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Assessment of Genetic Variability, Heritability and Genetic Advance for Quantitative Traits in Sunflower (*Helianthus annuus* L.)

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A B S T R A C T

A study was conducted to determine the genetic variability, heritability and genetic advance for several quantitative traits in 115 genotypes of sunflower during Kharif, 2014. The field experiments were carried out at Department of Oilseeds, TNAU, Coimbatore during Kharif, 2014. Analysis of variance showed significant differences among genotypes for all the characters indicating presence of sufficient variability among the genotypes for various traits. High estimate of genotypic and phenotypic coefficient of variation were observed for *Alternaria* leaf spot, 100- seed weight, seed yield per plant and oil yield per plant. All the characters studied exhibited high heritability except head diameter and oil content which exhibited medium heritability. High genetic advance is observed for 100 seed weight and oil yield. The results indicated the possibility for successful selection and can be used for further breeding programme.

Key words: Sunflower, Variability, Heritability, Genetic advance

Sunflower (*Helianthus annuus* L.) belongs to the family *Asteraceae*, genus containing 65 different species (Andrew *et al*. 2013). Sunflower is the world's fourth largest oil-seed crop and it is the third major source of edible oil in the world after soybean and groundnut. The name *Helianthus*, being derived from helios (the sun) and anthos (a flower). It is native to North America, also grown extensively in Russia, Argentina, France, Spain, USA and India. Breeding programmes aim at development of cultivars with high yield and yield components (Mallik *et al*. 2016). The seed yield of sunflower (*Helianthus annuus* L.) is a complex character, which is highly influenced by environmental variations. Information on nature and magnitude of variability present in a population due to genetic and non-genetic causes is an important prerequisite for systematic breeding programme. The magnitude of variability present in crop species is the deciding factor to exercise effective selection. Variability is a prerequisite for selection programme, it is necessary to detect and document the amount of variation existing within and between the populations. Thus, variability will aid the breeder to assess the character of importance and to choose the parents for hybridization programme.

Heritability magnitude indicates the reliability with which the genotype will be recognized by its phenotype expression (Chandrababu and Sharma 1999). Estimating the heritability, aid in determining the relative amount of heritable portion in variation and thus help the plant breeder in selecting elite genotypes from a diverse population. Heritability estimates along with genetic advance are normally more helpful in predicting the gain under selection than heritability estimates alone. Therefore, the present study was undertaken to study the genetic variability, heritability and genetic advance in 115 genotypes of sunflower.

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MATERIALS AND METHODS

The seed material of 115 genotypes for the field experiments were obtained from the Sunflower Unit at the Department of Oilseeds, Tamil Nadu Agricultural University (TNAU), Coimbatore (Table 1). The field experiments were carried out at Department of Oilseeds, TNAU, Coimbatore during Kharif, 2014. The trial was

conducted with two replications in a randomized block design. In each replication, each entry was raised in 4 m row, adopting a spacing of 60 cm between the rows and 30 cm between the plants. Normal agronomic practices were followed under irrigated condition. Data recorded on randomly chosen five plants for nine characters viz. days to 50% flowering, plant height (cm), head diameter (cm), 100-seed weight (g), volume weight (g/100 ml), seed yield per plant (g), oil content (%), oil yield per plant (g) and *Alternaria* leaf spot severity. The various genetic parameters like variability, genotypic coefficient variation (GCV), phenotypic coefficient variation (PCV), heritability and genetic advance as per cent mean were calculated by adopting the formulae given by Johnson *et al*. (1955).

Table 1 List of genotypes used in the research

S. No.	Genotypes	S. No	Genotypes
1	17B	59	CSFI 5291
2	1B	60	CSFI 5292
3	207 DS B	61	CSFI 5293
4	207B	62	CSFI 5298
5	234B	63	CSFI 5307
6	300B	64	CSFI 5330
7	400B	65	CSFI 5331
8	607B	66	CSFI 5334
9	60B	67	CSFI 5335
10	821B	68	CSFI 5336
11	850B	69	CSFI 5341
12	852B	70	CSFI 5347
13	86B	71	CSFI 5373
14	ARM 243B	72	CSFI 5377
15	CO 4	73	CSFI 5381
16	COSF 1B	74	CSFI 5387
17	COSF 2B	75	CSFI 5388
18	COSF 3B	76	CSFI 5389
19	COSF 5B	77	CSFI 5390
20	COSF 6B	78	CSFI 5393
21	COSF 7B	79	CSFI 5398
22	COSFV 5	80	CSFI 5401
23	CSFI 5019	81	CSFI 5406
24	CSFI 5021	82	CSFI 5411
25	CSFI 5040	83	CSFI 8002
26	CSFI 5055	84	CSFI 99
27	CSFI 5062	85	IR 3
28	CSFI 5075	86	M 1014-1
29	CSFI 5078	87	M 1014-3
30	CSFI 5082	88	M 1014-4
31	CSFI 5083	89	POP 440-1-2-1
32	CSFI 5084	90	POP 448-3-1-2
33	CSFI 5086	91	POP 449-1-2-1
34	CSFI 5090	92	POP 449-1-2-2
35	CSFI 5092	93	POP 449-1-2-3
36	CSFI 5124	94	POP 449-1-2-4
37	CSFI 5125	95	POP 449-2-1-1
38	CSFI 5133	96	POP 449-2-1-2
39	CSFI 5140	97	POP 449-2-1-3
40	CSFI 5152	98	POP 449-2-1-4
41	CSFI 5177	99	CSFI 13021
42	CSFI 5181	100	CSFI 13022
43	CSFI 5190	101	CSFI 13023
44	CSFI 5194	102	CSFI 13069
45	CSFI 5205	103	CSFI 13071
46	CSFI 5210	104	CSFI 13024
47	CSFI 5213	105	CSFI 13028
48	CSFI 5216	106	CSFI 13033
49	CSFI 5219	107	CSFI 13034

50	CSFI 5223	108	CSFI 13035
51	CSFI 5232	109	CSFI 13043
52	CSFI 5246	110	CSFI 13001
53	CSFI 5254	111	CSFI 13002
54	CSFI 5260	112	CSFI 13003
55	CSFI 5276	113	CSFI 13004
56	CSFI 5286	114	CSFI 13005
57	CSFI 5287	115	TNHSF 239-68-1-1-1
58	CSFI 5288		

RESULTS AND DISCUSSION

Phenotypic and genotypic coefficients of variation

The results obtained under the present investigation are presented in (Table 2-3). Analysis of variance revealed significant differences among the genotypes for all the characters (Table 2). The wide range of variation noticed in all the characters would offer scope of selection for improvement of desirable types. The phenotypic and genotypic coefficients of variation exhibited wide range for all nine characters. The phenotypic coefficient of variation (PCV) was high for the characters, oil yield per plant (50.12%), seed yield per plant (47.86%), *Alternaria* leaf spot (29.95%), hundred seed weight (25.53%). Moderate PCV values were noticed for head diameter (21.13%), plant height (18.60%), and volume weight (14.76%). Low PCV was exhibited by days to 50 % flowering (8.23%) and oil content (6.89%).

The genotypic coefficient variation (GCV) was high for the characters oil yield per plant (44.10%), seed yield per plant (42.25%), *Alternaria* leaf spot (23.45%), hundred seed weight (20.89%). Moderate GCV values were noticed for plant height (16.49%), followed by head diameter (14.63%) and volume weight (11.43%). Low GCV was exhibited days to 50 % flowering (7.37%) and oil content (5.33%) (Table 2). The presence of high GCV for oil yield per plant, seed yield per plant, *Alternaria* leaf spot and hundred seed weight suggested the possibility of improving and fixing these characters through effective selection.

Table 2 Analysis of variance for various characters

Source	Df	Mean sum of square								
		Days to 50% flowering (days)	Plant height (cm)	Head diameter (cm)	Alternaria leaf spot (%)	100seed weight (g)	Volume weight (g/100ml)	Seed yield per plant (g)	Oil content (%)	Oil yield per plant (g)
Treatment	114	41.38**	868.69**	9.26**	206.77**	2.06**	35.42**	226.89**	11.53**	38.63**
Error	114	4.53	104.00	3.26	49.64	0.41	8.86	28.16	2.90	4.92

**Significance at 1 per cent

The phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) may provide an idea about the magnitude of variability. The phenotypic and genotypic coefficients of variation exhibited wide range for all nine characters. Head diameter (cm), *Alternaria* leaf spot (%), hundred seed weight (g), seed yield per plant (g) and oil yield per plant (g) had recorded high PCV values, whereas *Alternaria* leaf spot (%), hundred seed weight (g), seed yield per plant (g) and oil yield per plant (g) recorded high GCV values. These results are in agreement with that of Rao *et al*. (2003), Seneviratne *et al*. (2004), Sridhar *et al*. (2006), Mijic *et al*. (2009), Dhillon *et al*. (2011). Moderate PCV values recorded for plant height (cm) and volume weight (g/100ml), whereas Moderate GCV values recorded for plant height (cm), head diameter and volume weight. These results are also in agreement with Dhillon *et al*. (2011). The result indicated that sufficient level of variability was present in the genotypes.

Table 3 Range and variability parameter of the genotypes

Character	Minimum	Maximum	Mean	PCV (%)	GCV (%)	h^2(%)	GAM (%)
Days to 50% flowering (days)	43.00	71.50	58.25	8.23	7.37	80.27	2.54
Plant height (cm)	62.40	177.49	118.58	18.60	16.49	78.62	1.21
Head diameter (cm)	6.95	17.74	11.84	21.13	14.63	47.92	5.77
Alternaria leaf spot (%)	14.27 (22.17)	90.12 (71.68)	38.23 (37.80)	29.95	23.45	61.28	2.61
100-seed weight (g)	1.98	7.79	4.35	25.53	20.89	66.95	25.94
Volume weight (g/ 100ml)	22.78	41.15	31.88	14.76	11.43	59.97	3.00
Seed yield per plant (g)	3.47	61.33	23.60	47.86	42.25	77.91	6.00
Oil content (%)	29.75	44.76	38.99	6.89	5.33	59.77	2.44
Oil yield per plant (g)	1.17	25.42	9.31	50.12	44.10	77.42	15.07

Where, GCV% and PCV% are genotypic and phenotypic coefficient of variation, respectively
GA (% of mean) is genetic advanced expressed as percent of mean

Heritability and genetic advance as percentage of mean (GAM)

All the characters studied exhibited high heritability except head diameter (47.92%) and oil content (59.77%) which exhibited medium heritability. Oil yield per plant (15.07%) recorded moderate genetic advance as a percentage of mean, whereas 100 seed weight (25.94%) recorded high genetic advance as a percentage of mean, while all the other traits recorded low value (Table 3). The heritability and genetic advance provide the proportion of heritable variation exist and the genetic gain can be obtained in subsequent generations. All the characters studied exhibited high heritability except head diameter, volume weight and oil content which exhibited medium heritability denoting the least influence of environmental factors. Similar findings were reported by Sridhar *et al*. (2006), Sujatha and Reddy (2009), Janamma *et al*. (2008), Sutar *et al*. (2010), Arshad *et al*. (2010), Makane *et al*. (2011).

High genetic advance as percentage of mean was recorded for 100 seed weight. High heritability and high genetic advance as percentage of mean indicates the possibility for successful selection. Directional selection for these traits would be more effective for desired genetic improvement. Similar findings were reported by Sridhar *et al*. (2006), Sujatha and Reddy (2009), Janamma *et al*. (2008), Makane *et al*. (2011). High heritability and low genetic advance as a percentage of mean were recorded for days to 50% flowering, plant height, PDI for *Alternaria* leaf spot, and seed yield per plant as reported by Sutar *et al*. (2010). It indicates that the expression of these traits is unstable due to environmental influence.

From the results and discussion, it could be concluded that the phenotypic and genotypic coefficients of variation exhibited wide range for all nine characters. *Alternaria* leaf spot, hundred seed weight, seed yield per plant and oil yield per plant recorded high phenotypic coefficient variation (PCV) and genotypic coefficient variation (GCV) values. The result indicated that sufficient level of variability was present in the genotypes. All the characters studied exhibited high heritability except head diameter and oil content which exhibited medium heritability. High genetic advance as percentage of mean was recorded for 100 seed weight and oil yield. High heritability and high genetic advance as percentage of mean indicated the possibility for successful selection. Directional selection for these traits would be more effective for desired genetic improvement.

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