

Gene action studies for yield and yield contributing characters in ten crosses of safflower (*Carthamus tinctorius* L.)

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SUMMARY

An object of present study was to know the nature of gene action in inter-varietal crosses of safflower (*Carthamus tinctorius* L.). Ten quantitative characters *i.e.* days to 50 per cent flowering, days to maturity, plant height (cm), number of primary branches, number of secondary branches, number of capitula per plant, number of effective capitula per plant, number of total seeds per capitula, test weight (g) and yield per plant (g) were studied with the help of generation mean analysis. Trial consisting of ten crosses *viz.*, MS 105 x Girna, MS 105 x Sharda, MS 104 x Sharda, MS 104 x PSF-14, MS 105 x PSF-14, MS 105 x 398-9-15, MS 105 x Annegiri-1, MS 104 x Bhima, MS 101 x Sharda and MS 101 x PSF-14, their parents, F₂ and backcross generations. Gene effects studies indicated that dominance gene effects were larger than additive gene effects. Epistatic gene interactions were also important. Complimentary as well as duplicate type of epistasis was observed in different crosses. The component like additive and additive x additive which are fixable were displayed by the crosses, MS-104 x Bhima, MS-104 x PSF-14 and MS-105 x Annegiri-1 indicating the possibility of obtaining transgressive variations for selecting these crosses for further improvement in grain yield.

Key words : Gene action, Safflower, Additive, Inheritance

Safflower (*Carthamus tinctorius* L.) crop is known as poor and marginal farmer's crop because it requires low inputs in terms of irrigation and fertilizers. In recent years, efforts are being made to improve the productivity of this crop using high yielding varieties and improved crop production technology. Yield being a complex character, knowledge of relative magnitude of additive and non-additive gene action forms the guidelines for choice of parents and handling the segregating material from the crosses. Several scientists worked on inheritance of different yield contributing characters. Predominance of non-additive gene action for majority of characters has been reported in safflower. Predominance of additive gene action for plant height and dominance gene effect for branches per plant, plant height and capitula per plant was also reported by several workers. It is important to estimate the additive and non-additive genetic component as well as to identify and estimate components of epistasis. It will facilitate in the choice of effective and efficient breeding methods. The present investigation includes estimation of six parameters using generation mean analysis, which estimates relative importance of additive and non-additive gene effects for controlling yield and

yield contributing characters. In order to obtain more precise estimates of gene effects, the present investigation was carried out on set of six types of segregating and non-segregating generations obtained from ten intervarietal crosses of safflower with a objective to study the gene action of yield and yield components.

MATERIALS AND METHODS

The present investigation was undertaken to study gene action of yield and yield components using generation mean analysis. Experimental material used in the present investigation comprised of nine diverse parental Safflower lines. The ten F₁'s *viz.*, MS 105 x Girna, MS 105 x Sharda, MS 104 x Sharda, MS 104 x PSF-14, MS 105 x PSF-14, MS 105 x 398-9-15, MS 105 x Annegiri-1, MS 104 x Bhima, MS 101 x Sharda, MS 101 x PSF-14 were developed using above lines in *rabi* 1998. Using these hybrids, F₂, BC₁ and BC₂ generations were developed at research farm of Department of Genetics and Plant Breeding during *rabi* 1999 and summer 1999. Six generations *i.e.* P₁, P₂, F₁, F₂, BC₁, BC₂ of each cross were studied in *rabi* 1999-2000 along with check DSH-129 (High yielding, bold seeded). The experimental material was sown in the randomized block design with two replications each having one row of P₁, P₂ and F₁, two rows of BC₁ and BC₂, and six rows of F₂. Each row was 3 mts length, 45 cm apart and with plant distance of 15 cm. From each replication data for ten quantitative characters *viz.*, days to 50 per cent flowering, days to maturity, plant height (cm), number of primary branches, number of secondary branches,

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