Genetic Evaluation and Characterization of Sunflower (*Helianthus annuus* L.) Genotypes as per DUS Guidelines

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Sixty-seven genotypes of sunflower were evaluated for yield and yield components to study the extent of variation for different quantitative traits. Analysis of variance revealed significant differences among the genotypes for all the quantitative traits. High heritability coupled with low genetic advance was recorded in respect of days to initiation of disk floret opening (96.3%), complete anthesis (92.2%) and days to maturity (84.6%). High heritability coupled with high genetic advance was observed for 1000 seed weight (88.2 and 55.06) and seed yield g/plant (73.7 and 59.1). Large head size was observed for P62R, P64R, P74R, P81R and NDR-2. Nineteen lines had high self-fertility exceeding 94.0%. Bold seeds (1000 seed weight >80 g) was the characteristic feature of P72R. The lines *viz*. P63R, P64R and P86R were found to be promising for developing short duration hybrids.

Key Words: Characterization, Genetic evaluation, Heritability, Phenotypic and genotypic Coefficients of variation

Introduction

Sunflower is one of the important edible oilseed crops of the world. The crop is spreading to diverse agroclimatic conditions and shows adaptability to all types of soils, which necessitates the development of more productive hybrids of diverse duration. Success of plant breeding, depends upon the nature and magnitude of variability present in the germplasm. Further more, the assessment of heritable and nonheritable components of total variability will have immense value in the choice of suitable breeding procedure. Characterization of germplasm is useful to identify suitable lines and also to avoid duplication. Qualitative characters being more stable over generations and environments are reliable for characterization of germplasm. Hence, the present study was planned to genetically evaluate the available germplasm for yield and related attributes. Attempt has also been made to identify some promising genotypes for use in sunflower breeding programme.

Material and Methods

The material for the present study comprised of 67 (55 restorers and 12 maintainers) genotypes of sunflower. The experiment was conducted at Punjab Agricultural University, Ludhiana, over two years during spring 2006 and 2007. The material was grown in a randomized block design with three replications. Each plot consisted of a single row of 4.5 m length with row to row spacing of 60 cm and plant to plant spacing of 30 cm. Recommended cultural practices were followed to raise the crop. The data were recorded in each genotype for days to initiation of disk floret opening (number of days from sowing to the date when one plant in a line showed disc floret opening), complete anthesis (when all the plants in the lines flowered), days to physiological maturity (when the back side of the heads turned yellowish brown) and on five plants for head diameter, plant height, autogamy (%), 1000 seed weight, seed yield/plant and oil content (%), in both the years. The overall means were calculated and used for statistical analysis. The phenotypic and genotypic coefficients of variation (PCV and GCV) were computed and classified as suggested by Burton and Dewana (1953), heritability (h^2) as per Hanson *et al.* (1956) and expected genetic advance (GA) as suggested by Johnson *et al.* (1995). The genotypes were characterized for 27 distinguishing morphological characters as per guidelines (Anonymous, 2009)

Results and Discussion

Analysis of variance revealed highly significant differences amongst genotypes for all the traits (Table1). The study has also revealed that the genotypes performed differently in two environments for 1000-seed weight, autogamy (%), plant height and head diameter. For these characters, genotype environment interaction was also observed to be significant. Different parameters *i.e.*, range, mean, phenotypic and genotypic coefficients of variance, heritability estimates and predicted genetic advance for the quantitative traits are presented in Table 2. The PCV and GCV was found to be the highest

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Table 1. Analysis of variance for nine quantitative characters in 67 genotypes of sunflower (Pooled over environments)

		Mean Squares								
Source of Variation	d.f.	Initiation of disk floret opening (days)	Complete anthesis (days)	Physiological maturity (days)	Head diameter (cm)	Plant height (cm)	Autogamy (%)	1000 seed weight (g)	Seed yield (g/pl)	Oil content (%)
Rep. (within Env.)	4	4.9	2.6	3.7	21.4**	180.8**	7.2	3.0	112.5	0.8
Genotypes	66	29.5**	30.1**	33.9**	45.5**	1635. 8**	84.2**	1218.1**	414.9**	97.9
Environment	1	37.0**	5.9	2.9	59.3**	10100.0**	573.5**	3746.2	58.0	547.7**
Genotype × Environment	66	1.1	2.3	5.2	7.2**	130.8**	48.6**	139.8**	109.0	32.3
Error	264	1.8	2.4	4.1	2.9	40.7	3.3	4.4	109.9	2.8

* Significant at 5% level.
** Significant at 1% level.

Table 2. Mean, Range and components of variability for nine quantitative traits in 67 genotypes of sunflower

Character	Mean ± SE	Range	PCV%	GCV%	h^2	GA
Initiation of disk floretopening (days)	61.1 ± 0.5	52.0–70.2	3.6	3.6	96.3	7.2
Complete anthesis(days)	66.9 ± 0.6	58.2–73.4	3.3	3.2	92.2	6.3
Physiological maturity (days)	90.6 ± 0.8	83.8–95.2	2.6	2.4	84.6	4.5
Head diameter (cm)	13.7 ± 0.8	7.9–19.2	20.1	18.4	84.3	34.3
Plant height (cm)	117.8 ± 3.1	77.8–151.7	14.0	13.4	92.0	26.5
Autogamy (%)	91.7 ± 1.4	80.3–95.9	4.8	0.0	42.3	3.5
1000 seed weight(g)	46.7 ± 2.3	21.8–89.3	30.5	28.7	88.3	55.6
Seed yield (g/plant)	21.4 ± 4.3	10.3–50.6	38.9	33.4	73.7	59.1
Oil content (%)	33.0 ± 1.2	22.3–42.8	12.2	10.0	67.0	16.9

PCV = Phenotypic coefficient of variance; GCV = Genotypic coefficient of variance; h^2 = heritability; GA = Genetic advance.

for seed yield/plant (38.9% and 33.4%) followed by 1000-seed weight (30.5% and 28.7%) and head diameter (20.1 and 18.5). This indicated presence of more variability which gives scope for improvement of these traits by selection. The high PCV and GCV observed for these traits is in conformation with earlier reports of Reddy and Reddy (2006). Moderate PCV and GCV were observed for plant height (14.0% and 13.4%) and oil content (12.2% and 10.0%). Very low variability was recorded for days to flowering, days to maturity and autogamy (%) thereby emphasizing the need for generating more variability with respect to these characters so that the germplasm lines having diverse maturity period could be effectively utilized in synthesizeding hybrids having different maturity duration.

High heritability was recorded for days of initiation of disk floret opening (96.3%), complete anthesis (92.2%) and days to maturity (84.6%), but these traits exhibited low genetic advance. High heritability coupled with high genetic advance was observed for 1000-seed weight (88.2 and 55.6) and seed yield (g/plant) (73.7 and 59.1), suggesting better scope for improvement of these characters through direct selection. Similar results have been reported by Reddy and Reddy (2006), Gangappa (1991) and Jayaramaiah *et al.* (1994). Moderate heritability with low genetic advance (67.01 and 16.89) was recorded for oil content. Low heritability (42.2) was observed for autogamy (%) along with very low genetic advance (3.5) which shows the greater influence of environment in the expression of these characters. On the contrary, Reddy and Reddy (2006) observed high heritability along with high genetic advance for these traits.

The characterization of genotypes revealed wide variation for all the qualitative characters among the genotypes. Earlier reports by Virupakshappa and Sindagi (1987) and Reddy and Reddy (2006) have also shown the presence of variation for these qualitative traits in sunflower accessions. Distinguishing characters of different genotypes are given in Table 3. Promising lines with desirable traits were identified as presented in Table 4. The genotype *viz*. P63R, P64R, P86R being early maturing were found to be promising for developing short duration hybrids. The genotypes P86R, P68R, P74R, P69R were dwarf with plant height of less than 100 cm. Large head size (>15 cm) was observed for P62R, P64R, P81R, P74R, P69R, NDR-2. A total of 19 genotypes were found to be having more than 94% self fertility. Bold seed (1000-seed weight >80.0 g) was the characteristic

Table 3. Distinguishing morphological characters of the genotypes

Character	Category	Genotype
Hypocotyle: Anthocyanin Coloration	Absent	P68R, SF-7R, NDR-2, CMS-44B, CMS-32B
Leaf size	Very Large	PISF-9R, RHA-856, PISF-3R, 179-2RP2, 12B
Leaf: colour	Light green	P84R, P81R, P69R
	Dark green	P62R, P64R, P83R, RCR8297
Leaf: blistering	Absent	P86R, P65R, P68R, P67R, P63R, P73R, PISF-12R, RHA83R6, PISF-18, LTRR-341, CMS-7-1B, CMS-10B, P69R
	Strong	P81R, P78R, P88R, P70R, P66R, P72R, RHA-297, RHA-265, R-801, RHA-17, LTRR-1822, RHA-859, 179-2RP2, CMS-18B, CMS-44B, CMS-12B, CMS-395, CMS-234B.
Leaf: fineness ofSerration	Fine	P88R, P72R, RHA-856, LTRR-1822, 32B, 207B.
	Acute	P69R
Leaf: angleof lateral veins	Right angle	PISF-9R, R273, 32B, RCR-8297
	Obtuse	P65R, P83R, P74R, P75R, 44B, 234B.
Leaf: hairiness	Dense	P64R, P84R, P83R, P73R, RHA-271, PISF-3R, PISF-IR, R-801, 1147-4, PISF-13R, 32B
Stem: pigmentation	Absent	P62R, P87R, P84R, P68R, P78R, P74R, P67R, P72R, RHA-297, P69R, SF-7R, RHA-265, PISF-9R, PISF-12R, PISF-18R, P35R, PISF-3R, R-272-IP9, NDR-2, RHA-17, LTRR-1822, 1147–4, SF-4R, PISF-13R, SF-1R, 179-2RP2, CMS-18B, CMS31B, CMS-44B, CMS7-1B, CMS-32B, CMS853B, CMS-10B, CMS-395B, CMS-234B, CMS207B.
	Strong	P86R, P83R, P70R, R-17, RHA-296, LTRR-341, RR-1, MR-6, RHA-85, RCR8297
Stem: flower: shape	Ovoid	P78R, P71R
Ray flower: colour	Orange	CMS-32B
Disk flower: Anthocyanin Coloration of stigma	Absent	P62R, P87R, P68R, P74R, P66R, P67R, P71R, P63R, P82R, P72R, RHA-297, P69R, SF-7R, RHA-265, RHA-856, RHA-271, PISF-1R, NDR-2, RHA-214, CMS-31B, CMS-7-1B, CMS-304B, CMS-32B, CMS-12B, CMS-853B, CMS-10B, CMS-395B, CMS-207B
Disk flower pollen Colour	White	MR-6
Bract: shape	Rounded	P68R, P78R, P70R, PISF-9R, PISF-12R, PISF-3R, P61R, P-801-RHA-17, 1147–4, 179-2RP2, 188, 31B, 853b, RCR-8297
Head: shape of grain side	Flat	395B, 234B, RCR8297
Plant: branching	Present	P86R, P68R, P70R, P72R, RHA-297, R-17, P69R, SF-7R, RHA-271RHA-296, P61R, PISF-1R, RCR-8297, R273, R-802, LTRR-1822, RR-1, MR-6, PISF-13, 395B

Table 4. Promising genotypes for different characters

Days to flowering	< 60	P86R
Days of maturity	< 90	P64R, P86R, P63R, R-17, RHA-856, RHA-296, PISF-1R, R-801
Plant height (cm)	< 100	P86R, P68R, P74R, P69R, RHA-83R6
Head diameter (cm)	> 15	P62R, P64R, P81R, P74R, P69R, RHA-83R6, R-801, NDR-2
Autogamy (%)	> 94	P87R, P65R, P83R, P81R, P88R, P66R, P75R, P71R, RHA-297, RHA-256, NDR-2, RHA-214,234B, 853B, 12B, 7-1B, 44B, 18B, RHA-859
1000-Seed weight (g)	> 60.0	P64R, P83R, P66R, P82R, PISF-3R, 179-2RP2, 12B, 853B, P69R
	> 80.0	P72R
Seed yield (g/plant)	> 30	P62R, P78R, PISF-18R, NDR-2
	> 40	PISF-9R, PISF-3R, 1147–4, 234B
Oil content (%)	> 37	P65R, RHA-271, PISF-1R, 234B

feature of P72R. For seed yield P62R, P78R, PISF-18R and NDR-2 had more than 31g seed yield/plant while PISF-9R, PISF3R, 1147-4 and 234 recorded more than >40 g seed yield/plant. Oil content was recorded to be high (>37%) for P65R, RHA271, PISF-1R, while 234B recorded the highest oil content of 42.8%.

The study revealed sufficient genetic variability both for quantitative and morphological characters among the genotypes, which can be exploited for developing superior hybrids. Different accessions have different promising traits. Therefore, a gene pool can be generated by crossing the germplasm lines of interest which can be further used as a source material to develop promising inbreds.

References

Anonymous (2009) Guidelines for the conduct of test for distinctiveness, uniformity and stability (DUS) on Sunflower. *Plant Variety J. India* **3(10)**.

Burton GW and EM Dewane (1953) Estimating heritability in tall fescue (*Festuca circulinaccae*) from replicated clonal material. *Agrono. J.* **45:** 478–481.

Gangappa E (1991) Evaluation of sunflower germplasm lines. *Crop Sci.* **15:** 77–78.

Jayaramaiah H, Virupakshappa K, Jayarame Gowda and Nagaraju (1994) Germplasm utilization and enhancement in sunflower. In: MVR Prasad *et al.* (eds) *Sustainability in Oilseeds*. Indian Society of Oilseeds Research, Hyderabad, pp 113–115.

Hanson GH, HF Robinson and RE Comstock (1956) Biometrical studies of yield in segregating population of Korean lespedeza, *Agron. J*. **48:** 267–282.

Johnson HW, HF Robinson and RE Comstock (1955) Estimates of genetic and environmental variability in soybean. *Agron. J*. **47:** 314–318.

Reddy A Vishnuvardhan and R Nagaraja Reddy (2006) Evaluation and characterization of sunflower, *Helianthus annuus L*. germplasm accessions. *J. Oilseeds Res*. **23:** 161–164.

Virupakshappa K and SS Sindagi (1987) Characterization, evaluation and utilization of sunflower germplasm accessions. Catalogue, Unit of the Project Coordinator, (Sunflower) GKVK, Bangalore.