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Research Note

Genetic variability studies for yield and yield components in sunflower (*Helianthus annuus* L.)

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Abstract

Genetic variability is a crucial tool for improvement of seed yield in sunflower. The analysis of variance of 23 hybrids revealed significant differences for all nine characters studied. The genotypic and phenotypic variation was high for seed yield per plant, head diameter and test weight indicating these characters were amenable for improvement by selection. All characters studied were least affected by environment as shown by correspondence between phenotypic co-variance (PCV) and genotypic co-variance (GCV). High heritability coupled with the high genetic advance was recorded for plant height, test weight, seed yield per plant, volume weight and head diameter. High heritability along with moderate genetic advance was observed for days to 50 per cent flowering and oil content indicating additive gene action controlling these traits.

Keywords

Genetic variability, genetic advance, heritability, sunflower

India is among the largest vegetable oil economies in the world next only to USA and China. In the agricultural economy of India, oilseeds are important next to food grains. Sunflower is one of the important oilseed crops after Groundnut, Rapeseed-Mustard and Soybean. Sunflower is an important crop for production of healthy edible oil for cardiac problems due to which sunflower oil has great demand in commence. Breeding programmes aim at development of cultivars with high yield and yield components. 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 development of an effective plant breeding program is dependent upon the existence of genetic variability. Hence, an insight into the magnitude of variability present in a cross combinations is an indirect indication of genetic variability present in crop species. The coefficients of variation expressed at phenotypic and genotypic levels are used to compare the variability observed among different characters. A wide range of variation has been reported for seed yield, seed number and other important components of yield (Virupakshappa and Sindagi, 1988). The heritability estimates aid in determining the relative amount of heritable portion in variation and thus help plant breeder in selecting the elite inbreds 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 23 hybrids.

The experimental materials consist of 23 sunflower hybrids sown in randomized complete block design (RBD) with three replications at MARS, Raichur during *Kharif*, 2014. Each hybrid was raised in two rows of 3m length with spacing of 60 x 30 cm. Recommended agronomic practices were followed to raise good crop. Observations were recorded on days to 50 per cent flowering, plant height (cm), head diameter (cm), days to maturity, test weight (g), volume weight (g/100ml), seed yield per plant (g) and oil content (%). The data were recorded on five randomly selected plants in each entry in each replication. The analysis of variance, coefficient of variation was calculated as per Burton and Devane (1953). Heritability in broad sense and genetic advance were calculated as per Hanson (1956) and Johanson *et al.*, (1955), respectively.

The success of any breeding programme depends upon the extent of genetic variability in base population and it is essential to subject a population for selection for achieve improvement in a particular trait. The mean squares from analysis of variance for different characters were presented in the Table 1. Analysis of variation indicated that the mean squares of the genotypes were highly significant for all the characters taken under study. This indicated that there was enough variability in the present material. The range of variation, as well as genotypic and phenotypic coefficient of variations were high for seed yield per plant, head diameter and test weight indicating the scope of improvement through simple selection procedure for obtaining high yield . The results obtained are in confirmatory with the findings of Teklewold (2000); Gowda (1994); Reddy and Reddy (1979) and Mogali (1993). Plant height, volume weight and oil content registered moderate phenotypic and genotypic co-efficient of variation. Mogali (1993) and Patil *et al*. (1996) reported similar results. Low variability was observed for days to 50 % flowering and days to maturity. This is in line with the results of Gangappa (1991); Mogali (1993); Gowda (1994) and Patil *et al*. (1996). Singh *et al*. (1977) reported low variability for days to maturity. This is due to presence of both positive and negative alleles for these characters in the material (Table 2 and Fig. 1).

High heritability estimates were observed for all the characters studied, Among these traits plant height followed by volume weight, test weight, days to 50 per cent flowering, oil content, seed yield per plant, head diameter and days to maturity recorded maximum heritability estimate. These results are in confirmatory with the findings of Sathisha (1995); Patil *et al*. (1996) and Lakshmanaiaha (1979). This indicated that these characters were least influenced by the environment and generally, selection based on phenotypic observation would be effective. Heritability in conjunction with genetic advance would give more reliable index of selection value (Johanson *et al.,* 1955). A combination of high heritability and genetic advance was observed for plant height, test weight, seed yield per plant, volume weight and head diameter which showed that these characters were amenable for improvement by phenotypic selection, particularly through mass selection (Ashok *et al*., 2000). Such values of high heritability and genetic gain might attribute to additive gene effect (Panse, 1957). Thus direct selection could be employed for improving these traits. High heritability coupled with moderate genetic advance was observed for days to 50 per cent flowering and oil content indicating the prevalence of narrow range of variability suggesting that these characters could also be considered for improvement through selection as these were more likely to be controlled by additive gene action. Seed yield and oil content are two important characters in sunflower. It is desirable to evolve hybrids with high seed yield coupled with high oil per cent. High variability, heritability and genetic advance as percent of mean were observed for seed yield indicating additive gene action controlling the trait. While the character oil content showed moderate variability, high heritability and moderate genetic advance as per cent of mean. The results are in agreement with the findings of Perumal and Rajashekaran (1994).

It can be concluded from the results that there is a better scope for selection for seed yield per plant, head diameter and test weight. The lower variability coefficients for days to 50 per cent flowering and maturity indicated that there was less genetic variation for this trait in the material evaluated, which needed to search for variation for this trait in other material. Selection is effective for the characters like plant height, test weight, seed yield per plant, volume weight and head diameter with high heritability estimate with high genetic advance.

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Table 1. ANOVA for eight characters in 23 hybrids of sunflower

Sl. No.	Source of variation	Df	Mean Sum of Squares							
			Days to 50% flowering	Plant height (cm)	Head diameter (cm)	Days to maturity	Test weight (g)	Volume weight (g/100ml)	Seed yield/ Plant (g)	Oil content (%)
1	Genotype	22	34.77 *	1389.40*	44.10*	13.45*	3.03*	65.94*	122.97*	47.52*
2	Replication	2	1.84	8.10	13.04	0.10	0.05	3.91	4.62	1.39
3	Error	44	1.27	8.34	4.07	1.66	0.06	1.29	6.66	2.18
4	S.Em±	-	0.65	1.66	1.16	0.74	0.14	0.65	1.49	0.85
5	CD at (5%)	-	1.86	4.75	3.32	2.12	0.40	1.87	4.24	2.43

*,**-indicates significance at 5% and 1% level respectively

Table 2. Estimation of mean and genetic variability parameters for eight quantitative characters in 23 sunflower hybrids

Sl. No.	Characters	Mean ± SE	Range		PCV (%)	GCV (%)	h^2 (bs) (%)	GAM (%)
			Minimum	Maximum				
1	Days to 50 per cent flowering	63 ± 0.6	56	69	5.6	5.3	89.7	10.3
2	Plant height (cm)	136 ± 1.7	93	167	15.9	15.7	98.2	32.1
3	Head diameter (cm)	17 ± 1.1	11	25	24.2	21.2	76.6	38.2
4	Days to maturity	93 ± 0.7	89	96	2.5	2.1	70.3	3.7
5	Test weight (g)	4.6 ± 0.1	2.3	6.3	22.4	21.7	94.2	43.5
6	Volume weight (g/100 ml)	33.8 ± 0.6	22.8	41.0	14.1	13.7	94.3	27.5
7	Seed yield/plant (g)	19.55 ± 1.5	9.76	33.58	34.46	31.83	85.3	60.6
8	Oil content (%)	37.8 ± 0.8	30.3	42.5	10.9	10.2	87.3	19.7

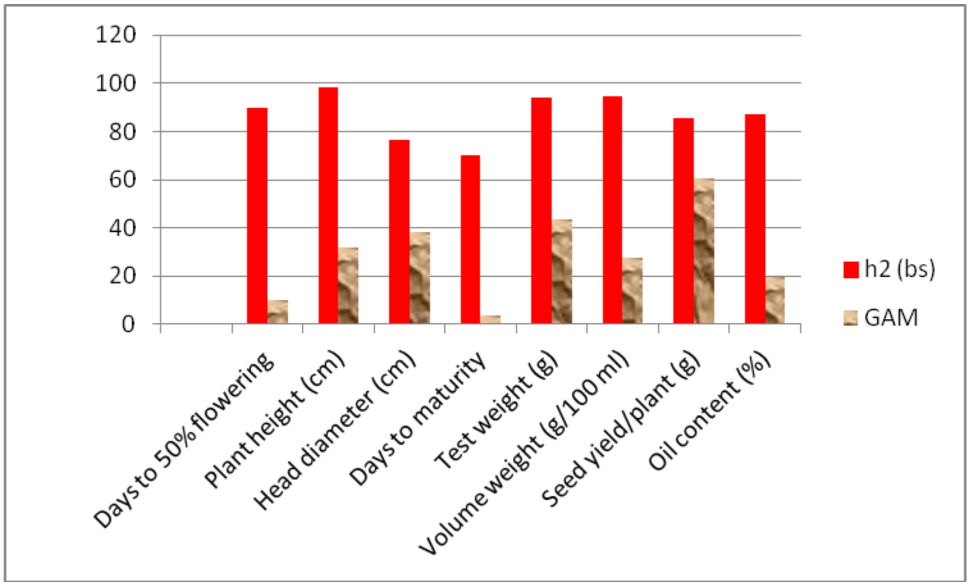

Fig. 1. Heritability (h^2) and Genetic advance as per cent of mean (GAM) for eight quantitative traits in hybrids of sunflower