability for the traits which are especially characteristic features of the confectionery type such as 100-seed weight, 100-kernel weight, percent husk and seed oil content. In addition to these traits, days to 50 percent flowering also seemed not to be much influenced by the environment. These results suggested that the significant differences among the 52 genotypes were largely due to genotypic differences. Further it was interesting to note that these traits also exibited medium to high heritability coupled with medium to high predicted genetic advance. Jayaramegowda (1994), Hebura (1958), Suma (1993) and Laxmanaiah (1978) reported high heritability for oil content. Furthermore, the genotypes SG-1142, SG-1262, SG-1266, SG-1419, SG-1501, SG-1601, SG-433, SG-354 and SG-914 have been identified as promising confectionery type sunflowers based on the attributes such as low seed oil content, low husk percent, high 100-seed weight, high 100-kernel weight and high seed yield. Kovačik et al. (1993) reported that Hungarian hybrid Toma with large achenes was the only culinary cultivar suitable for cultivation in the Czech Republic.

Table 3: List of the genotypes used in the study

1.	SG-246	27.	SG-1168-1
2.	SG-377-1	28.	SG-1174
3.	SG-433	29.	SG-1187-1
4.	SG-1281	30.	SG-1197-2
5.	SG-1291	31.	SG-1254
6.	SG-1279-1	32.	SG-1485
7.	SG-1271-1	33.	SG-1486
8.	SG-1266	34.	SG-1505
9.	SG-1265	35.	SG-1504
10.	SG-1263	36.	SG-1501
11.	SG-1262	37.	SG-1540
12.	SG-1258	38.	SG-1870
13.	SG-1261	39.	SG-1582
14.	SG-1376	40.	SG-1601
15.	SG-1419	41.	SG-1401
16.	SG-1426	42.	SG-1424
17.	SG-892	43.	SG-1224
18.	SG-914	44.	SG-1583
19.	SG-912	45.	SG-AR21
20.	SG-1142	46.	RHA-359
21.	SG-1039	47.	SG-3998
22.	SG-916	48.	SG-3538
23.	SG-1139	49.	KBSH-1
24.	SG-1135	50.	Morden
25.	SG-1149	51.	EC-68415
26.	SG-1153-1	52.	EC-68414

From these results it is evident that selection of genotypes with high 100-seed weight, high kernel weight, low husk percent and low oil content would be effective.

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LA EVALUACIÓN DE GENOTIPOS PARA USO DIRECTO COMO

RESUMEN

Se evaluaron 52 accesiones de germoplásma de girasol para su uso directo como semilla. El análisis de varianza mostró diferencias significativas entre los genotipos para todos los carácteres. Los valores de los coeficientes de variabilidad de los fenotipos y genotipos fueron altos para los carácteres de producción de semillas, porcentaje de la cáscara, el diámetro del capítulo y el número de semillas llenas por planta. Se observaron elevadas estimaciones de herediabilidad para los carácteres: días hasta 50% de floración, número de hojas por planta, porcentaje de cáscara, y contenido de aceite en la semilla; el avance genético fue considerable para los carácteres: número de semillas llenas por planta, porcentaje de semillas llenas y de la cáscara. Las accesiones de germoplasma SG-1142, SG-1262, SG-1266, SG-1419, SG-1501, SG-1505, SG-1601, SG-433, SG-354 y SG-914 han sido identificadas como tipo para girasol prometedores por lo que se refiere a su uso como artículo de uso directo basándose en atributos como: bajo contenido en aceite, bajo porcentaje de cáscara, alto peso de 100 pipas, alto peso de 100 frutos, y una elevada producción de semillas.

EVALUATION DE GÉNOTYPES DE TOURNESOL DE BOUCHE

RÉSUMÉ

52 numéros de germplasm de tournesol ont été évalués pour une utilisation de type tournesol de bouche, l'analyse de variance révèle pour tous les caractères des différences significatives entre génotypes. Les valeurs des coefficients de variation phénotypique et génotypique sont élevées pou les caractéristiques de rendement en graines, de pourcentage en coques, de diamètre du capitule et du nombre de graines pleines par plante. Des estimations d'héritabilité élevée sont détectées pour les caractères, nombre de jours pour 50% de floraison, nombre de feuilles par plante, pour-cent de coque et teneur en huile; le progrès génétique est élevé pour le nombre de grains pleins par plante, le pourcentage de grains pleins et le pourcentage de coque. Les numéros de germplasm SG-1142, SG-1262, SG-1266, SG-1419, SG-1501, SG-1505, SG-1601, SG-433, SG-354 et SG-914 sont identifiés comme des tournesols de bouche prometteurs, sur la base de critères tels que la faible teneur en huile, la faible teneur en coque, le poids de 1000 grains élevé, le poids élevé de 1000 amandes ou le rendement élevé.