## Research Note

# Genetic divergence studies in safflower (*Carthamus tinctorius* L.) germplasm lines

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**Abstract**
Ninety safflower genotypes representing diverse geographic regions were studied for genetic divergence using Mahalanobis $D^2$ static. The genotypes were grouped into 12 clusters. Seed yield contributed maximum to the total divergence. The maximum inter cluster distance was observed between cluster VIII and cluster XI whereas minimum distance between the clusters IV and XII. The accession 41 is the distinct one which can be highly utilized in further breeding programme. Selection of the genotypes from these clusters for hybridization programme may result in good recombinants.

**Keywords:** Safflower, genetic divergence,

Safflower (*Carthamus tinctorius* L) is an important rabi oil seed crop grown on residual soil moisture, referred to as a hardy and drought tolerant crop. Safflower is grown in about 1-2 million hectares with annual production of 0.79 million tons. Genetic variability or divergence present in the material plays a vital role in framing a successful breeding programme. Success of any crop improvement programme depends upon the extent of genetic variability, choice of parents for hybridization and selection procedure adopted. The choice of genetically diverse parents is important in hybridization programme to create variation for selection of useful recombinants. $D^2$ static developed by Mahalanobis (1936) is a powerful tool to measure genetic divergence among genotypes in any crop. It appears that relatively very little work has been reported so far in Andhra Pradesh which is emerging potential safflower growing state in India. Hence, an attempt has been made to study the genetic divergence among 90 different safflower genotypes useful for future hybridization programme in safflower.

The experimental material for the present study cconsisted of 90 safflower germplasm accessions were grown in a randomized block design at Agricultural Research Station, Tandur during rabi 2008-09. Each entry was sown in a plot consisting of single row of 5m length and replicated twice. The inter and intra row spacing was maintained at 45 x 20 cm, respectively. All the recommended agronomic practices were followed to raise a good crop. Data were recorded on five randomly selected competitive plants from each plot for quantitative traits, *viz.,* days to 50% flowering, days to maturity, number of capitula per plant and test weight (g) and seed yield was computed on plot basis and converted to kg/ha. The analysis of genetic divergence was carried out using Mahalanobis $D^2$ statistics. The ninety genotypes studied were grouped in clusters by the Tochers' method suggested by Rao (1952).

Analysis of variance showed the significant differences among the traits studied. By adopting Tochers' procedure, group constellation resulted in the distribution of the ninety accessions into 12 clusters. Cluster II was the largest with 16 genotypes followed by cluster IX with 13 and cluster VII with 12 genotypes, cluster IV, V and VIII each containing 8 genotypes. The cluster XII had solitary accession i.e., 1 as it was not clubbed with any other genotypes. The two clusters IX and VII together included 25 genotypes reflecting genetic closeness and narrow genetic diversity among them which may be attributed to similarity in the base material from which they have been evolved. Cluster IX included 13 genotypes and exhibited highest cluster distance from other clusters.

The results in the present study revealed that distribution of genotypes into different clusters was at random and no relationship was observed between geographic origin and genetic diversity as the genotypes developed from different geographic regions were included in the same cluster (Table 1). These results were in agreement with the earlier findings of Patel (1990). The maximum contribution towards genetic divergence (Table 2) is by seed yield (97.70%) followed by number of capitula per plant (1.07%) and days to 50% flowering (0.90%) The cluster means for the characters studied are represented in Table 3. The cluster VIII recorded highest seed yield of 1608.50kg/ha followed by cluster IX (1343.46 kg/ha) and cluster X (1221.00kg/ha) for that trait indicating that the high yielding genotypes fell in the neighboring clusters. Similar results were reported by Ghongade and Navale (1995).

The average intra and inter cluster distances are presented in Table 4. The intra cluster D2 values ranged from 0 (cluster XII) to 97.73 (cluster IX). The maximum intra cluster distance of 97.75 was observed in cluster IX followed by cluster VIII

(96.84) and cluster XI (78.69). Such intra cluster genetic diversity among the genotypes may be due to heterogeneity, genetic architecture of the populations and past history of selection in development traits. The cluster XII with 0 intra cluster distance had only one genotype (41) indicating the distinctness of the genotype with respect to the traits studied. Similar results were reported by Patil *et al.,* 1991 and Pawar *et al.,* 2006. Cluster X had the low intra cluster distance of 19.90 indicating the similarity among the genotypes included in this cluster. The genotypes among diverse clusters when crossed may through up high heterotic combinations for the traits under consideration.

The data on inter cluster distances and *per se* performances of genotypes were used to select genetically diverse and agronomically superior genotypes. The intercrossing of genotypes belonging to diverse clusters would lead to genetic base in the base populations and greater opportunities for crossing over to occur, which may release hidden variability by breaking close linkages among gene constellations. The results indicate that inclusion of genotypes grouped in cluster VIII (GMU 3216**,** GMU 3237, GMU 3197, GMU 3248, GMU 3212, GMU 3206, GMU 3219, GMU 3249) and cluster XI (GMU 3173, GMU 3180, GMU 3170, GMU 3238, GMU 3163, GMU 3183) with high inter cluster distances in the hybridization programme in safflower is expected to give useful segregants in subsequent generations.

**References**

Pawar, K.M., Joshi, B.M., Jagtap, P.K. and Jawanjal. 2006. Genetic divergence in safflower, *Carthamus tinctorius* L. *J. Oilseeds Res.*, **23**: 96-97.

Mahalanobis, P.C. 1936. On the generalized distance in statistics. *Proceedings on Natural Institute of Sciences*, India, **2**: 49-55.

Rao, C.R. 1952. *Advanced statistical methods in biometrical research*. John Wiley and Sons, Inc. New York.

Patel, D. P. 1990. Genetic divergence in safflower (*Carthamus tinctorius* L.). *Indian J. Pl. Genet. Res.,* **3**: 13-20.

Patil, B. R., Dudhe, R. S., Ghorpade, P. B., Dhumale, D. B. and Deshmukh, M. P. 1991. Studies on genetic divergence in safflower. *J. Maharashtra. Agric. Univ.,* **16**:59-62.

Ghongade, R. A. and Navale, D. A. 1995. Genetic divergence in safflower. *J. Maharashtra. Agric. Univ.,* **20**:249-251.

**Table 1 Distribution of 90 safflower GMU germplasm in different clusters**

| Cluster No | Genotype |
|---|---|
| I | GMU 3157, GMU 3174, GMU 3167, GMU 3191 |
| II | GMU 3178, GMU 3198, GMU 3160, GMU 3239, GMU 3215, GMU 3240, GMU 3250, GMU 3246, GMU 3243, GMU 3192, GMU 3244, GMU 3200, GMU 3224, GMU 3190, GMU 3252, GMU 3188 |
| III | GMU 3229, GMU 3235, GMU 3210, GMU 3227, GMU 3185, GMU 3179, GMU 3165, GMU 3231, GMU 3193 |
| IV | GMU 3234, GMU 3236, GMU 3241, GMU 3211, GMU 3201, GMU 3195, GMU 3217, GMU 3232 |
| V | GMU 3209, GMU 3228, GMU 3218, GMU 3169, GMU 3186, GMU 3189, GMU 3162, GMU 3161 |
| VI | GMU 3164, GMU 3205, GMU 3168 |
| VII | GMU 3182, GMU 3233, GMU 3187, GMU 3181, GMU 3176, GMU 3166, GMU 3203, GMU 3159, GMU 3204, GMU 3230, GMU 3245, GMU 3175. |
| VIII | GMU  3216, GMU 3237, GMU 3197, GMU 3248, GMU 3212, GMU 3206, GMU 3219, GMU 3249 |
| IX | GMU 3221, GMU 3242, GMU 3194, GMU 3207, GMU 3247, GMU 3184, GMU 3251, GMU 3213, GMU 3226, GMU 3225, GMU 3171, GMU 3208, GMU 3172 |
| X | GMU 3177, GMU 3223 |
| XI | GMU 3173, GMU 3180, GMU 3170, GMU 3238, GMU 3163, GMU 3183 |
| XII | GMU 3199 |

**Table 2 Percentage contribution towards genetic divergence in safflower**

| Character | % contribution |
|---|---|
| Days to 50% flowering | 0.90 |
| Days to maturity | 0.32 |
| Number of capitula per plant | 1.07 |
| 100-seed weight (g) | 0.01 |
| Seed  yield (kg/ha) | 97.70 |

**Table 3  Cluster means for various yield attributes in safflower**

| Cluster | Days to 50% flowering | Days to maturity | Number of capitula per plant | 100-seed weight (g) | Seed yield (kg/ha) |
|---|---|---|---|---|---|
| **I** | 66.75 | 96.75 | 19.50 | 4.32 | 440.00 |
| **II** | 76.06 | 106.19 | 22.19 | 4.71 | 865.13 |
| **III** | 79.00 | 109.00 | 28.00 | 4.56 | 1133.56 |
| **IV** | 76.63 | 107.38 | 24.25 | 5.17 | 972.50 |
| **V** | 77.75 | 107.75 | 23.75 | 4.44 | 552.88 |
| **VI** | 81.67 | 110.67 | 16.33 | 4.16 | 351.67 |
| **VII** | 75.92 | 105.92 | 24.75 | 4.66 | 736.50 |
| **VIII** | 74.00 | 104.25 | 36.50 | 5.14 | 1608.50 |
| **IX** | 77.92 | 108.15 | 30.69 | 5.23 | 1343.46 |
| **X** | 72.00 | 102.00 | 40.00 | 4.27 | 1221.00 |
| **XI** | 72.00 | 102.00 | 17.50 | 5.05 | 178.83 |
| **XII** | 81.00 | 111.00 | 33.00 | 3.22 | 1052.00 |

**Table 4  Average inter and intra cluster distances in safflower**

| Cluster | I | II | III | IV | V | VI | VII | VIII | IX | X | XI | XII |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **I** | 25.82 | 426.37 | 694.58 | 533.48 | 120.11 | 95.94 | 301.46 | 1170.53 | 906.25 | 781.53 | 266.64 | 612.69 |
| **II** | | 36.45 | 271.16 | 112.76 | 315.13 | 514.85 | 140.33 | 746.69 | 483.65 | 357.38 | 688.66 | 188.98 |
| **III** | | | 42.36 | 165.28 | 582.40 | 782.96 | 401.25 | 480.20 | 221.98 | 93.73 | 956.60 | 86.51 |
| **IV** | | | | 35.67 | 421.69 | 621.95 | 242.44 | 639.78 | 377.65 | 250.41 | 795.70 | 83.60 |
| **V** | | | | | 51.85 | 206.07 | 193.44 | 1058.21 | 794.14 | 669.33 | 379.17 | 500.41 |
| **VI** | | | | | | 46.64 | 389.19 | 1258.95 | 994.49 | 870.23 | 182.61 | 701.05 |
| **VII** | | | | | | | 74.14 | 875.87 | 612.68 | 487.47 | 562.29 | 319.66 |
| **VIII** | | | | | | | | 96.84 | 280.75 | 392.91 | 1432.13 | 560.27 |
| **IX** | | | | | | | | | 97.73 | 140.23 | 1167.73 | 298.97 |
| **X** | | | | | | | | | | 19.90 | 1043.69 | 169.92 |
| **XI** | | | | | | | | | | | 78.69 | 874.87 |
| **XII** | | | | | | | | | | | | 0.00 |