

GENETIC VARIABILITY, HERITABILITY AND GENETIC ADVANCE STUDIES FOR YIELD AND ITS COMPONENTS TRAITS IN SAFFLOWER (*Carthamus tinctorius* L.)

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Abstract

*In order to examine the genotypic and phenotypic variability, genotypic and phenotypic coefficient of variation, heritability, and genetic advance per cent of mean, sixty safflower accessions were evaluated during rabi 2020–21. All characters including days to 50% flowering, plant height, number of primary branches per plant, number of secondary branches per plant, capitulum diameter, number of capitula per plant, number of seeds per capitulum, hundred seed weight, and seed yield per plant showed high GCV and PCV, indicating that these traits were highly genetically variable. The high genetic advance as a percentage of mean seen for all characteristics, along with high heritability, indicated that this character's selection may be successful.***Key words:** Safflower, PCV, GCV, heritability and Yield.

Introduction

Safflower (*Carthamus tinctorius* L.) is a prominent oilseed crop in the Compositae (Asteraceae) family. It is the only cultivated species of the genus *Carthamus* which contains 2n=24 chromosomes (Singh, 2007). It is a generally self-pollinating species (Johnson et al., 2007). Out crossing ranges between 15 and 20per cent, depending on insect activity (Claassen, 1950). Safflower is a traditional oilseed crop which is extensively cultivated grown under the hot and dry climate of the Middle East, the centre of its origin and diversity (Hugar *et al.*, 2021). It is a drought-tolerant multi-purpose crop which is planted not just for oil but also for the petals, which are used to extract the orange-red dye (carthamin). The petals contain a variety of therapeutic characteristics and can be used to treat a wide range of chronic diseases (Li and Mundel, 1996). Traditionally, this crop was cultivated for various purposes such as flowers, fabric dyes, food colouring and medicinal value (Weiss 2000). Safflower is a spiny crop in general, containing many sharp spines on the leaves and bracts in

most genotypes (Bradley *et al.*, 1999). It is cultivated in 45,890 ha in India, with a production of 24,640 t and a productivity of 537 kg/ha. The main safflower-growing states are Karnataka and Maharashtra, which account for more than 90% of India's safflower production (Neelima *et al.*, 2021). Success of any breeding programme purely depends upon the variability present in the population. The purpose of this study was to determine the magnitude of phenotypic coefficient of variation, genotypic coefficient of variation and heritability in broad sense in safflower genotypes.

Materials and Methods

A total of sixty safflower genotypes sourced from the Directorate of Oilseeds Research, Hyderabad including two checks viz., CO-1 and NARI-6 were evaluated in Randomized Block Design with three replications in the Department of Plant Breeding and Genetics, Agricultural College and Research Institute, Tamil Nadu Agricultural University, Madurai during *rabi* 2020- 2021. The safflower genotypes sown on ridges and furrows with a spacing of 45cm between the rows and 15 cm between the plants. Recommended agronomic practices were followed to raise good crop. The following nine biometrical observations were taken such as days to 50% flowering, plant height (cm), number of primary branches per plant, number of secondary branches per plant, capitulum diameter (mm /cm), number of capitula per plant, number of seeds per capitulum, 100 seed weight (g) and single plant yield (g). The recorded mean data used for statistical analysis to calculate genotypic (GCV) and phenotypic (PCV) coefficient of variation, heritability and genetic advance as per cent of mean. Phenotypic coefficient of correlation was computed according to Al-Jibouri *et al.*, (1958). The phenotypic correlation was partitioned into direct and indirect effects as suggested by Dewey and Lu (1959).

Results and discussion

Greater variability in safflower will increase the chances of selection, which will benefit the breeding effort. The study of PCV, GCV, heritability, and genetic advances aids in the assessment of genes and environmental factors that are useful for improved selection. The genetic variability parameters for nine characters were presented in **Table 1, Figure 1 and 2**. Higher the value of PCV than the GCV implies that the variability present in traits was partially influenced by environmental factors. The moderate level of PCV and GCV were recorded in days to 50% flowering (10.68%), plant height(19.34%), number of primary branches per plant(19.97%), number of secondary branches per plant(19.20% capitulum diameter(19.95% number of capitula per plant (15.79, number of seeds per capitulum (17.17% and 16.94% respectively), 100 seed weight(16.14% and 15.93% respectively) and single plant yield(19.53% and 19.37% respectively). the germplasm collection possess moderate variability for economically important traits, hence selection of diverse parental lines for breeding programmes is possible. Pushpavalli and Kumar (2017) reported similar results for traits like 100 seed weight (17.62%), number of capitula per plant (19.19%) and number of seeds per capitulum (20.561%). Rathod *et al.*, (2021) recorded for traits days to 50% flowering, 100-seed weight and plant height.

The single plant yield (98.35 %) showed a high heritability estimate followed by number of primary branches per plant (98.27%), plant height (98.24%), number of secondary branches per plant (98.01), capitulum diameter (98.00%), 100 seed weight (97.41%), number of seeds per capitulum (97.408%), number of capitula per plant (97.16%) and days to 50% flowering (92.61%). These characters having a high heritability with less influenced by environment. So, selection for enhancement of such characters may be useful. Similar reports were recorded by Rathod *et al.*, (2021) for number of secondary branches per plant, single plant yield, number of seeds per capitulum, plant height, 100-seed weight, days to 50% flowering. Pushpavalli and Kumar (2017) for seed yield and 100-seed weight.

High GAM was recorded for traits days to 50% flowering, plant height, number of primary branches per plant, number of secondary branches per plant, Capitulum diameter, number of capitula per plant, number of seeds per capitulum, 100 seed weight and Single plant yield. As a result, simple selection would be more effective in developing these traits. Rathod *et al.*, (2021) noted the same results for the traits like number of secondary branches per plant, single plant yield, number of seeds per capitulum, number of primary branches per plant, number of effective capitula per plant, plant height and 100- seed weight. All traits had high heritability coupled with high GAM, indicating that additive gene action is present in the genetic control of these traits. The traits plant height, single plant yield, number of seeds per capitulum registered for high heritability coupled with high GAM by Rathod *et al.*, (2021).

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Table 1. Genetic variability parameters for different traits in safflower

Characters	Mean	PCV (%)	GCV (%)	h ² (%)	GAM (%)
Days to 50% flowering	71.58	10.68	10.28	92.61	20.39
Plant height (cm)	58.51	19.34	19.17	98.24	39.15
Number of primary branches per plant	5.59	19.97	19.79	98.27	40.43
Number of secondary branches per plant	1.99	19.20	19.01	98.01	38.77
Capitulum diameter (cm)	2.01	19.95	19.75	98.00	40.28
Number of capitula per plant	18.12	15.79	15.57	97.16	31.62
Number of seeds per capitulum	26.20	17.17	16.94	97.40	34.45
100 seed weight (g)	3.99	16.14	15.93	97.41	32.39
Single plant yield (g)	19.86	19.53	19.37	98.35	39.58

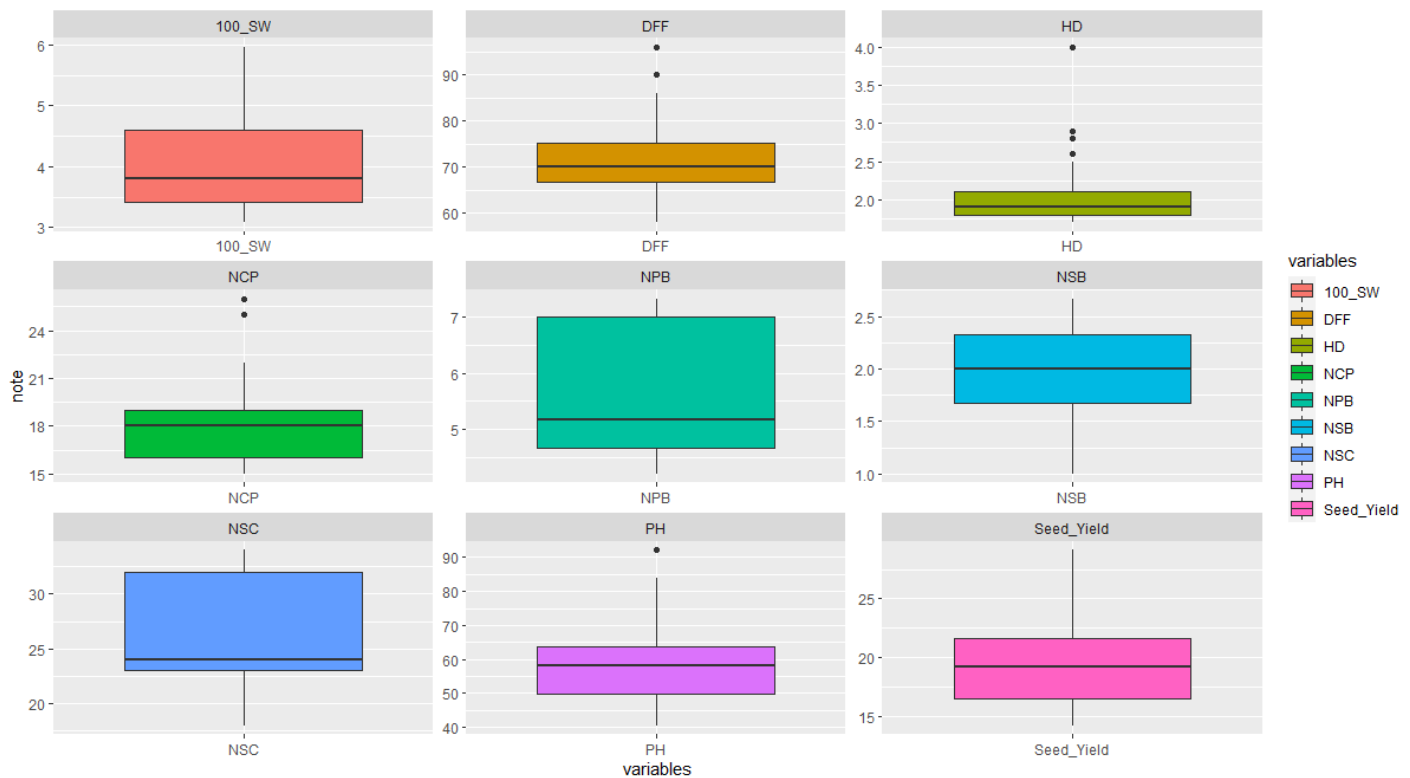
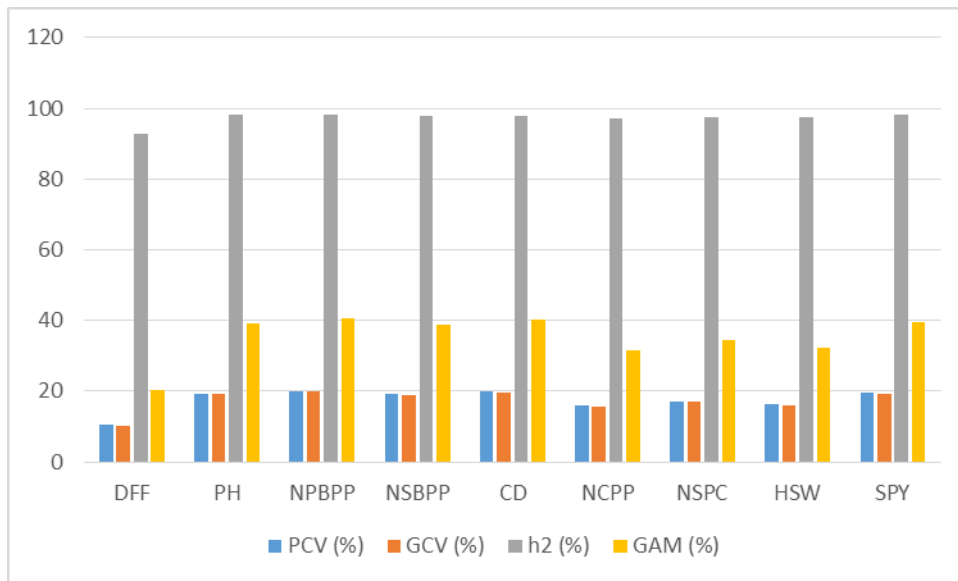


Figure 1. Multiple box plot for nine phenotypic traits in safflower



(DDF-Days to 50% flowering, PH-Plant height, NPBPP-Number of primary branches per plant, NSBPP-Number of secondary branches per plant, CD-Capitulum diameter, NCPP- Number of capitula per plant, NSPC-Number of seeds per capitulum, HSW-100 seed weight and SPY- Single plant yield)

Figure 2. Phenotypic coefficient of variation, genotypic coefficient of variation, heritability and genetic advance over mean for nine phenotypic traits in safflower