

GENETIC VARIABILITY STUDIES FOR YIELD AND YIELD COMPONENT CHARACTERS IN SAFFLOWER (*CARTHAMUS TINCTORIUS* L.)

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ABSTRACT

The field experiment was conducted with 40 genotypes of safflower at the Experimental Farm of College of Agriculture, Latur, during Rabi 2020–2021, with the purpose of exploring genetic diversity, heritability, and genetic progress for yield and yield contributing features in safflower. The presence of wide genetic variability in the experimental materials was demonstrated by an analysis of variance involving 40 safflower genotypes for ten quantitative characters, which revealed significant differences for all of the traits under study. Seed yield per plant, number of branches per plant, number of seeds per capitulum, test weight, and number of effective capitulum per plant all had a significant genotypic coefficient of variation and phenotypic coefficient of variation magnitudes. The character seed yield per plant, hull content, plant height, and test weight were similarly linked to the greatest broad sense heritability scores. The number of seeds per capitulum, number of effective capsules per plant, number of branches per plant, oil content, and days to 50% flowering were also associated with high broad sense heritability values. Characters, such as the number of branches per plant, number of effective capitulum per plant, number of seeds per capitulum, test weight, plant height, and seed yield per plant were associated with high heritability values in the broad sense, along with high expected genetic advance, indicating the role of additive genes in governing the inheritance of these traits, which could be improved through simple segregation.

Keywords: Genetic variability, Heritability, Genotypic coefficient of variation, Phenotypic coefficient of variation, Genetic advance, Safflower.

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INTRODUCTION

Safflower is one of the oldest oilseed crops (*Carthamus tinctorius* L.). According to archeological traces dating as far as 2500 BC, it was first farmed in Mesopotamia. Safflower has been grown in India since the beginning of time, and it is known in ancient scriptures as kuswtiba. It is frequently grown in the hot and arid climate of the Middle East, whence it derives its origins and diversity. The Arabic name quartilum or gurtum refers to the color of safflower flower dye, and *Carthamus* is a Latinized synonym for it. Safflower is one of India's most significant Rabi oilseed crops, and it is heat, drought, and salinity resistant. The safflower (*C. tinctorius* L.) is an important tropical oil seed crop.

Safflower belongs to the compositae family, *Asteraceae* subfamily, tubiflorae tribe, and phanerogams division of the angiosperms. The safflower plant is a bushy, herbaceous perennial with many primary, secondary, and tertiary branches, all of which terminate in a spherical structure known as the capitulum. There are 36 species in the *Carthamus* genus, with *C. tinctorius* L. (2n=24) being the only cultivated safflower used for oil extraction and the rest being wild species. Plants range in height from 30 to 150 cm, with globular flower heads (capitula) with bright yellow, orange, or red flowers. Safflower oil offers excellent cooking qualities, with an average of 75% linoleic acid and tocopherols, which have an antioxidant effect and a high Vitamin E concentration. India produces the most safflower in the world (43.67 MT) and has the most acreage (5.17 lakh hectares); however, the average production in 2019–2020 is just 843 kg/ha. Maharashtra and Karnataka are the two most important safflower-growing states, with 72 and 23% of area and 63 and 35% of production, respectively. (Ministry of Agriculture and Farmers Welfare, Government of India).

MATERIALS AND METHODS

During Rabi 2020–2021, forty genotypes of safflower were investigated at the College of Agriculture, Lature, under of V.N.M.K.V., Parbhani. Each

genotype was cultivated in a single row of 4 m × 3 m in length with a spacing of 50 cm between rows and 20 cm between plants within a row by using a randomized block design with two replications. To raise a good crop, a recommended package of operations was followed. Five plants were identified and labeled at random from each row and replication for recording observations, and the mean of the five plants was employed for statistical analysis. The data were recorded for days to 50% flowering, days to maturity, plant height at maturity (cm), number of branches per plant, number of effective capitula per plant, number of seeds per capitulum, 100-seed weight (g), seed yield per plant (g), hull content (%), oil content (%). Analysis of variance was performed to test the significance of differences between the genotypes for all the characters. The analysis of variance was done as suggested by Panse and Sukhatme (1985). Broad sense heritability was estimated for various characters as per the formulae suggested by Lush (1949). The genetic advance was calculated in percent as per the formula suggested by Johnson et al., (1995).

RESULTS AND DISCUSSION

The analysis of variance for a set of 40 safflower genotypes for ten quantitative characters revealed highly significant differences among genotypes for the characters studied, including days to 50% flowering, day to maturity, plant height, number of branches per plant, number of capsules per plant, number of seed per capsule, test weight, hull content, and oil content. For all ten characters studied, the mean sum of the square was non-significant due to replication. The general analysis of variance was carried out for each character to find out the amount of variation for various characters given in (Table 1). Phenotypic variance (V_p) values were more than the genotypic variance (V_g) for all the characters. High genotypic and phenotypic variances were observed for the characters' plant height and seed yield per plant. The present findings are in close agreement with those of Lakshyadeep et al. (2005) and Inchanal et al. (2010), Sreelakshmi (2015) and Monpara and Khairnar (2016).

CONCLUSION

The treatment differences in the analysis of variance were found statistically significant for all of the characters. The magnitude of genotypic and PCV also indicated the presence of a good amount of variability in the experimental materials. In the present study, high estimates of genotypic and PCV were observed for various characters. High heritability values in a broad sense coupled with high expected genetic advance were associated with the characters, such as the number of branches per plant, number of effective capitulum per plant, number of seeds per capitulum, test weight, plant height, and seed yield per plant. High heritability coupled with a high genetic advance expressed as percent of the mean offers the most effective condition for selection.

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