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Research Note

Genetic variability studies for yield and its component traits in newly developed sunflower (*Helianthus annuus*L.) hybrids

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Abstract

The present study was conducted in order to estimate the genetic variability and variability parameters among the parental lines and crosses for 18 characters in sunflower. The investigation was carried out at Regional Agricultural Research Station, Nandyal during *rabi*, 2018-19, in a Randomized block design with two replications. ANOVA studies reported highly significant differences for all the traits. High GCV and PCV recorded for oil yield, leaf area index, seed yield, autogamy per cent, number of seeds per head and specific leaf area indicating more variability of these traits and less influence of environment. High heritability and genetic advance noted for the traits *viz*., leaf area index, plant height, specific leaf area, the number of leaves per plant, oil yield, seed set per cent, seed yield, 100 seed weight, the number of seeds per head, head diameter and autogamy per cent indicates these traits were governed by additive gene action and selection will be rewarding for the crop improvement. The traits days to 50 per cent flowering, oil content, volume weight, SPAD chlorophyll meter reading and hull content reported high heritability coupled with moderate genetic advance indicating the role of both additive and non-additive gene action and population improvement by reciprocal recurrent selection can be useful.

Keywords

Sunflower, genetic variability and variability parameters

India is the fourth largest producer of edible oil seeds after USA, China and Brazil (DVVOF, 2017). In the agricultural economy of India, edible oil seeds are important next to pulses. Sunflower emerging as a new potential oil seed crop in India competes with other three major oil seeds crops like groundnut, soybean, rapeseed and mustard (Rao, 2012). Sunflower oil, however, is nutritionally better and more stable than soybean oil and hence it is better for human consumption. The oil concentration in whole seeds varies from 30 to 45 % depending on the genotype and growing conditions. It's edible oil is premium owing to light colour, bland flavor, high smoke point, good nutritional quality, lack of linolenic acid and presence of high concentration of monounsaturated fatty acids *viz*., oleic acid (55 - 60 %) and linoleic acid (25 - 30 %) that are known to reduce the risk of coronary diseases. The higher levels of compounds present in sunflower seeds *viz*., tocopherols (vit E), choline, betaine and phenolic acid makes "the sunflower could be a power house for health benefits". The seed yield of sunflower is a complex trait, which is highly influenced by the environmental variations due to narrow genetic base, while the production of superior hybrids which yield more for seed yield and oil content would become a great lacuna in the present scenario.

Hence, the development of superior hybrids with desired characters is dependent on the existence of genetic variability present in the material. While, the coefficient of variation expressed at genotypic and phenotypic levels are used to compare the variability observed among different characters. The heritability estimates help in determining the relative amount of heritable portion in variation and thus help a plant breeder in selecting the elite inbreds from a diverse population. Heritability estimates in conjunction with genetic advance are more helpful in predicting the genetic gain under selection than heritability alone (Supriya *et al*. 2016). Therefore, an attempt was made in the present investigation to assess the variability, heritability and genetic advance studies in twenty four hybrids and ten parents for eighteen characters.

Four CMS lines *viz*., NDLA-3, NDLA-4, CMS-17 A and CMA-30 A were crossed with six restorer lines *viz*., NO-15, R-106, CPI-1, RHA-271, NGM-16 and NO-30 in L x T fashion to generate 24 hybrids during *kharif*2017. The developed 24 hybrids were evaluated along with 10 parents and four standard checks NDSH-1012, DRSH-1, KBSH-44 and Kaveri during *rabi,* 2018-19 at RARS, Nandyal in a Randomized Block Design with two replications. Each genotype was raised in two rows in a row length of 3 m with spacing of 60 cm between rows and 30 cm within the row. All the recommended agronomic practices were followed to raise the crop successfully. The observations were recorded by tagging five selected competitive plants randomly in each entry per replication. Observations were recorded on these five plants for plant height, head diameter, the number of leaves per plant, stem girth and 100 seed weight, seed yield per plant. The traits days to 50 % flowering and days to maturity were recorded on a plot basis.

SPAD chlorophyll meter reading was recorded at the time of anthesis with SPAD 502 plus meter for upper, middle and lower leaves and average of them was noted. Leaf area index was calculated by taking fully opened five leaves from each plant at anthesis and the area was measured by leaf area meter (LI-3000, Lincoln Nebraska, USA) and was calculated as per the method suggested by Watson (1952).

$$\text{Leaf Area Index} = \frac{\text{Leaf area}}{\text{Ground area}}$$

For deriving Specific leaf area, the dry weight of the same five leaves taken for LAI estimation was used and it was calculated as the method advocated by Watson (1952).

$$\text{SLA} = \frac{\text{Leaf area (cm}^2\text{)}}{\text{Leaf dry weight (g)}}$$

Number of seeds trait was estimated by counting the total number of filled seeds per head.

Seed set (%) was calculated as

$$\text{Seed set (\%)} = \frac{\text{Number of filled seeds}}{\text{Number of filled + unfilled seeds}} \times 100$$

Autogamy (%) was calculated as the per cent ratio of seed set under bagging to that of seed set under open pollination.

$$\text{Autogamy (\%)} = \frac{\text{Seed set under bagging}}{\text{Seed set under open pollination}} \times 100$$

Seeds were filled up to the mark in 100 ml beaker and the weight of those seeds was recorded as volume weight in grams.

Hull content was estimated by taking a sample of 100 seeds per genotype and these were dehulled and estimated as

$$\text{Hull content (\%)} = \frac{\text{Weight of hull}}{\text{Weight of seeds}} \times 100$$

The seed oil content per cent was determined directly with Nuclear Magnetic Resonance (NMR) spectrometer available at IIOR, Rajendranagar, Hyderabad.

Oil yield on hectare basis was calculated as

$$\text{Oil yield (kg/ha)} = \frac{\text{Seed yield (kg/ha) x Oil content (\%)}}{100}$$

Genotypic and phenotypic correlation coefficients were calculated using the method given by Johnson *et al.* (1955) and path coefficients as per the formula given by Wright (1921) and adopted by Dewey and Lu (1959).

Selection is a prime requisite for the crop improvement programme and is dependent on the extent of genetic variability present in the breeding material. The mean squares from the general analysis of variance for different characters (**Table 1**) revealed significant differences of mean squares for all the characters indicating a good amount of variability in the experimental material.

The estimates of range and genetic variability parameters were assessed for 18 characters were presented in **Table 2**. In the present study, maximum range was observed for the trait seed yield (556 - 4167) followed by oil yield (185 - 1537), the number of seeds per head (333 - 1564), plant height (80 - 206), autogamy per cent (33 - 134), specific leaf area (67.79 - 150.86), seed set per cent (46 - 86), volume weight and hull content (32 - 54). These results were in accordance with the findings of Neelima *et al.* (2016), Supriya *et al.* (2016) and Latha *et al.* (2017) for seed yield.

Table 1. General ANOVA for yield and yield components in sunflower

S. No.	Characters	Mean squares		
		Replications (df : 1)	Genotypes (df : 37)	Error (df : 37)
1	Days to 50 % flowering	0.84	14.93**	0.17
2	SPAD chlorophyll meter reading	2.92	12.84**	1.17
3	Leaf area index	0.15	10.72**	0.11
4	Specific leaf area (cm2/g)	1.29	973.12**	58.29
5	Plant height (cm)	32.89	1714**	33.38
6	Stem girth (cm)	0.21	2.15**	0.70
7	Head diameter (cm)	1.07	15.63**	2.69
8	Number of leaves per plant	0.33	39.21**	2.30
9	Days to maturity	0.47	12.18**	0.12
10	100 seed weight (g)	0.001	2.11**	0.23
11	Number of seeds/head	384.75	134219.21**	20058.75
12	Volume weight (g/100ml)	2.96	33.05**	3.01
13	Seed set (%)	38.37	154.70**	14.75
14	Autogamy (%)	13.47	1075.21**	201.37
15	Seed yield (kg/ha)	16741.89	1728070.22**	176862.44
16	Hull content (%)	6.96	58.08**	12.74
17	Oil content (%)	0.05	15.81**	0.93
18	Oil yield (kg/ha)	2760.05	253873.43**	23215.54

*- Significant at 5% level** - Significant at 1% level

Table 2. Range, mean, coefficient of variation, heritability (broad sense) and genetic advance as per cent of mean for 18 characters in 38 sunflower genotypes.

S. No.	Character	Range		Mean	Coefficient of variation		Heritability (%) (Broad sense)	Genetic advance as per cent of mean (%) (GAM)
		Min.	Max.		Geno typic	Pheno typic		
1	Days to 50 % flowering	45.00	60.00	54.00	5.02	5.08	98	10.24
2	SPAD chlorophyll meter reading	31.60	43.00	38.11	6.27	6.87	83	11.80
3	Leaf area index	2.35	10.00	6.59	34.94	35.31	98	71.24
4	Specific leaf area (cm^2/g)	67.79	150.86	97.00	22.07	23.44	89	42.82
5	Plant height (cm)	80.00	206.00	156.00	18.59	18.95	96	37.55
6	Stem girth (cm)	6.00	10.00	8.00	10.55	14.77	51	15.52
7	Head diameter (cm)	8.00	22.00	17.00	15.12	17.98	71	26.17
8	Number of leaves per plant	24.00	40.00	34.00	12.79	13.56	89	24.84
9	Days to maturity	79.00	92.00	86.00	2.87	2.90	98	5.85
10	100 seed weight (g)	2.75	7.15	5.49	17.72	19.74	81	32.79
11	Number of seeds/head	333.00	1564.00	872.00	27.39	31.84	74	48.54
12	Volume weight (g/100ml)	32.00	54.00	44.00	8.85	9.70	83	16.64
13	Seed set (%)	46.00	89.00	72.00	11.61	12.77	83	21.74
14	Autogamy (%)	33.00	134.00	74.00	28.35	34.26	68	48.31
15	Seed yield (kg/ha)	556.00	4167.00	2649.00	33.24	36.84	81	61.79
16	Hull content (%)	32.00	54.00	41.00	11.74	14.57	65	19.47
17	Oil content (%)	26.93	39.68	34.45	7.92	8.40	89	15.37
18	Oil yield (kg/ha)	185.00	1537.00	924.00	36.75	40.28	83	69.08

Whereas, the range was narrowed for number of leaves per plant (24 -40), days to 50 per cent flowering (45 - 60), head diameter (8 - 22), days to maturity (79 - 92), oil content (26.93 -39.68) and SPAD chlorophyll meter reading (31.60 - 43.00). Similar variation for these traits was also reported by Baraiya *et al*. (2018). However, the range was very narrow for the traits leaf area index (2.35 - 10.00), 100 seed weight (2.75 - 7.15) and stem girth (6 - 10). The same trend was also reported by Rani *et al*. (2016).

The coefficient of variance revealed high GCV and PCV values for leaf area index, specific leaf area, the number of seeds per head, autogamy per cent, seed yield and oil yield supporting the presence of substantial magnitude of genetic variability in the experimental material and better scope for improvement of these traits through simple selection for obtaining higher yield. Similar results for seed yield were also reported by Rao (2012), Kumar *et al*. (2014), Sudrik *et al*. (2014), Baloch *et al*. (2016), Supriya *et al*. (2016) and Baraiya *et al*. (2018), whereas for seed yield and oil yield by Hassan *et al*. (2015). However, the traits *viz*., plant height, stem girth, head diameter, the number of leaves per plant, 100 seed weight, seed set per cent and hull content reported moderate GCV and PCV values. These results were in line with Sudrik *et al*. (2014), Latha *et al*. (2017) and Baraiya *et al*. (2018). While, the traits *viz*., days to 50 per cent flowering, SPAD chlorophyll meter reading, days to maturity, volume weight and oil content have shown low GCV and PCV values. The expression of low coefficients of variation for these traits indicates that there was low amount variation in the material evaluated, which requires search for variation in other material (Supriya *et al*., 2016) or also due to presence of both positive and negative alleles for those in the population (Rao, 2012). The same results for the above traits were also given by Kumar *et al*. (2014), Hassan *et al*. (2015) and Sheshaiah and Shankergoud (2015) and Latha*et al*. (2017). However, contrast results were reported for oil content with moderate GCV and PCV (Rao, 2012 and Sudrik *et al*., 2014) and Baraiya *et al*. (2018) with high GCV and PCV for the above traits.

The GCV and PCV values for the traits *viz*., days to 50 per cent flowering, SPAD chlorophyll meter reading, days to maturity, leaf area index and plant height were differed slightly in the experimental material indicating the stable expression of these traits and least influence of environment.The heritability values ranged from 51 (moderate) to 98 (high) and the estimates were high for all the traits studied (except stem girth) indicating that these were least influenced by the environment and selection based on phenotypic observations would be effective. The studies were in consonance with Rao (2012), Kumar *et al*. (2014), Rani *et al*. (2016) and Baraiya *et al*. (2018) for seed yield.

High heritability in conjunction with genetic advance observed for the traits *viz*., leaf area index, specific leaf area, plant height, head diameter, number of leaves per plant, 100 seed weight, seed set per cent, number of seeds per head, autogamy per cent, seed yield and oil yield indicating the role of additive gene action and directional selection for these traits would be more effective. These results were in agreement with Sudrik *et al*., 2014 and Baraiya *et al*., 2018 (plant height, head diameter, the number of leaves per plant, 100 seed weight and seed yield); Sheshaiah and Shankergoud, 2015 (plant height and the number of leaves per plant); Neelima *et al*., 2016 (plant height, 100 seed weight and seed yield); Supriya *et al*., 2016 (plant height, head diameter, the number of leaves per plant, 100 seed weight and seed yield) and Latha *et al*., 2017 (leaf area index, plant height, head diameter, number of leaves per plant, 100 seed weight, the number of seeds per head, autogamy per cent and seed yield). However, Kumar *et al*. (2014) for seed yield, head diameter and 100 seed weight reported contrast results.

The traits *viz*., days to 50 per cent flowering, SPAD chlorophyll meter reading, volume weight, hull content and oil content recorded high heritability coupled with moderate genetic advance indicating the role of both additive and non-additive gene actions and population improvement by reciprocal recurrent selection can be useful. The results were in accordance withRao, 2012 (days to 50 per cent flowering), Sheshaiah and Shankergoud, 2015 (SPAD chlorophyll meter reading), Sudrik *et al*., 2014 (days to 50 per cent flowering, seed set per cent, oil content and hull content), Supriya*et al*., 2016 (days to 50 per cent flowering and oil content), Latha*et al*., 2017 (days to 50 per cent flowering and SPAD chlorophyll meter reading).

The character days to maturity alone recorded high heritability and low genetic advance (Rao, 2012, Sudrik *et al*., 2014, Supriya *et al*., 2016 and Neelima *et al*., 2016 and Baraiya *et al*., 2018) suggesting that the role of favourable environment rather than the genotype and the selection is not rewarding.

Moderate heritability and genetic advance exhibited by the trait stem girth indicates the influence of environment to a considerable level and selection for this trait was not much effective. This result was disagreeable with Hassan *et al*. (2015), Sheshaiah and Shankergoud (2015) and Baraiya *et al*. (2018) for stem girth (high heritability and genetic advance).

The analysis of various genetic parameters in the present study reveals higher values of GCV, PCV, heritability and genetic advance as per cent of mean for the traits *viz*., leaf area index, specific leaf area, the number of seeds per head, autogamy per cent, seed yield and oil yield. Hence the seed yield in segregating generations can be taken as a criteria for selection of a single plantand for promoting to next generation. Moderate values of PCV, GCV coupled with high heritability and genetic advance was recorded for plant height, head diameter, the number of leaves per plant, 100 seed weight and seed set per cent. Low values of GCV, PCV coupled with high heritability and low genetic advance for days to maturity.

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