



Genetic Variability Studies For Yield and Its Attributes in Sunflower (*Helianthus annuus* L.)

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ABSTRACT

The present study was undertaken at Regional Agricultural Research Station, Nandyal during rabi, 2016-17. Seventy genotypes of sunflower were evaluated in a randomized complete block design replicated thrice for assessment of genetic variability. Highly significant differences were observed for all the characters studied. The traits viz., plant height, number of leaves per plant, head diameter, 100 achene weight, number of achenes per head, autogamy per cent, volume weight, achene yield per plant, hull content and leaf area index showed high heritability and genetic advance indicating the role of additive gene action. The traits days to 50% flowering, days to maturity, oil content and SPAD chlorophyll meter reading recorded high heritability with moderate genetic advance implying the role of non-additive gene action.

Received 20.07.2017

Revised 06.08.2017

Accepted 27.08.2017

INTRODUCTION

Edible oil seeds occupy a prominent role in the Indian economy next to pulses. India is the third largest producer of edible oils after U.S.A and China. Among the edible oil seeds, sunflower ranks fourth in position after groundnut, soybean, rapeseed and mustard. Sunflower oil is premium oil due to its light colour, bland flavor, high smoke point, towering level of unsaturated fatty acids, good nutritional quality and lack of linolenic acid. Besides, the crop can be grown on a large area owing to its inherent traits viz., short duration, day neutrality and thus fits in any cropping season and can be cultivated throughout the year. Sunflower is a potential source for vegetable oil and protein. However the area under sunflower cultivation is declining in the recent years due to varied reasons and the current level of production cannot meet the demand of growing population. Hence there arises the need of increasing crop production levels. Exploitation of genetic variability is the foremost important for further genetic upgradation of the crop as genetic variation is the base for effective plant improvement programme. Hence, an insight into the nature and magnitude of genetic variability is a prime requisite for adoption of appropriate breeding procedure in order to develop genotypes with higher productivity and wider adaptability. Genetic variability is very crucial item in the breeding programs (Sujatha *et al.* 2002). Magnitude and nature of genotypic variation and non-genotypic variation in the morphological characters is the stipulation for the breeding process (Safavi *et al.* 2011). Estimates of heritability provides vital information about index of transmissibility of quantitative characters of economic importance that pave way for designing effective crop breeding strategy. Besides, genetic advance provides comprehensive information of segregating generations to facilitate selection. Higher estimates of heritability and genetic advance offers ample scope for selection in developing newer genotypes with desired features.

MATERIALS AND METHODS

The experimental material comprised of 70 genotypes in sunflower sown in a randomized complete block design replicated thrice at Regional Agricultural Research Station, Nandyal, Andhra Pradesh during *rabi*, 2016-17. Each genotype was raised in a single row of 3m length with a spacing of 30cm between the plants and 60cm between the rows. Recommended agronomic practices were adopted to raise good crop. Data were recorded on five randomly selected plants in each entry per replication for 15 quantitative traits *viz.*, days to 50 per cent flowering, days to maturity, plant height, number of leaves per plant, head diameter, 100 achene weight, number of achenes per head, autogamy per cent, volume weight, achene yield per plant, hull content, oil content, SPAD chlorophyll meter reading, specific leaf area and leaf area index. The analysis of variance, coefficient of variation were calculated as per Burton and Devane(1953). Genetic advance and heritability in broad sense were calculated as per Johnson *et al.*, (1955) and Hanson *et al.* (1956) respectively.

RESULTS AND DISCUSSIONS

Selection is a prime requisite for crop improvement programme and is dependent on the extent of genetic variation available in the breeding material. The mean squares from analysis of variance for different characters were presented in Table 1. Results of analysis of variance revealed significant differences of mean squares for all the characters studied indicating the presence of considerable amount of variability in the material evaluated. Results of genetic parameters were presented in Table 2 (Fig 1,2). High genotypic and phenotypic coefficients of variation were shown by the traits number of achenes per head and achene yield. The results are in line with Supriya *et al.* (2016), Kumar *et al.* (2014), Neelima *et al.* (2012) and Khan *et al.* (2007). Moderate values of genotypic and phenotypic coefficient of variation were observed for the traits plant height, number of leaves per plant, head diameter, 100 achene weight, volume weight, hull content, specific leaf area and leaf area index. The results obtained are in consonance with the findings of Supriya *et al.* (2016), Neelima *et al.* (2016), Prasad and Reddy (2015), Kumar *et al.* (2014) and Neelima *et al.* (2012). Lesser amount of variability was observed for days to 50% flowering, days to maturity, oil content and SPAD chlorophyll meter reading. Similar findings were noted by Neelima *et al.* (2016) and Kumar *et al.* (2014).

High heritability estimates were observed for all the traits except specific leaf area that displayed moderate heritability. Genetic advance in conjunction with heritability present more reliable index of selection value (Johnson *et al.* 1955). High heritability and genetic advance were reported for the traits plant height, number of leaves per plant, head diameter, 100 achene weight, number of achenes per head, autogamy per cent, volume weight, achene yield, hull content and leaf area index imply the role of additive gene action in these traits and suggest simple selection strategies rewarding for crop improvement. Similar works were reported by Supriya *et al.* (2016), Amrita *et al.* (2013) and Sujatha *et al.* (2002).

High heritability coupled with moderate genetic advance was registered for the traits *viz.*, days to 50% flowering, days to maturity, oil content and SPAD chlorophyll meter reading indicating the existence of both additive and non-additive genetic effects. The results are in accordance with the findings of Supriya *et al.* (2016) and Amin *et al.* (2016). The trait specific leaf area alone showed moderate heritability and genetic advance implying the role of non-additive gene action and selection to be ineffective for this trait.

Existence of high variability, heritability and genetic advance as per cent of mean were observed for achene yield indicating additive gene action controlling the trait. The results are in consonance with the findings of Supriya *et al.* (2016) and Kumar *et al.* (2014).

A perusal of results implies the presence of wide range of variability for the traits *viz.*, achene yield and number of achenes per head indicating their scope for simple selection. The traits *viz.*, plant height, number of leaves per plant, head diameter, 100 achene weight, number of achenes per head, volume weight, hull content and leaf area index having high heritability and genetic advance as per cent mean implies the role of additive gene action and signifies their scope for further improvement. Lower extent of variability was registered by the traits days to 50% flowering, days to maturity, oil content and SPAD chlorophyll meter reading indicating the need to search for variation of these traits in other material.

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Table.1 Analysis of variance for yield and yield contributing traits in seventy genotypes of sunflower

S. No.	Characters	Mean squares		
		Replications (df:2)	Genotypes (df:69)	Error (df:138)
1.	Days to 50% flowering	2.10	50.21**	0.96
2.	Days to maturity	1.95	63.62**	1.24
3.	Plant height (cm)	377.24	1216.96**	46.67
4.	Number of leaves per plant	2.65	48.92**	0.89
5.	Head diameter (cm)	14.24	16.15**	2.50
6.	100 achene weight (g)	0.04	2.91**	0.25
7.	Number of achenes per head	1314.57	62900.45**	4899.88
8.	Autogamy (%)	543.17	1017.57**	253.74
9.	Volume weight (g/100ml)	0.13	35.15**	1.29
10.	Achene yield (g/plant)	4.10	239.99**	12.63
11.	Hull content (%)	6.52	137.28**	1.81
12.	Oil content (%)	0.31	13.80**	0.61
13.	SPAD Chlorophyll meter reading (SCMR)	0.53	18.86**	0.20
14.	Specific leaf area (cm ² /g)	843.64	1567.80**	658.85
15.	Leaf area index	0.02	0.92**	0.10

* Significant at 5% level; ** Significant at 1 % level

Table 2. Range, Mean, Coefficients of variation, Heritability (broad sense) and Genetic advance as per cent of mean for 15 characters in 70 sunflower genotypes

Sl. No.	Character	Range		Mean	Coefficient of Variation		Heritability (Broad sense) (%)	Genetic Advance as per cent of Mean (%) (GAM)
		Min.	Max.		Genotypic	Pher otypic		
1.	Days to 50% flowering	47.00	66.00	56.01	7.23	7.30	98	14.76
2.	Days to maturity	74.00	97.00	84.83	5.38	5.43	98	10.96
3.	Plant height	61.00	153.6 7	116.14	17.01	17.34	96	34.35
4.	Number of leaves per plant	14.45	32.59	23.86	16.77	16.93	98	34.24
5.	Head diameter	6.67	19.67	14.06	15.18	16.51	85	28.76
6.	100 achene weight	2.90	7.20	5.26	17.90	18.72	91	35.26
7.	Number of achenes per head	116.15	800.0 6	425.77	32.66	34.01	92	64.60

8.	Autogamy	48.37	121.9 9	84.09	18.97	21.90	75	33.87
9.	Volume weight	24.67	42.33	32.68	10.28	10.48	96	20.79
10.	Achene yield	3.44	44.69	22.47	38.74	39.80	95	77.68
11.	Hull content	21.21	46.72	34.04	19.74	19.87	99	40.39
12.	Oil content	27.18	41.07	33.97	6.17	6.31	96	12.43
13.	SPAD Chlorophyll meter reading	34.52	46.16	39.32	6.34	6.38	99	13.00
14.	Specific leaf area	129.61	267.5 6	165.59	10.51	13.81	58	16.48
15.	Leaf area index	1.53	3.77	3.08	17.07	18.03	90	33.29

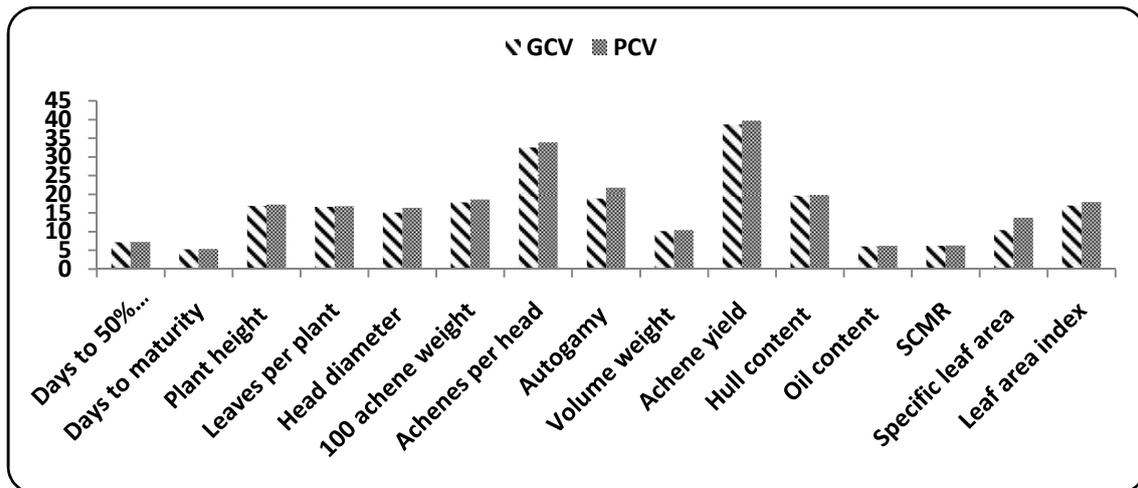


Fig 1: Graph representing the extent of variability of 15 characters

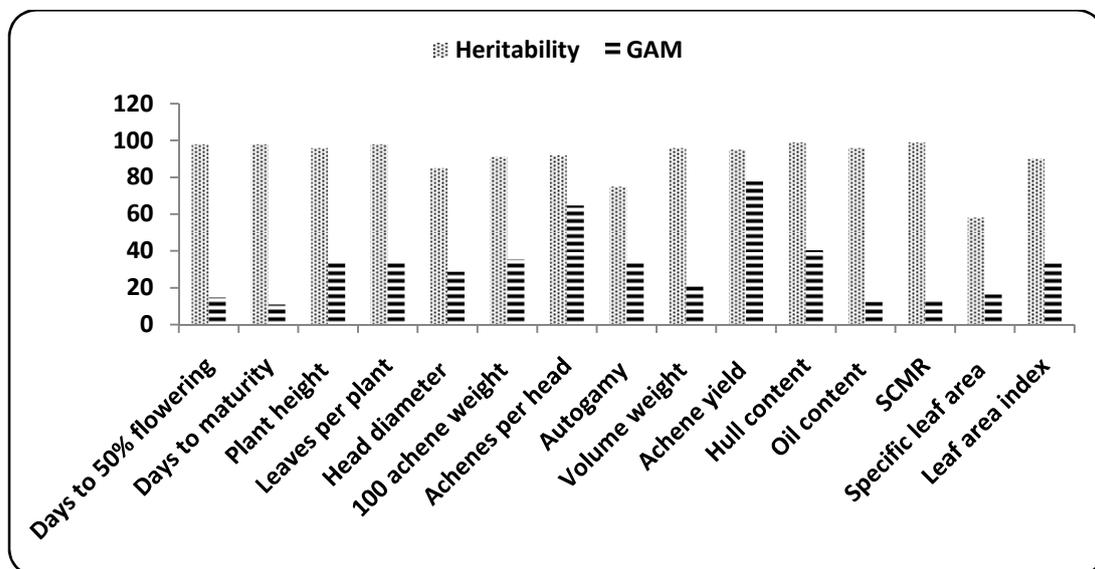


Fig 2: Graph showing the pattern of heritability and genetic advance as per cent of mean for the traits studied

CITATION OF THIS ARTICLE

K. Madhavi Latha, A.V.S. Durga Prasad, S. Neelima, P. Uma Maheswari. Genetic Variability Studies For Yield and Its Attributes in Sunflower (*Helianthus annuus* L.). Bull. Env. Pharmacol. Life Sci., Vol 6 Special issue 2, 2017: 117-120