



## Genetic Divergence and Variability Studies for Yield and Yield Component Traits in Safflower

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### ABSTRACT

An experiment was conducted with 60 genotypes of safflower to assess variability, heritability, genetic advance, direct and indirect effects of different characters on seed yield and genetic diversity. Wide variability was observed for seed yield and other yield attributes. High phenotypic and genotypic coefficients of variation were found for number of seeds per capitulum followed by seed yield. The high heritability with high genetic advance as per cent of mean for seed yield, plant height and test weight revealed that these characters were controlled by additive gene action. The genotypes were grouped into nine clusters and seed yield contributed maximum towards genetic divergence followed by plant height and number of seeds per capitulum. The intra cluster distance ranged from 124.26 (cluster V) to 21.05 (cluster III). The maximum inter cluster distance was observed between clusters VII and IX followed by clusters IV and IX and clusters VII and VIII.

**Key words :** Genetic divergence, Safflower, Variability.

The cultivated safflower (*Carthamus tinctorius* L. ) has emerged as one of the major edible oilseeds crop in the world due to its oil having high PUFA content and as a healthy cooking medium. Genetic variability and diversity is the basic requirement for successful breeding programme and the success depends on the extent of genetic variability, choice of parents for hybridization and the selection procedure adopted. The choice of genetically diverse parent is important in hybridization programme to create variation where useful recombinants can be identified. D<sup>2</sup> statistic developed by Mahalanobis (1936) is a powerful tool to measure genetic divergence among genotypes.

The estimation of genetic correlation coefficient between yield and its component characters has been of immense help for the indirect selection of desired plant ideotype. Yield is dependent on correlation among morpho-physiological characters for developing effective selection strategies. Path analysis divides correlation coefficients into direct and indirect effects. With this, the breeder can determine the magnitude of direct and indirect effects of different characters on seed yield. The objectives of the experiment was to assess quantum of variability, heritability, genetic advance, direct and indirect effects of different characters on seed yield and genetic diversity in available germplasm so that breeding efforts can be initiated to evolve high yielding safflower varieties.

### MATERIAL AND METHODS

A field experiment was conducted with 60 diverse genotypes of safflower at Agricultural Research Station, Tandur during *rabi* 2009. The soil of the experimental site is deep black cotton soil. The crop was raised under rainfed situations. Each genotype was raised in one row of 5m length with a spacing of 45cm between rows and 20cm within the row. Recommended agronomic practices were followed to raise a healthy crop. Five plants were selected randomly from each plot and observations for eight characters were recorded namely, days to 50% flowering, days to maturity, plant height, number of capitula per plant, number of seeds per capitulum, test weight (g), oil content (%) and seed yield (kg ha<sup>-1</sup>). Oil content was estimated by the Nuclear Magnetic Resonance (NMR) technique. The analysis of genetic divergence was carried out using Mahalanobis D<sup>2</sup> statistic. The 60 genotypes studied were grouped into clusters by the Tocher's method as described by Rao (1952). Genotypic and phenotypic correlation coefficients were calculated as per Johnson *et al.* (1955). The direct and indirect contribution of various characters to yield was calculated through path coefficient analysis by Wright (1921) and Dewey and Lu (1959).

### RESULTS AND DISCUSSION

Analysis of variance revealed significant differences among genotypes for all the characters studied. Wide variability was observed for seed yield

Table 1. Genetic parameters for various quantitative traits in safflower.

Character	Mean	PCV	GCV	Heritability (bs) (%)	GA as % of mean
Days to 50% flowering	77.4	11.59	6.64	32.80	6.06
Days to maturity	108.6	4.03	3.71	84.70	7.63
Plant height (cm)	67.7	19.42	19.21	97.90	26.50
Number of capitula per plant	25.7	25.50	21.36	70.00	9.43
Number of seeds per capitulum	18.6	30.58	28.35	85.90	10.09
Test weight (g)	5.45	42.41	12.20	8.30	0.39
Seed yield (kg ha <sup>-1</sup> )	1332.70	28.63	28.63	100.00	786.24
Oil content (%)	21.40	92.75	15.98	3.00	1.21

Table 2. Grouping of 60 genotypes of safflower in different clusters.

Cluster No.	Number of genotypes	Name of the genotype
I	21	GMU 3363, GMU 3408, GMU 3384, GMU 3371, GMU 3378, GMU 3365, GMU 3393, GMU 3368, GMU 3359, GMU 3352, GMU 3358, GMU 3405, GMU 3394, GMU 3373, GMU 3343, GMU 3387, GMU 3382, GMU 3395, GMU 3390, GMU 3347, GMU 3355
II	14	GMU 3351, GMU 3396, GMU 3350, GMU 3402, GMU 3409, GMU 3372, GMU 3391, GMU 3346, GMU 3385, GMU 3348, GMU 3397, GMU 3374, GMU 3349, GMU 3354.
III	3	GMU 3383, GMU 3392, GMU 3356
IV	9	GMU 3367, GMU 3369, GMU 3389, GMU 3388, GMU 3353, GMU 3401, GMU 3345, GMU 3381, GMU 3386
V	9	GMU 3344, GMU 3377, GMU 3399, GMU 3404, GMU 3410, GMU 3366, GMU 3411, GMU 3361, GMU 3364
VI	1	GMU 3403
VII	1	GMU 3375
VIII	1	GMU 3376
IX	1	GMU 3400

Table 3. Per cent contribution of various quantitative traits towards genetic divergence in safflower.

Character	% contribution
Days to 50% flowering	0.28
Days to maturity	0.17
Plant height (cm)	1.98
Number of capitula per plant	0.34
Number of seeds per capitulum	0.73
Test weight (g)	0.00
Seed yield (kg ha <sup>-1</sup> )	96.33
Oil content (%)	0.17

Table 4. Intra and inter cluster distances in safflower.

	I	II	III	IV	V	VI	VII	VIII	IX
I	<b>94.29</b>	376.22	178.34	645.89	312.35	549.82	922.98	726.70	1081.58
II		<b>117.38</b>	212.54	295.97	665.84	911.06	564.89	1088.50	1443.63
III			<b>21.05</b>	478.55	467.12	711.49	755.49	889.36	1245.13
IV				<b>96.81</b>	939.23	1186.82	289.58	1364.58	1720.16
V					<b>124.26</b>	265.64	1217.48	437.86	790.00
VI						<b>0.00</b>	1466.51	181.16	534.57
VII							<b>0.00</b>	1644.02	2000.06
VIII								<b>0.00</b>	356.23
IX									<b>0.00</b>

Bold and diagonal values indicate intercluster distances.

*i.e.*, from 533 kg ha<sup>-1</sup> (GMU 3375) to 2533 kg ha<sup>-1</sup> (GMU 3400) (Table 1). The genotype GMU 3374 was found earliest in days to 50% flowering (64 days) and maturity (95 days). The range of plant height was from 47cm (GMU 3346) to 92cm (GMU 3348), number of capitula per plant from 16 (GMU 3396) to 47 (GMU 3405), number of seeds per capitula from 10 (GMU 3348) to 32 (GMU 3365), test weight from 4.02g (GMU 3369) to 6.74g (GMU 3365) and oil content from 12.6% (GMU 3366) to 27.4% (GMU 3378). High magnitudes of phenotypic as well as genotypic coefficients for number of seeds per capitulum followed by seed yield indicated the presence of ample amount of variation for these characters. The high heritability combined with high genetic advance as per cent of mean for seed yield, plant height and test weight revealed that these characters were controlled by additive gene action suggesting direct selection for these traits would be effective for crop improvement. These results are

in agreement with earlier findings of Diwakar *et al.* (2006).

As per the Mahalanobis D<sup>2</sup> statistic, the 60 genotypes were grouped into nine clusters (Table 2). The per cent contribution towards genetic divergence by all the eight contributing characters is presented in Table 3. Amongst the characters, seed yield contributed maximum towards genetic divergence (96.33%) followed by plant height (1.98%) and number of seeds per capitulum (0.73%). Similar results were also reported by Patil *et al.* (1991). The average intra and inter cluster distances are presented in Table 4. The intra cluster distance ranged from 124.26 (cluster V) to 21.053 (cluster III). The maximum inter cluster distance was observed between clusters VII and IX (2000.06) followed by clusters IV and IX (1720.16) and clusters VII and VIII (1644.02) suggesting wide diversity between genotypes of these clusters. Therefore, genotypes belonging to these clusters may be used

Table 5. Cluster means for various quantitative traits in safflower

	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of capitula per plant	Number of seeds per capitulum	Test weight (g)	Seed yield (kg ha <sup>-1</sup> )	Oil content (%)
I	76.71	107.71	68.81	27.33	18.71	5.69	1453.43	22.27
II	77.64	108.07	65.57	25.14	19.57	5.25	1091.64	21.08
III	75.33	104.67	68.67	25.00	25.00	6.27	1288.00	23.53
IV	78.22	108.44	64.67	22.67	17.22	5.19	814.11	19.51
V	77.11	109.89	67.44	24.00	17.22	5.42	1747.44	20.37
VI	80.00	118.00	54.00	36.00	21.00	4.77	1999.00	23.40
VII	80.00	109.00	90.00	27.00	16.00	5.53	533.00	20.60
VIII	79.00	109.00	84.00	29.00	11.00	4.50	2177.00	21.20
IX	81.00	112.00	76.00	27.00	19.00	5.05	2533.00	25.60

Table 6. Genotypic correlation coefficients in safflower.

Character	Days to flowering	Days to maturity	Plant height (cm)	Number of capitula per plant	Number of seeds per capitulum	Test weight (g)	Oil content (%)	Seed yield (kg ha <sup>-1</sup> )
Days to 50% flowering	<b>1.0000</b>	0.3648*	-0.1733	0.1321	0.0135	-0.0596	-0.0111	-0.0419
Days to maturity		<b>1.0000</b>	-0.2086*	0.3153*	-0.2095*	-0.2221	0.0009	0.1321
Plant height (cm)			<b>1.0000</b>	-0.1126	-0.1605	0.0625	-0.1609	0.0882
Number of capitula per plant				<b>1.0000</b>	0.1580	0.4801*	0.0713	0.2193*
Number of seeds per capitulum					<b>1.0000</b>	0.4566*	-0.1358	-0.3180*
Test weight (g)						<b>1.0000</b>	-0.0953	0.1440
Oil content (%)							<b>1.0000</b>	0.1613
Seed yield (kg ha <sup>-1</sup> )								<b>1.0000</b>

\*- Significant at 5% level

in hybridization programme for improvement of safflower for isolating better segregants. The least inter cluster distance was observed between the clusters I and III (178.34) followed by VI and VIII (181.16) indicating close relationship between the genotypes of these clusters.

The diversity was also supported by the appreciable amount of variation among the cluster means of different characters (Table 5). The highest cluster mean was revealed by cluster IX for seed yield, oil content and days to 50% flowering; cluster VI for days to maturity and number of capsules per plant and cluster VIII for plant height and number of clusters per plant. These results showed that

different clusters were superior for different characters and genotypes from these characters would offer a good scope for safflower improvement through rational selection.

Since genotypes with narrow genetic base are more vulnerable to diseases and adverse climatic conditions, therefore, the availability of the genetically diverse genotypes for hybridization programme becomes more important. In the present study, the maximum inter cluster distance observed between clusters VII and IX and clusters IV and IX, and crosses among genotypes *viz.*, GMU 3375, GMU 3400, GMU 3367, GMU 3369, GMU 3389, GMU 3388, GMU 3353, GMU 3401, GMU 3345, GMU 3381

Table 7. Direct and indirect effects of different traits in safflower.

Character / Genotype	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of capitula per plant	Number of seeds per capitulum	Test weight (g)	Oil content (%)	Seed yield (kg/ha)
Days to 50% flowering	<b>-0.1166</b>	-0.0426	0.0202	-0.0154	-0.0016	0.0069	0.0013	<b>-0.0419</b>
Days to maturity	0.0773	<b>0.2120</b>	-0.0442	0.0067	-0.0444	-0.0471	0.0002	<b>0.1321</b>
Plant height (cm)	-0.0282	-0.0340	<b>0.1629</b>	-0.0183	0.0262	0.0102	-0.0262	<b>0.0882</b>
Number of capitula per plant	0.0306	0.0073	-0.0261	<b>0.2193</b>	0.0366	0.0111	0.0165	<b>0.2193</b>
Number of seeds per capitulum	0.0000	0.0004	0.0003	-0.0003	<b>-0.0018</b>	-0.0008	0.0002	<b>-0.0380</b>
Test weight (g)	-0.0030	-0.0112	0.0031	0.0024	0.0229	<b>0.0502</b>	-0.0048	<b>0.0140</b>
Oil content (%)	-0.0019	0.0001	-0.0280	0.0124	-0.0236	-0.0166	<b>0.1740</b>	<b>0.1613</b>

Diagonal bold values are direct effects.

and GMU 3386 would be resulted into transgressive segregants.

Correlation studies provide better understanding of yield components which helps the plant breeder during selection. Seed yield reflected high positive and significant correlations with number of capitula per plant and number of seeds per capitula (Table 6). These results are in agreement with those of Ghongade and Navale (1995). Significant positive correlation of days to maturity was observed with days to 50% flowering and number of capitula per plant while negative significant association with plant height and number of seeds per capitula. Test weight exhibited positive significant association with number of capitula per plant and number of seeds per capitula.

Path coefficient analysis revealed that days to maturity had direct positive association with days to maturity coupled with positive correlation with seed yield (Table 7). Genotypic correlation coefficient of number of capitula per plant with seed yield was almost equal to its direct effect both in direction and magnitude. Such correlation indicates true relationship and direct selection through this trait will be effective. Considering the direct and indirect effects along with character association, the present study suggested that numbers of capitula per plant, number of seeds per capitulum and test weight are the important characters to be considered for selecting high yielding safflower genotypes suitable for cultivation.

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