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Assessment of genetic variability, heritability and genetic advance for seed yield and its contributing traits in elite germplasm accessions of safflower (*Carthamus tinctorius* L.)

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Abstract

The present investigation was undertaken at the IGKV research and instructional farm in Raipur (C.G.) during rabi 2019-20. The experimental materials include 12 trait-specific elite germplasm lines with 3 checks collected from the Indian Institute of Oilseeds Research IIOR, Hyderabad. Analysis of variance indicated that all the characters *viz.*, rosette period, days to 50% flowering, days to maturity, plant height, number of primary branches plant⁻¹, number of capitulum plant⁻¹, 100 seed weight and oil content showed presence of significant variability, except traits like number of seeds capitulum⁻¹ and seed yield (g plant⁻¹). This showed that the chances of improvement in genotypes through characters showing significant variability are possible. Seed yield (g plant⁻¹), plant height (cm), and number of seeds capitulum⁻¹ had higher phenotypic and genotypic coefficient of variations. High heritability accompanied with high genetic advance was present in oil percentage followed by plant height (cm). It indicates presence of additive genes in the trait and suggested these traits were governed by non-additive genes thus, the direct selection with such characters would not be beneficial.

Keywords: safflower, heritability, phenotypic and genotypic variability

Introduction

Safflower (*Carthamus tinctorius* L.) is a dry land oilseed crop from the *Asteraceae* family, genus *Carthamus*, tribe *Tubiflorae*, sub division *Angiosperm*, division *Phanerogams* (Singh and Nimbkar, 2005) [8]. Safflower with 2n=24 chromosomes is the only cultivated variety. It is an effective multipurpose oilseed crop that has been used for dye and quality oil in a wide range of geographical regions since ancient times (Knowles, 1989) [3]. Fake saffron, bastard saffron, thistle saffron, and dyers saffron are all terms for a less expensive saffron replacement (Weiss, 1983). Safflower is primarily valued for its seed oil, which contains both high linoleic acid (typically 64–79 percent of total fatty acids) and high oleic acid (typically 10–81 percent of total fatty acids). Less seed production, plant shininess and maturity period are the main bottlenecks with this crop. To increase the crop's seed yield, researchers must look into the relationships between the important traits that contribute the most to seed yield. Seeds are now the most commonly used plant component, resulting in high-quality edible and industrial oils as well as for birds feed (Knowles, 1989; Bergman *et al.*, 2001) [3, 1]. Current applications cover specific oil forms to boost human dietary (Velasco and Fernandez – Maryinez, 2001), biofuel (Bergman and Flynn, 2001) [1], and the manufacture of transgenic pharmaceuticals (Lacey *et al.*, 1998) [4] due to the ease with which oleosin proteins can be extracted from the seed of the safflower (Lacey *et al.*, 1998) [4].

Material and Methods

The present investigation was undertaken at the IGKV research and instructional farm in Raipur (C.G.) during the *rabi* 2019-20. The experimental materials include 12 trait-specific elite germplasm lines with 3 checks collected from the Indian Institute of Oilseeds Research IIOR, Hyderabad. Experiment was laid out in Randomized block design in three replications on 20 November, 2019. The plot size was 1.35m x 5m and had three rows. Plant to plant spacing was 20cm and row to row spacing was 45cm. Crop was sown in an irrigated condition, with two irrigations: one at the come-up stage, i.e. after seed sowing, and the other at the 60-day crop stage, i.e. branching stage. Fertilizer was applied at a rate of 40N: 30P: 20K kg/ha. After 60 days of crop irrigation, the remaining half of the nitrogen was administered as a basal

dose. P₂O₅ and K₂O were employed as the starting doses.

Result and Discussions

At various growth stages of crop, observations were recorded. 10 traits were observed, including: rosette period, days to 50% flowering, days to maturity, plant height, number of primary branches plant⁻¹, number of capitulum plant⁻¹, number of seeds capitulum⁻¹, 100 seed weight, seed yield and oil percentage to measure genetic parameters such as mean, range, PCV (%), and GCV (%), heritability (h²b) (%), genetic advance, and GA (% mean). Apart from these correlation and path analysis were also estimated to know the association and direct and indirect effects among the characters.

Analysis of variance

All the characters *viz.*, rosette period, days to 50% flowering, days to maturity, plant height, number of primary branches plant⁻¹, number of capitulum plant⁻¹, 100 seed weight and oil content showed presence of significant variability, except

traits like number of seeds capitulum⁻¹ and seed yield (g plant⁻¹). This showed that the chances of improvement in genotypes through characters showing significant variability are possible.

The current results confirm the previous researchers findings Sarang *et al.*, (2004) and Sirel and Aytac (2016)^[6,9].

Genotypic and Phenotypic coefficient of variance:

The estimated value of PCV is found to be greater than the values of GCV for all traits because PCV includes both genotypic and environmental effects. Characters such as seed yield (g plant⁻¹) (PCV=32.85%, GCV=27.87%), plant height (cm) (PCV=24.04%, GCV=23.17%) and number of seeds capitulum⁻¹ (PCV=21.82%, GCV=7.98%) showed higher phenotypic and genotypic coefficient of variance. This indicates that these characteristics have a stronger selection response.

The current result confirms the studies of previous researchers Tariq *et al.*, (2014) and Pavithra *et al.*, (2016)^[10,5].

Table 1.1: Analysis of variance of 10 traits in Safflower (*Rabi*: 2019-20)

Source of variation	D.F.	1	2	3	4	5	6	7	8	9	10
Replication	2	4.01	0.41	2.26	2.76	0.66	0.47	1.46	2.52	5.90	1.53
Treatment	14	41.19*	5.96*	33.16*	40.06*	6.84*	3.25*	1.46	36.13*	0.69	87.02*
Error	28	1.351	41.989	4.243	35.367	0.841	18.075	30.765	0.023	32,109.517	0.805

* Significant at 5% level

1- Rosette period, 2- Days to 50% flowering, 3- Days to maturity, 4- Plant height (cm), 5- Number of primary branches plant-1, 6- Number of capitulum plant-1, 7- Number of seeds capitulum-1, 8- 100 seed weight (g), 9- Seed yield (g plant-1), 10- Oil percentage

Table 1.2: Genetic parameters for yield and its contributing traits in safflower (*Rabi*: 2019-20)

Traits	Mean	Range		PCV %	GCV%	Heritability (h ² b) (%)	GA	GA % (mean)
		Min.	Max.					
Rosette period	32.84	30.00	39.00	13.43	12.95	93.05	8.45	25.74
Days to 50% flowering	98.71	84.33	111.33	10.69	8.44	62.35	13.56	13.74
Days to maturity	138.66	124.33	144.66	5.08	4.86	91.46	13.28	9.58
Plant height (cm)	92.60	53.33	121.00	24.04	23.17	92.86	42.60	46.00
Number of primary branches plant ⁻¹	8.71	6.66	10.66	18.07	14.69	66.06	2.14	24.60
Number of capitulum plant ⁻¹	25.77	21.33	31.66	21.81	14.28	42.85	4.96	19.26
Number of seeds capitulum ⁻¹	27.31	19.00	33.00	21.82	7.98	13.38	1.64	6.01
100 seed weight (g)	4.30	3.40	5.00	12.55	12.05	92.27	1.02	23.86
Seed yield (g plant ⁻¹)	1,029.71	786.66	1,543.33	32.85	27.87	71.95	501.48	48.70
Oil Percentage	25.11	18.79	28.53	19.46	19.13	96.63	9.72	38.73

Heritability and Genetic Advance

Character with high heritability indicated character is less influenced by environment and selection for enhancement of such characters may be beneficial. High heritability with high genetic advance indicated presence of additive genes in the trait and suggested these traits were governed by non-additive genes thus, the direct selection with such characters would not be beneficial. High heritability accompanied with high genetic advance was present in oil percentage followed by plant height (cm).

The current result confirms the findings reported by previous researchers Camas and Esendal (2006), Shivani *et al.*, (2012) and Pavithra *et al.* (2016)^[2,7,5].

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