

Genetic variability, heritability and genetic advance studies for economically important traits in sunflower (*Helianthus annuus* L.)

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(Received: October 24, 2020; Revised: March 20, 2021; Accepted: March 22, 2021)

ABSTRACT

The present investigation was carried out to study genetic parameters for eight different traits viz., days to 50 per cent flowering, days to maturity, plant height, head diameter, 100 seed weight, volume weight, seed yield/plot and oil content at ICAR-Indian Institute of Oilseeds Research during *rabi* 2019-2020. The study included a total of 67 genotypes including 5 CMS lines and 10 newly developed restorer lines and their 50 F₁ hybrids along with two checks (KBSH-44 and DRS-1). Analysis of variance revealed significant differences for all the traits. High variation was observed for plant height and seed yield/plant and lowest was observed for 100 seed weight, oil content and head diameter. The difference between GCV and PCV was low for all the characters indicating less influence of environmental factors on the expression of these traits. High heritability with high genetic advance was observed for plant height, head diameter, 100 seed weight and seed yield/plant indicating additive gene action in the expression of these traits. Simple phenotypic selection may be effective for improving these characters. High heritability coupled with low genetic advance was observed for oil content suggesting involvement of non-additive gene action in the expression of this trait indicating little scope for further improvement through individual plant selection.

Keywords: Genetic advance, GCV, Heritability, PCV, Sunflower

Oilseed crops occupy a prime position in agricultural economy after food grains, and among them sunflower (*Helianthus annuus* L.) is one of the prominent oilseed crop grown in world as well as in India. It is the fourth most important oilseed crop next to soybean, groundnut and rapeseed (Shamshad *et al.*, 2016; Yamgar *et al.*, 2018) which is originated from North America. The crop has much importance especially for its oil content due to presence of high concentration of polyunsaturated fatty acids (PUFA) with 55 to 60% of linoleic acid and 25 to 30% of oleic acid, which reduces the risk of coronary diseases by reducing blood cholesterol levels (Joksimovic *et al.*, 2006). In India, sunflower is cultivated over an area of 2.5 lakh ha with a production of 2.2 lakh tonnes and productivity of 886 kg/ha (Directorate of Economics and Statistics, 2018-19). The requirement of high yield and quality edible oil is raising day by day and therefore, there is a need to increase the area, production and productivity of the crop which is possible through crop improvement strategies. Success of any crop improvement programme depends upon the genetic variability present in the material. Sometimes phenotypic selection based on their performance may not be sufficient because these genotypes may perform poor in further segregating generations, so it is essential to select the genotypes based on genetic worth of the genotypes i.e., based

on heritability and genetic advance (Hamouda *et al.*, 2016). Genetic variability along with heritability estimates would provide the amount of genetic gain expected out of selection (Burton, 1952; Swarup and Chaugle, 1962). Information on variability and heritability is useful to formulate selection criteria for improvement of seed yield and its component traits. Heritability estimates along with genetic advance are normally more helpful in predicting the gain under selection than heritability estimates alone (Paul *et al.*, 2006). So, taking all these aspects into consideration, the present study was conducted to evaluate the extent of genetic variability, heritability and genetic advance over mean for seed yield and its component traits in sunflower.

The present investigation was carried out during *rabi*, 2019-20 at ICAR-Indian Institute of Oilseeds Research, Rajendranagar, Hyderabad. Study material consisted of 67 genotypes (Table 1). Each genotype was sown in two rows of 3.0 m length following a spacing of 60 cm between the rows and 30 cm between the plants in randomised block design (RBD) with three replications. Standard agronomic practices were performed uniformly for all the experimental units. At maturity five plants from each accession were selected randomly for recording data on days to 50% flowering, days to maturity, plant height (cm), head diameter (cm), 100 seed weight (g), volume weight (g/100 ml), seed yield/plant (g) and oil content (%). Mean performance of the genotypes were calculated and the genotypic coefficient (GCV) and phenotypic coefficient of variation (PCV) was estimated by using the formula given by Burton (1952). The estimates of PCV and GCV were classified as low (0-10%),

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moderate (10-20%) and high (>20%) according to Sivasubramanian and Madhavamenon (1973). Heritability in broad sense ($h^2 b$) was estimated according to the formula

suggested by (Johnson *et al.*, 1955) and (Hanson *et al.*, 1956). Estimation of genetic advance was done following the formula given by Johnson *et al.*, (1955) and Allard (1960).

Table 1 List of genotypes used in the present study in sunflower

S. No.	Experimental Material	Source
CMS Lines (Lines)		
1.	CMS-234A	UAS, GKVK, Bengaluru
2.	ARM-243A	ICAR-IIOR, Hyderabad
3.	CMS-335A	UAS, GKVK, Bengaluru
4.	HA-430A	ICAR-IIOR, Hyderabad
5.	CMS-1010A	ICAR-IIOR, Hyderabad
Testers		
6.	PM-81	UAS, Raichur
7.	RHA-6D1	ICAR-IIOR, Hyderabad
8.	RGP-21-P2-S2	ICAR-IIOR, Hyderabad
9.	RGP-28	ICAR-IIOR, Hyderabad
10.	RGP-30-P3-S1	ICAR-IIOR, Hyderabad
11.	RGP-46-P2	ICAR-IIOR, Hyderabad
12.	RGP-49-P4	ICAR-IIOR, Hyderabad
13.	RGP-50-P1-S4	ICAR-IIOR, Hyderabad
14.	RGP-50-P2-S1	ICAR-IIOR, Hyderabad
15.	RGP-58-P4-S2	ICAR-IIOR, Hyderabad
Crosses		
16.	CMS-234A x PM-81	41. CMS-335A x RGP-46-P2
17.	CMS-234A x RHA-6D1	42. CMS-335A x RGP-49-P4
18.	CMS-234A x RGP-21-P2-S2	43. CMS-335A x RGP-50-P1-S4
19.	CMS-234A x RGP-28	44. CMS-335A x RGP-50-P2-S1
20.	CMS-234A x RGP-30-P3-S1	45. CMS-335A x RGP-58-P4-S2
21.	CMS-234A x RGP-46-P2	46. HA-430A x PM-81
22.	CMS-234A x RGP-49-P4	47. HA-430A x RHA-6D1
23.	CMS-234A x RGP-50-P1-S4	48. HA-430A x RGP-21-P2-S2
24.	CMS-234A x RGP-50-P2-S1	49. HA-430A x RGP-28
25.	CMS-234A x RGP-58-P4-S2	50. HA-430A x RGP-30-P3-S1
26.	ARM-243A x PM-81	51. HA-430A x RGP-46-P2
27.	ARM-243A x RHA-6D1	52. HA-430A x RGP-49-P4
28.	ARM-243A x RGP-21-P2-S2	53. HA-430A x RGP-50-P1-S4
29.	ARM-243A x RGP-28	54. HA-430A x RGP-50-P2-S1
30.	ARM-243A x RGP-30-P3-S1	55. HA-430A x RGP-58-P4-S2
31.	ARM-243A x RGP-46-P2	56. CMS-1010A x PM-81
32.	ARM-243A x RGP-49-P4	57. CMS-1010A x RHA-6D1
33.	ARM-243A x RGP-50-P1-S4	58. CMS-1010A x RGP-21-P2-S2
34.	ARM-243A x RGP-50-P2-S1	59. CMS-1010A x RGP-28
35.	ARM-243A x RGP-58-P4-S2	60. CMS-1010A x RGP-30-P3-S1
36.	CMS-335A x PM-81	61. CMS-1010A x RGP-46-P2
37.	CMS-335A x RHA-6D1	62. CMS-1010A x RGP-49-P4
38.	CMS-335A x RGP-21-P2-S2	63. CMS-1010A x RGP-50-P1-S4
39.	CMS-335A x RGP-28	64. CMS-1010A x RGP-50-P2-S1
40.	CMS-335A x RGP-30-P3-S1	65. CMS-1010A x RGP-58-P4-S2
Checks		
66.	KBSH-44	UAS, GKVK, Bengaluru
67.	DRSH-1	ICAR-IIOR, Hyderabad

The analysis of variance exhibited a significant difference for all the traits considered in the study indicating sufficient amount of variation present in the material utilised. The results pertaining to analysis of variance are presented in Table 2. The results pertaining to mean, variability, heritability and genetic advance of each trait in the present study is represented in Table 3. Wide range of variation was

observed for plant height (85.8-206.4 cm) followed by seed yield/plant (5.9-68.5 g) and lowest for 100 seed weight (2.4-7.1g) followed by oil content (32.5-40.3%) and head diameter (7.4-16.6 cm). Highest variation for plant height was also reported by Sutar *et al.* (2010) and Reena *et al.* (2017).

Table 2 Analysis of variance for different characters in sunflower

Source of variation	d.f.	DF	DM	PH	HD	SW	VW	SY/Plant	OC
Mean of sum of squares									
Replication	2	52.93	58.85	6,691.90	0.09	1.29	68.01	183.52	1.72
Treatment	66	70.79**	71.35**	1,505.9**	14.79**	2.96**	25.99**	621.57**	7.44**
Error	132	1.92	2.09	105.1	1.05	0.22	3.45	31.34	0.65
Total	201	125.64	132.3	8302.9	15.93	4.48	97.45	836.43	9.81

** - Significant at 1% level; * - significant at 5% level; d.f. - Degrees of freedom; DF - Days to 50 per cent flowering (days); DM - days to maturity (days); PH - Plant height (cm); HD-Head diameter (cm); SW-100 Seed weight (g); VW-Volume weight (g/100 ml); SY/ Plant-Seed yield/plant (g); OC-Oil content (%)

Table 3 Mean, range, coefficient of variation, heritability and genetic advance as per cent of mean for different traits in sunflower

Character	Mean	Range		Coefficient of Variation		Heritability (%)	Genetic advance as per cent of mean
		Minimum	Maximum	GCV (%)	PCV (%)		
Days to 50 % flowering	65.0	52.0	76.0	7.41	7.72	92.28	14.67
Days to maturity	95.0	82.0	106.0	5.07	5.30	91.69	10.01
Plant height (cm)	154.0	85.8	206.4	14.04	15.53	81.63	26.12
Head diameter (cm)	13.5	07.4	16.6	15.83	17.55	81.30	29.40
100 seed weight (g)	4.98	02.4	7.1	19.21	21.43	80.32	35.46
Volume weight (g/100 ml)	41.4	32.2	46.8	6.62	8.00	68.56	11.30
Seed yield per plant (g)	36.5	05.9	68.5	38.42	41.37	86.26	73.51
Oil content (%)	36.6	32.5	40.3	4.11	4.66	77.60	7.45

The PCV ranged from 5.30 (days to maturity) to 41.37 (seed yield/plant); whereas, GCV ranged from 5.07 (days to maturity) to 38.42 (seed yield/plant). High GCV and PCV was recorded for seed yield/plant (38.42, 41.37). Further, moderate GCV and PCV was recorded for plant height (14.04, 15.53) and head diameter (15.83, 17.55). The character 100 seed weight recorded high PCV (21.43) coupled with moderate GCV (19.21). Low GCV and PCV were recorded for the trait days to maturity (5.07, 5.30); days to 50 per cent flowering (7.41, 7.72); volume weight (6.62, 8.00) and oil content (4.11, 4.66). In the present study values of PCV were higher for all characters than corresponding GCV and the difference between PCV and GCV was narrow indicating less influence of environment over the expression of these characters. Similar reports of high PCV and GCV for seed yield/plant was reported by Dudhe *et al.* (2019); moderate PCV for head diameter by Reena *et al.* (2017) and moderate GCV for plant height, head diameter and 100 seed

weight by Kumar *et al.* (2014) and Neelima *et al.* (2016). Further, low PCV for the characters volume weight, days to 50 per cent flowering, days to maturity and oil content was also reported by Kalukhe *et al.* (2010) and Makane *et al.* (2011).

The estimates of heritability ranged from 68.56 (volume weight) to 92.28% (days to 50 per cent flowering) whereas, genetic advance as percentage of mean ranged from 7.45 (oil content) to 73.51% (seed yield/plant). Heritability and genetic advance are important selection parameters. Heritability estimates are more useful when combined with the genetic advance of corresponding trait. Hence, high heritability estimates along with high genetic advance is more useful in predicting genetic gain under selection than heritability estimates alone. High heritability coupled with high genetic advance as percent of mean was observed for the characters seed yield/plant, 100 seed weight, plant height and head diameter indicating that these characters are governed by additive gene action. Hence, good response to

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selection can be attained for improvement of these traits. Similar reports of high heritability along with high genetic advance for seed yield/plant, 100-seed weight, plant height was reported by Neelima *et al.* (2016). High heritability estimates coupled with moderate genetic advance was manifested by the traits *viz.*, days to 50 per cent flowering, volume weight and days to maturity indicating involvement of both additive and non-additive gene action in the inheritance of these traits. Similar results were reported by Madhavi Latha *et al.* (2017) for days to 50 per cent flowering, days to maturity and plant height and Supriya *et al.* (2016) for days to 50 per cent flowering. Further, oil content exhibited high heritability coupled with low genetic advance suggesting non-additive gene action in inheritance of this trait. Hence, this trait can be further improved through heterosis breeding.

From the present study, it could be concluded that the traits like seed yield/plant, plant height, 100 seed weight and head diameter are controlled by additive gene action suggesting that these traits can be improved by simple selection. The character oil content was under the influence of non-additive gene action and can be improved through heterosis breeding.

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