

## Genetic correlation studies in safflower (*Carthamus tinctorius* L)

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Safflower (*Carthamus tinctorius* L.) is a member of the composite, family Asteraceae. There are twenty five species in this genus. Out of which only *Carthamus tinctorius* L. (2n = 24) is cultivated. Safflower is cultivated mainly for its seeds, which yield edible oil traditionally. Besides, it contains 30% oil in Indian varieties. The oil constitutes 76 per cent of Linoleic acid (PUFA) which helps in reducing cholesterol level in human blood. Earlier varieties of safflower have the genetic potential to give yield of 15-20 q/ha with oil content of about 30-40% under optimum condition. However attempts to further improve the yield and oil content were not successful for the last three decades. This may be due to, use of pedigree selection technique in population derived from two line crosses and negative correlation between seed yield and oil content. Conventional breeding methods have not been very efficient for improving quantitatively inherited characters like seed yield and oil content. Moreover regular methods of breeding have several limitations to use available genetic resource (Jensen, 1970). These limitations may be overcome by application of recurrent selection method in self pollinated crop. Therefore, present study was conducted to estimate the correlations among the different parameters which is directly correlated with seed yield and oil content in safflower with other traits.

The experimental material consisted of random mating population developed by using HUS-305 MS-2, genetic male sterile line with 12 parental lines viz. Bhima, A<sub>1</sub>, AKS-112, AKS-207, BLY-652, Sharada, S-251, N-7, JLSF-88, PH-39, AKS-68 and AKS-215. The population was grown for random-mating and development of half-sib families in *Rabi* 2007. Approximately 900 half sib were developed in *Rabi* 2007. Out of which 80 half sib families with sufficient seeds were selected and grown in *Rabi* 2009 along with check varieties viz., Bhima and A<sub>1</sub> for evaluation in randomized complete block design with two replication as suggested by Panse and Sukhatme (1954).

Each replication consisted of two blocks with 40 half sib along with two check in each block. The plant spacing within a row between plant to plant 30 cm and row to row spacing were 45 cm. Two seeds per hill were initially sown in each dibble and latter thinning was practiced to retain only one plant per hill. Recommended package of practices were followed to raise the good crop. The data were recorded on five competitive fertile plants for characters days to 50% flowering, days to maturity, plant height (cm), number of branches per plant, number of capitula per plant, number of seeds per capitula, 100 seed weight and seed yield per plant. Mean values of data were used for statistical analysis.

The recurrent selection experiments are mainly designed and conducted for improving seed yield per plant. However, this does not mean that other traits are unimportant. Selection for high yield does to some extent is indirect selection for disease and insect resistance and for traits correlated with yield (Gardner, 1978). However, if selection is for high seed yield alone undesirable correlated response may occur in other traits as pointed out by Doggett (1972). The genetic correlations among different traits were estimated and analyzed. Days to 50% flowering has positive and significant correlation with days to maturity (0.355\*\*) and plant height (0.249\*). Plant height has positive and significant correlation with number of primary branches (0.414\*\*), number of capitula per plant (0.643\*\*), number of seeds per capitulum (0.393\*\*), 100 seed weight (0.375\*\*). Number of primary branches per plant has positive correlation with number of capitula per plant (0.909\*\*), number of seeds per capitulum (0.553\*\*), 100 seed weight (0.326\*\*). Number of capitula has positive and significant correlation with number of seeds per capitulum (0.841\*\*), 100 seed weight (0.496\*\*), and number of seeds per capitulum has positive and significant correlation with 100 seed weight (0.681\*\*). In the present study random mating population in a

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**Table 1 : Genetic correlation among eight quantitative characters for half- sib family selection**

Characters	Days to maturity	Plant height (cm)	No. of primary branches/plant	No. of capitula /plant	No. of seeds /capitulum	100 seed weight (g)	seed yield /plant (g)
Days to 50 % flowering	0.355**	0.249*	0.117	0.072	0.053	-0.093	0.207
Days to maturity		0.149	0.114	0.040	0.133	-0.205	0.201
Plant height (cm)			0.414**	0.643**	0.393**	0.375**	0.631**
No. of primary branches / plant				0.909**	0.553**	0.326**	0.866**
No. of capitula / plant					0.841**	0.496**	0.973**
No. of seeds /capitulum						0.681**	0.989**
100 Seed weight (g)							0.803**

\* and \*\* indicate significance of values at P=0.05 and 0.01 is (0.217) and (0.283), respectively

safflower segregating for genetic male sterility. Seed yield per plant has positive and significant correlation with plant height (0.631\*\*), number of primary branches per plant (0.866\*\*), number of capitula per plant (0.973\*\*), number of seeds per capitulum (0.989\*\*) and 100 seed weight (0.803\*\*). These results of estimates are in agreement with those reported in safflower true breeding lines (Pure lines) by various workers (Mummaneni, 2003). Except the association between seed yield per plant to days to 50 % flowering and days to maturity was non significant correlated indicating breaking of linkages, Neole (2004) reported negative and significant correlation between seed yield per plant and days to maturity (-0.377\*\*) shows that unfavorable gene combination can be broken by recurrent selection. This will facilitate selection recombinant lines with high yield and earliness.

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