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Genetic Analysis of Yield, its Attributing Traits and Oil Content in Multi-headed Sunflower (*Helianthus annuus* L.) Restorer Lines

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Abstract

Genetic variability, phenotypic and genotypic coefficients of variation, heritability and genetic advance for eight traits related to yield, its attributing traits and oil content in 120 restorer lines of sunflower was studied. The analysis of variance revealed highly significant differences for all the characters among the restorer lines. The magnitude of differences between phenotypic coefficients of variation (PCV) and genotypic coefficients of variation (GCV) was relatively low for all the traits, indicating less environmental influence. The estimates of GCV and PCV were high for seed yield plant^{-1}, head diameter, 100 seed weight and plant height. High heritability in broad sense estimates (>90%) were recorded for all the traits under study indicating, the predominance of additive gene action and selection of genotypes based on these characters would be more effective for target plant selection in early generation. Majority of the restorer lines were multi headed, early flowering with medium plant height, small head diameter and medium volume weight. Among various restorer lines studied the promising restorer lines (K-3, C-18, G-17-1, N-16, M-19-1, B-21-1, D-11 and C-30) were selected in comparison with checks based on the presence of high seed yield plant^{-1} and oil content. These selected lines can be promoted in future hybridization program to achieve desired segregants or can be used as parental lines to develop sunflower hybrids with high seed yield and oil content.

Keywords : Restorer lines, Seed yield, Oil content, GCV, PCV, Heritability, GAM

Sunflower represents the second most important crop based on hybrid breeding after maize. It is mainly used for its seed oil with up to 12 per cent of the global production of vegetable oils worldwide. Sunflower takes position number four after palm oil, soybean and canola oil (Rauf *et al*., 2020). Apart from its use for human nutrition, sunflower oil has a number of industrial applications as basic component for polymer synthesis, biofuel, emulsifier or lubricants (Dimitrijevic *et al*., 2017). Sunflower oil is considered as premium quality oil and standard sunflower oil is usually composed of polyunsaturated linoleic acid (18:2) and monosaturated oleic acid (18:1) in ratios of 70:20 per cent. Although the content of these two fatty acids could vary due to the effect of the environment, it is typical for sunflower oil that they jointly make about 90 per cent of the total fatty acid content in the oil. In a lower percentage, there are also unsaturated palmitic (16:0) and stearic acids (18:0), which together make up 5 - 15 per cent of fatty acids. Similar oil composition has been reported for some Argentinian populations of wild *H. annuus* (Cantamutto *et al*., 2010).

Seed yield remains the most important objective of sunflower breeding, selection for higher seed yield and its attributing traits should begin during inbred line creation by defining the effects of heterosis and analyzing and evaluating the correlations among them to develop a productive hybrid with the desired traits. Therefore, the selection of high-yielding restorer lines in sunflower is an important prerequisite (Mascagni *et al*., 2018).

Understanding the nature and magnitude of genetic variation governing the inheritance of relatively quantitative traits like yield and its attributing traits and oil content in sunflower restorer gene pool is essential. Plant breeder has to analyze certain genetic variability parameters like genetic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), Heritability and genetic advance (GA) of various economic

important quantitative traits to plan future crop improvement programs. Heritability is the heritable portion of phenotypic variance and is a good index of the transmission of the characters from parents to offspring (Falconer, 1981). Genetic advance is also of considerable importance because it indicates the magnitude of the expected genetic gain from one cycle of selection (Hamdi *et al.,* 1992). The analysis of genetic variability in sunflower restorer lines based on seed yield and oil content plays an important role in plant breeding to select valuable genetic resources to be utilized later in breeding programmes to achieve superior combining ability that plant breeders look for when trying to obtain high yielding hybrid combinations, hence with this background the present investigation was undertaken to study the genetic variability, heritability and genetic advance in restorer lines of sunflower and also to select the promising restorer lines based on yield plant^{-1} and oil content.

Material and Methods

A field experiment was conducted with 120 restorer lines of sunflower, in alpha lattice design in 12 blocks with 10 restorer lines each in a block with two replications during *kharif* 2019 at Zonal Agriculture Research Station (ZARS), GKVK, Bengaluru, Karnataka. Each restorer line was sown in a single row of three-meter length with a row spacing of 60 cm and 30 cm between plants within a row. Five representative plants for each restorer line in each replication were randomly selected to record observations on days to fifty per cent flowering (DFF), plant height (PH), head diameter (HD), stem girth (SG), seed yield per plant (SYP), volume weight (VW), 100 seed weight (100 SW) and oil content (OC).

The mean of the 120 restorer lines was analyzed statistically by the method outlined by Ostle (1966). The analysis of variance for different characters was carried out in order to assess the genetic variability among genotypes. The level of significance was tested at 5 and 1 per cent using F table values given by Fisher and Yates (1963). Both phenotypic and genotypic coefficient of variability for all characters as estimated using the formula of Burton and De Vane (1953). The broad sense heritability (h^2) was estimated for all characters as the ratio of genotypic variance to the total or phenotypic variance as suggested by Lush (1949). Genetic advance for each character was estimated by using the formula of Johnson *et al.* (1955). Genetic advance as per cent mean was categorized as suggested by Johnson *et al.* (1955).

Table 1

ANOVA for yield and yield attributing traits of sunflower restorer lines

Source of variation	Mean Sum Squares (MSS)				CV (%)
	Replications	Treatments	Block	Error	
Degrees of freedom (d.f)	1	119	9	110	-
Days to Fifty percent Flowering (Days)	0.504	16.521 **	0.226	0.117	5.027
Plant Height (cm)	8.971	351.459 **	1.32	1.318	11.274
Head Diameter (cm)	0.817	9.119 **	0.211	0.223	21.852
Stem Girth (cm)	0.004	0.072 **	0.003	0.004	10.991
Seed Yield Plant^{-1} (g)	0.196	15.339 **	0.182	0.070	24.466
Volume Weight (g/100 ml)	0.717	16.876 **	0.527	0.535	7.806
100 Seed weight (g)	0.037	0.849 **	0.080	0.045	17.484
Oil Content (%)	0.140	9.809 **	0.505	0.498	6.696

** Significant at 1per cent level

RESULTS AND DISCUSSION

The mean sum of squares for eight characters in 120 genotypes under study is presented in Table 1. Analysis of variance revealed highly significant differences among restorer lines for all the characters under study indicating the presence of adequate variability among the restorer lines.

The estimates of mean, range, phenotypic and genotypic coefficients of variation, heritability and genetic advance in per cent of mean for the respective characters were estimated (Table 2). A wide range of variation was observed in the restorer lines of sunflower for all the yield, its attributing traits and also in oil content. However, widest range of variability was recorded for plant height (92.5 - 142.5 cm) followed by days to fifty per cent flowering (52 - 68 days) andseed yield per plant (5.8 - 19.2 g), while it was lowest in the case of stem girth (1.32 - 2.3 cm) and 100-seed weight (2.16 - 5.2 g). Similar results were also reported by Ramya *et al*. (2019), Singh *et al*. (2019) and Dudhe *et al*. (2020).

The estimates of Phenotypic Coefficient of Variation were slightly higher than their corresponding Genotypic Coefficient of Variation (Fig. 1) for all the traits under this study indicating the less influence of environment on expression of these traits. The traits with almost equal value of PCV and GCV can be considered as stable. The phenotypic and genotypic variances measure the magnitude of variation arising out of differences in phenotypic and genotypic values. The genotypic estimates of variability (Vg) and GCV are the most consequential parameters that avails in the quantification of the contribution of the genotype to the expression of a particular character and gives clue to compare the genetic variability for different characters. This gives scope for selection of plants which contribute for better yield attributing traits (Bharath *et al*., 2020).

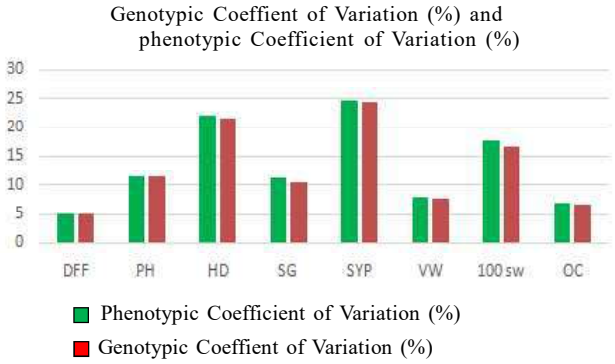

Fig.1 : Graphical representation of Phenotypic Coefficient of Variation(PCV) per cent and Genotypic Coefficient of Variation (GCV) per cent

TABLE 2

Mean performance and genetic variability of sunflower restorer lines for yield and its attributing traits

Character	Mean	Standard Error of Mean	Range		Coefficient of variation %		Heritability (%)	Genetic Advance as Mean (%)
			Low	High	Genotypic Coefficient of Variation	Phenotypic Coefficient of Variation		
Days to Fifty per cent Flowering (Days)	57.276	0.355	52	68	5.001	5.039	98.486	10.223
Plant Height (cm)	117.571	1.148	92.5	142.5	11.254	11.296	99.253	23.096
Head Diameter (cm)	9.873	0.472	5.00	14.5	21.360	21.888	95.234	42.939
Stem Girth (cm)	1.775	0.068	1.32	2.3	10.317	11.013	87.752	19.909
Seed Yield Plant^{-1} (g)	11.325	0.281	5.8	19.2	24.411	24.537	98.975	50.028
Volume Weight (g/100ml)	37.727	0.732	31	44.3	7.576	7.821	93.852	15.120
100 Seed weight (g)	3.823	0.219	2.16	5.2	16.546	17.512	89.276	32.206
Oil Content	33.835	0.706	28.31	41.11	6.378	6.711	90.328	12.487

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The estimates of heritability in broad sense (h^2) and Genetic Advance as per cent of Mean (GAM) were presented in Table 2 and Fig. 2. High heritability in broad sense estimates (>90%) were recorded for all the characters under study indicating, characters are least influenced by environment and selection for improvement is rewarding. The highest heritability in this study was observed in plant height (99.25%) followed by seed yield per plant (98.97%) and days to fifty per cent flowering (98.48 %). High heritability estimates indicated a high response to selection for these traits; the high heritability and genetic advance values have explained the predominance of additive gene action and selection for these traits can be carried in early generations. Therefore, selection of genotypes based on these characters would be more effective to be successful for target plant selection and these findings were also reported earlier by Lakshman *et al*. (2021), Riaz *et al*. (2019) and Hasan *et al*. (2020). Heritability is a measure of the extent of phenotypic variation caused by the action of genes and high heritability estimates indicates a high response to selection for these traits; the high heritability and genetic advance values have explained the predominance of additive gene action and selection for these traits can be carried in early generations. Therefore, selection of restorer lines based on these characters would be more effective to be successful for target plant selection and these findings are in accordance with the findings of Mangin *et al*. (2017) and Ankesh *et al*. (2019).

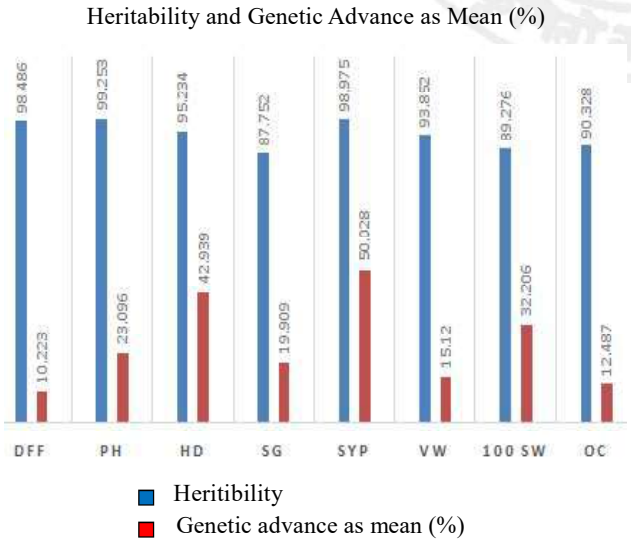

Fig. 2 : Graphical representation of Heritability (h^2) and Genetic Advance as Mean (%)

TABLE 3

Grouping of sunflower restorer lines on the basis of quantitative characters

Days to 50% flowering (days)	Early (<60)	93	77.5
	Medium (60-75)	27	22.5
	Late (>75)	0	0
	Veryshort (<80)	0	0
	Short (80-110)	38	31.6
Plant height (cm)	Medium (111-140)	78	65
	Tall (141-170)	04	3.4
	Verytall (>170)	0	0
	Small (<12)	104	86.6
Head diameter (cm)	Medium (13-20)	16	13.4
	Large (>20)	0	0
	Low (<35)	22	18.3
Volume Weight (g/100ml)	Medium (35-40)	59	49.1
	High (>40)	39	32.6
	Low (<4)	67	55.8
100 Seed weight (g)	Medium (4-6)	53	44.2
	High (>6)	0	0
Oil content (%)	Low (<35)	85	70.8
	Medium (35-40)	32	26.6
	High (40-43)	03	2.6
	Very high (>43)	00	0
Seed yield per Plant (g)	Low (<35)	120	100
	Medium (35-40)	0	0
	High (40-50)	0	0
	Very high (>45)	0	0

Classification and characterization of all 120 sunflower restorer lines into different categories of quantitative traits was done (Table 3). The restorer line B-22 exhibited late maturity (68 days), while G-40-2 exhibited the highest plant height (142.5 cm). Among the entire population, around 65 per cent were found with medium height (111-140 cm) and 77.5 per cent of population showed early flowering (<60 days). Around 86.6 per cent of the population exhibited smaller head diameter (<12), where as the highest head diameter was exhibited by the restorer line J-3 (14.5 cm). Encheva *et al.* (2010) and Onemli and Gucer (2010)

reported significant differences in plant height, head diameter and period of flowering in sunflower restorer lines. The highest 100 seed weight was exhibited by L-23 (5.2 cm), while 44.2 per cent of the population possessed medium seed weight (2.16-5.12) and the restorer line M-19-1 exhibited the highest oil content (41.11). The restorer lines which have high seed weight and oil content are categorized as potential lines because seed weight is one of important considerable yield component (Dehkhoda *et al.,* 2013 and Ion *et al.,* 2015).

Based on the above studies five promising restorer lines were selected from 120 restorer lines comparing with checks based on the presence of high seed yield per plant (Table 4a) and high oil content (Table 4b).

TABLE 4 (a)

Selection of top five promising sunflower restorer lines based on seed yield per plant

Restorer Line	Seed yield plant^{-1} (g)	Days to 50% flowering	Plant height (cm)	Head diameter (cm)	Stem Girth (cm)	Volume weight (g/100ml)	100 seed weight (g)	Oil Content (%)
K-3	19.1	59	127	11	2.25	39.63	5.05	32.86
C-18	18.4	55	126	13	2.14	38.16	4.55	34.32
G-17-1	18.3	62	139	13	2.06	38.45	4.09	37.75
N-16	17.8	58	121.2	10	2.11	35.23	3.54	38.92
M-19-1	17.5	58	130.5	11	1.55	35.87	5.01	41.11
RHA-95-C-1 (Check-1)	12.17	68	111	12.4	1.24	42.57	4.23	35.56
RHA-6D-1 (Check-2)	12.75	65	145	15.2	2.36	40.58	3.89	37.02
S. Em ±	0.281							
CD at P=0.05	5.40							
CD at P=0.01	7.22							

TABLE 4 (B)

Selection of top five promising sunflower restorer lines based on oil content

Restorer Line	Oil Content (%)	Days to 50% flowering	Plant height (cm)	Head diameter (cm)	Stem Girth (cm)	Volume weight (g/100ml)	100 seed weight (g)	Seed yield plant^{-1} (g)
M-19-1	41.11	58	130.5	11	1.55	35.87	5.01	17.5
B-21-1	40.11	55	127.5	9	1.78	36.97	4.16	12.46
N-16	38.92	58	121.2	10	2.11	35.23	3.54	17.8
D-11	38.89	54	122.5	9	1.86	43.14	3.54	13
C-30	38.26	54	126	13	2.13	37.65	3.71	17.54
RHA-95-C-1 (Check-1)	35.56	68	111	12.4	1.24	42.57	4.23	12.17
RHA-6D-1 (Check-2)	37.02	65	145	15.2	2.36	40.58	3.89	12.75
S. Em±	0.706							
CD at P=0.05	4.23							
CD at P=0.01	6.19							

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The restorer lines K-3 (19.1 g), C-18 (18.4 g), G-17-1 (18.3 g), N-16 (17.8 g) and M-19-1 (17.5 g) are the promising restorer lines selected based on high seed yield per plant, while the restorer lines M-19-1 (41.11 %), B-21-1 (40.11 %), N-16 (38.92 %), D-11 (38.92 %) and C-30 (38.26 %) are the promising restorer lines selected based on high oil content whereas M-19-1 and N-16 are the promising restorer lines in terms of both seed yield per plant (17.5g and 17.8 g, respectively) and oil content (41.11 and 38.92, respectively).

In the present investigation, useful variation among 120 multi-headed sunflower restorer lines were observed for yield, its attributing traits and oil content. Hence, these lines can be utilized in crossing programs to develop sunflower hybrids with desirable combination of traits in them. The promising restorer lines selected from this study with high seed yield plant^{-1} and oil content can be used in future hybridization program to achieve desired segregants or can be used as parental lines to develop sunflower hybrids with high seed yield and oil content. These lines should be confirmed in further studies across the locations as they could serve as valuable genetic stock for sunflower breeding programme.

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