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Screening The Pattern Of Genetic Variability For Yield And Drought Tolerance In *Carthamus Tinctorius*

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Abstract

An experiment comprising of 40 genotypes of safflower was undertaken to elucidate information on the nature and magnitude of genetic variability, Observations were recorded for twelve characters, The data were subjected to variability and multivariate analysis. Lower branch height showed highest phenotypic and genotypic coefficient of variation followed by number of branches per plant, number of capitula per plant, number of seeds per capitulum, biological yield per plant, 100 seed weight. Heritability in broad sense and genetic advance as per cent of mean were higher for lower branch height, number of branches per plant, number of capitula per plant, number of seeds per capitulum, biological yield per plant, 100 seed weight, harvest index and seed yield per plant.

Introduction

Safflower (Carthamus tinctorius L.) is commonly known as kusum in India, is predominantly self-pollinated crop and is a member of the family Compositae or Asteraceae, genus *Carthamus*. There are two types of safflower varieties the type that produces high in mono unsaturated fatty acids (oleic acid), and those with high concentration of polyunsaturated fatty acids (linoleic acid). Safflower oil is rich in poly unsaturated fatty acids (Linoleic Acid 78%) which play an important role in reducing blood cholesterol level and is considered as a healthy cooking medium. This oil can also be used as a diesel fuel substitute. The meal that remains after oil extraction is used as a protein (24%) supplement for livestock.

Major producer of safflower are India, United state, Mexico , Kazakhstan, Argentina, China, Ethiopia, Russia and Australia. Some states like Madhya-Pradesh, Andhra Pradesh, Orissa, Bihar, West Bengal *etc.,* account for about 5% area and 2% production. There are many constraints of its low productivity in the state, out of which non-availability of seeds of high Yielding Variety which perform under moisture stress condition of Malwa region.

One of the constraints regarding its low productivity that it is mainly cultivated in rabi season on residing residual soil moisture and crop faces moisture stress during growing season .Thus, it is necessary to screen genotypes for tolerance to drought condition. Information on the nature and magnitude of variability present in the existing material and association among the various morphological characters is a pre-requisite

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for any breeding programme to be initiated by the local breeder for high yields. Thus the experiment was planned to study the existence of genetic variability present in the experimental material and to screen the Safflower genotype for drought tolerance. The experiment was laid out in Randomized Block Design with three replications. Pandya *et al.* (1996) reported that the genotypic coefficients of variation were highest for grain yield per plant, number of capitula per plant, 100-seed weight and number of secondary branches per plant. Chowdhury *et al.* (1999) observed 100-seed weight and seed yield per plant showing greater consistency in respect of GCV (genotypic coefficient of variation) and heritability. Reddy *et al.* (2003) found high estimates of genotypic and phenotypic coefficients of variation for seed yield per plant, number of seeds per capitulum, number of primary and secondary branches, and number of capitula per plant, and moderate for test weight and oil content. Aanjani (2005) conducted an experiment to assess the feasibility of transfering desirable traits from wild safflower (*C. oxyacantha*) to cultivated safflower (*C. tinctorius*) and to understand the extent of variability in wild safflower. Beena *et al.* (2006) reported high heritability estimates for days to 50% flowering, days to maturity, seed yield per plant, 100-seed weight, plant height and number of seeds per capitulum. Pandey A and Singh B.P. (2012) reported that analysis of variance for all the character studid, exibit great variability.

Material And Methods

The experiment was carried out at All India Coordinated Research Project on Safflower, College of Agriculture, Indore (M.P.), which is situated between latitude 20°43’ N and longitude 76°54' E and at an altitude of 567 meters above the mean sea level. The experimental material used in the present study comprised of forty Safflower genotypes.

Table 3.2: list of genotypes

9	Name of genotype		Name of genotype
1	GMU-4058		GMU-4093
2	GMU-4060		GMU-4095
3	GMU-4062		GMU-4098
4	GMU-4065		GMU-4100
5	GMU-4066		GMU-4101
6	GMU-4067		GMU-4102
7	GMU-4070		GMU-4104
8	GMU-4072		GMU-4105
9	GMU-4075		GMU-4106
10	GMU-4076		GMU-4107
11	GMU-4077		GMU-4108
12	GMU-4080		GMU-4109
13	GMU-4081		GMU-4110
14	GMU-4082		GMU-4111
15	GMU-4084		GMU-4112

16	GMU-4085		GMU-4114
17	GMU-4088		GMU-4115
18	GMU-4089		GMU-4116
19	GMU-4091		GMU-4117
20	GMU-4092		GMU-4118

The experiment was laid down in a Randomized Block Design with three replications. Each entry was sown in four rows plot of 4 m length with a row spacing of 45-cm. and plant distances was maintained as 20 cm. The material was sown on November 28, 2012. All recommended package of practices were followed during the conduction of experiment to raise a good crop.Observations were recorded on plot as well as single plant basis. Observations on plot basis were recorded for days to flower initiation, days to 50% flowering and days to maturity. Five competitive plants selected at random from each plot for recording observations. Average of these five plants in respect of plant height, lower branch height, number of branches, number of capitula per plant, number of seeds per capitulum, biological yield per plant, 100 seed weight, harvest index and seed yield per plant were taken for statistical analysis.

The following observations were recorded:

(a) Yield contributing traits:-

1. Days to flower initiation 2. Days to 50% flowering:3. Days to maturity:4. Plant height (cm) 5.Lower branch height: (cm) 6. Number of branches per plant 7. Number of capitula per plant 8. Number of seeds per capitulum 9. Biological yield per plant 10.100-seed weight 11. Seed yield per plant 12. Harvest index

b) Traits for Drought Tolerance:

Observations recorded on leaf tempreture, transpiration rate, and relative water content and water saturation deficit at pre flowering stage to identify the genotypes for drought tolerance. The former two observations were recorded under field conditions whereas, observations on RWC and WSD was recorded in laboratory. The number of plants selected for observations were same as mentioned for above characters i.e. five from each plot. The values obtained were used to calculate mean for further analysis.

The equipments used were Porometer (transpiration rate, leaf temperature),

The following observations were recorded

1. Leaf temperature and transpiration rate

Leaf temperature and transpiration rate were recorded with the help of Steady State Porometer at preflowering and post flowering stages. Three leaves were randomly selected from upper, middle and lower portion of each plant .The time for recording was between 11.30 to 13.30.

2.Relative water content and water saturation deficit

Ten leaf samples from each plot were collected and relative water content and water saturation deficit was measured. The samples were put in plastic bag and transferred to laboratory on ice. Then fresh weight was measured by electronic scale. Afterward leaf samples were immerged in distilled water at room temperature and placed in dark place. After 16-18 h saturated weight was measured and finally

dry weight was registered after leaf drying 70o C for 48 h. Relative water content was calculated according to following formula (Ritchie et al., 1990).

RWC = FW-DW/SW-DW ×100

WSD= SW-FW/SW-DW × 100

Where FW= Fresh weight, DW = Dried weight, SW = Saturated weight,

Statistical procedures:

Analysis of variance and covariance:

The data on various characters were subjected to statistical analysis by using appropriate method of analysis of variance and covariance as described by Panse and Sukhatme (1954). The range and estimates of mean, phenotypic, genotypic and environmental variances and covariances, standard error, coefficient of variation and critical difference were obtained for all the 12 traits. The significant differences between genotypes for various characters were tested.

Estimation of phenotypic and genotypic coefficients of variation:

The phenotypic and genotypic coefficients of variation in per cent were computed by the following formulae given by Burton (1952).

PCV (%)= √

GCV (%)= √

where, PCV = Phenotypic coefficient of variation

GCV = Genotypic coefficient of variation

Estimation of heritability and genetic advance:

Heritability:

Heritability in broad sense in per cent was estimated by the following formula given by Singh and Choudhary (1977):

Heritability (h2) =

Genetic advance:

The estimates of expected genetic advance from selection, G(s), was obtained by the formula suggested by Robinson, Comstock, and Harvey (1949).

G(s) = k × hb2 × σp

where,

k = Selection differential in standard deviation units which is 2.06 for 5% selection intensity,

hb2 = Heritability in broad sense, and

σp = Phenotypic standard deviation

Results

The present experiment was carried out to assess the nature and extent of genetic diversity among fourty genotypes of Safflower. The experimental results are presented under following headings.

1. Analysis of variance
2. Mean performance
3. Phenotypic and genotypic coefficient of variation
4. Heritability
5. Genetic advance

Analysis of variance:

The mean sum of squares due to various sources of variation for twelve characters are presented in Table 4.1. The variations due to genotypes were highly significant at 0.001% level of probability in respect to all the characters namely, days to flower initiation, days to 50% flowering and days to maturity, plant height, lower branch height, number of branches, number of capitula per plant, number of seeds per

capitulum, biological yield per plant, 100 seed weight, seed yield per plant and harvest index.

Mean performance and Range

The mean performance of safflower genotypes for quantitative as well as drought tolerance traits are presented in Appendix I(a) and I(b). The value of mean, range, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability, genetic advance expressed as per cent mean for all the twelve quantitative characters studied are presented in Tables 4.2.

Phenotypic and genotypic coefficients of variation (PCV and GCV):

The estimates of phenotypic and genotypic coefficient of variation were worked out and are presented in Table 4.2. The genotypes under study showed high PCV for seven characters and GCV values for six characters, moderate PCV for two characters and moderate GCV for three characters low for three characters.

Heritability:

Estimates of heritability in broad sense are furnished in table 4.2. The genotypes under study showed high heritability values for eleven characters while moderate heritability for one and two characters, respectively.

Table 4.1 Analysis of Variance for yield and its components in Safflower

Sources of variance	d.f	Days to flowering initiaiion	Days to 50% flowering	Days to maturity	Plant height	Lower branch height	No. of branchs per plant	No. of capitula Per plant	No. of Seeds per capitulum	Biological Yield per palnt	100 Seed Weight	Seed yield per plant	Harvest index
Replications	2	0.25	1.81	1.88**	81.12	0.13	3.11**	4.35**	8.76**	2.56**	0.10**	0.46**	0.11
Genotypes	39	56.72**	56.09**	25.06**	671.70**	1131.99**	282.32**	262.13**	214.811**	265.18**	2.33**	34.67**	139.58**
Error	78	0.91	1.15	0.85	82.73	0.84	0.77	0.94	1.125	0.60	3.46	9.81	0.65

** **Significant at p=0.01**

Maximum heritability was recorded for the trait or lower branch height (99.8%) followed by biological yield per plant (99.3%), seed yield per plant (99.2%),no. of branches of plant (99.2%) , number of capitula per plant (98.9%), harvest index (98.6%), number of seeds per capitulum (98.4%), 100 seed weight (95.7), days to flower initiation (95.3%), days to 50% flowering (94.1%), days to maturity (90.5%). Moderate heritability was noticed for plant height (70.4%).

Genetic advance:

The estimates of expected genetic advance expressed as percentage of mean of the twelve characters ranged from 4.16 to 75.03 % (Table 4.2). The maximum and minimum were recorded by lower branch height per plant and days to maturity. The characters which recorded high (>20 percent) genetic advance as per cent of mean were number of seeds per capitulum (75.03%), number of capitula per plant (69.15%), number of branches per plant(67.17%), biological yield per plant (62.59%), seed yield per plant (56.63%), 100 seed weight (39.81%), harvest index (34.24%), plant height (21.07%). The traits that recorded low (<10 percent) genetic advance as per cent of mean were days to flowering initiation (9.42), days to 50% flowering (8.15) and days to maturity (4.16).

Table 4.2: Estimates of various parameters of genetic variability for different traits in safflower

S. No	Characters	Mean	Range	PCV (%)	GCV (%)	Heritability (Broad sense) (%)	Genetic advance	Genetic advance as % of mean
1	Days to flower initiation	92.10	80.00 - 99.00	4.80	4.68	95.3	8.68	9.42
2	Days to 50% flowering	104.97	94.00 - 112.00	4.20	4.08	94.1	8.55	8.15
3	Days to maturity	133.58	128.67 - 142.00	2.24	2.13	90.5	5.57	4.16
4	Plant height	114.86	90.67 - 140	14.54	12.20	70.4	24.21	21.07
5	Lower branch height (cm)	42.90	3.00 - 73.67	45.30	45.25	99.8	39.96	93.14
6	Number of branches	29.58	15.00 - 58.00	32.88	32.75	99.2	19.87	67.17
7	Number of capitula per plant	27.65	13.00 - 55.67	33.92	33.74	98.9	19.12	69.15
8	Number of seeds per capitulum	22.99	10.00 - 46.00	37.00	36.71	98.4	17.25	75.03
9	Biological yield per plant	30.80	19.67 - 64.00	30.59	30.48	99.3	19.28	62.59
10.	100 seed weight (g)	4.42	2.83 - 6.47	20.23	19.79	95.7	1.76	39.81
11.	Seed yield per plant (g)	12.29	6.33 - 20.30	27.73	27.61	99.2	6.96	56.63
12.	Harvest index (%)	40.65	23.18 - 49.57	16.86	16.74	98.6	13.92	34.24

Discussion

The success of the safflower improvement programme success of depends entirely on the existence and magnitude of the genetic variability in the base population and heritability.

Analysis of variance

In the present study, forty genotypes of safflower were evaluated to assess their potential in respect of yield and its components. Analysis of variance revealed highly significant differences for all the characters.

Mean performance: Yield and yield related traits

Based on mean performance, the genotypes GMU-4092 were found early in flower initiation, while the genotypes like GMU-4066, GMU-4092, and GMU-4107 were early in 50% flowering. The genotype GMU-4093 exhibited maximum biological yield per plant while genotype GMU-4084 recorded maximum 100 seed weight. Genotypes GMU-4089 and GMU-4105 exhibited maximum harvest index while genotype GMU-4075 and GMU-4092 produced highest seed yield per plant.

Mean performance: drought tolerance

In present study,it was observed that genotypes GMU-4100,GMU-4065, GMU-4107 and GMU-4114 has lowest value for leaf temperature and highest transpiration rates at pre flowering were noted in genotype GMU-4114 Plants exposed to water stress closed their stomata to maintain their inner moisture content and consequently, their transpiration rate and photosynthetic rates and productivity decreased (Gollan et al.1986, Termatt et al. 1985, Turner 1986).It may be concluded that lower mean value of leaf temperature and water saturation deficit along with high relative water content and high transpiration rate may be considered favourable for drought tolerance and selection can be done on this basis. In present study genotypes GMU-4065, GMU-4100, GMU-4107 and GMU-4114 may be considered comparatively better performer based on these parameters.

Variability, heritability and genetic advance

In the present investigation, the phenotypic and genotypic coefficients of variation were the highest for lower branch height, number of branches per plant number of capitula per plant, number of seeds per capitulum, biological yield per plant, 100 seed weight and seed yield per plant. Moderate values of PCV and GCV observed for harvest index and plant height. In general, phenotypic coefficient of variation was higher than correspondly genotypic coefficient of variation. It indicated that the influence of environment for all the traits under study.

The heritability estimates separate the environmental influence from the total variability and indicates the accuracy with which a genotype can be identified by its phenotypic performance, thus making the selection more effective. High heritability estimates were recorded for lower branch height, biological yield per plant, no. of branches per plant, seed yield per plant, number of capitula per plant, harvest index, number of seeds per capitulum, 100 seed weight, days to flower initiation, days to 50% flowering and days to maturity.

High heritability was coupled with high genetic advance was observed for lower branch height, number of branches per plant, number of capitula per plant, number of seeds per capitulum, biological yield per plant, 100 seed weight, harvest index and seed yield per plant. This implied that, these traits were not much influenced by environmental factors which inturn indicated that these traits are mostly controlled by additive and additive × additive gene interactions and is expected to respond to direct selection for improvement.

Moderate heritability with moderate genetic gain was observed for plant height, hence these are conditioned by additive and non-additive gene components and selection based on

phenotypic observations alone may not be very effective for these traits. High heritability values associated with moderate values of genetic gain was observed for days to flower initiation, days to 50% flowering, days to maturity.

To conclude, the genotypes from most distant cluster i.e. GMU-4070, GMU-4072, GMU-4093, GMU-4100, GMU-4081, GMU-4084 and GMU-4092 could be exploited in hybridization programme to obtain desirable variability in segregating generations. Hybridization among the genotypes from these clusters might produce high yielding genotypes having broad genetic base.

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