# GENETIC DIVERGENCE, CORRELATION AND PATH ANALYSIS FOR THE YIELD COMPONENTS OF SAFFLOWER GENOTYPES (CARTHAMUS TINCTORIUS L.)

SNCVL PUSHPAVALLI, T. RAJESHWAR REDDY, G. KUMAR, C. SUDHAKAR

**Abstract:** Genetic divergence and relationship among yield and yield components has been studied among a set of forty seven safflower genotypes at Agricultural Research Station, Tandur during Rabi 2015-16. The genotypes were clustered into ten different groups based on Mahalonobis $D^2$ statistics. Genotypes in cluster VI recorded highest mean values for number of effective capitula/plant, and cluster IX for number of seeds/capitula. 100-seed weight contributed to maximum genetic divergence followed by days to 50% flowering among the genotypes studied. Broad sense heritability estimates was highest for 100-seed weight followed by number of seeds/capitulum. Significant and positive correlation was observed between seed yield and number of capitula/plant. Path coefficient analysis indicated that 100-seed weight exhibited maximum direct effect followed by number of seeds/capitulum.

**Keywords:** Safflower, Genetic divergence, Path coefficient analysis, Correlation, Principal Component Analysis

**Introduction:** Safflower (Carthamus tinctorius L.) is a drought tolerant oilseed crop grown under residual soil moisture conditions. The knowledge of the extent of variability prevalent in each attribute in germplasm, would increase the scope for improving the character through selection. The genetic variability existing in safflower genotypes needs to be studied for breeding high seed yielding varieties. Knowledge of interrelationship between yield and yield contributing traits significantly helps in making selections in breeding material and thus increases the efficiency of breeding program. The success of breeding program also depends on as to how much of the phenotypic variation of a trait is heritable (Kearsey and Pooni 1996), since the efficiency of selection is mainly dependent on the magnitude of genetic variation and heritability of a trait (Falconer and Mackay 1996).

The present study was carried out to assess the magnitude of phenotypic and genotypic variability, phenotypic and genotypic coefficient of variation, heritability in broad sense, expected genetic advance, correlation coefficient and path analysis for utilizing the information in development of superior genotypes of safflower suited to rainfed situations of Telangana state.

**Materials and Methods:** Forty seven safflower genotypes evaluated in Random Block Design at Agricultural Research Station, Tandur during Rabi 2015-16. The entries were sown in 5m long five row plots with a spacing of 45cm between the rows and 20cm between the plants. All the recommended agronomic practices and plant protection methods have been followed to raise a good crop. Data was recorded on five random plants of the following six characters viz, days to 50% flowering, days to maturity, Number of effective capitula/plant, number of seeds/capitula, test weight (g) and seed yield (kg/ha) in each treatment across all replications. Mahalonobis $D^2$ statistic (Rao, 1952) and Principal Component Analysis (PCA) (Jackson, 1991) have been used to analyze genetic divergence among safflower genotypes. The data has been subjected to statistical analysis to calculate genetic divergence genotypic (GCV) and phenotypic (PCV) coefficients 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:** The Mahalonobis $D^2$ values have grouped the forty seven safflower genotypes to ten distinct clusters. The average intra and inter cluster distances are depicted in (Table 1). The maximum intra $D^2$ value is 2.93 (cluster I). The maximum inter cluster distance is between cluster X and VI (8.27) and minimum inter cluster distance is 1.39 between IV and II. Cluster VI recorded highest mean values for number of effective capitula/plant, 100-seed weight (29.73) and seed yield (1159.27) while cluster IX recorded highest number of seeds/capitula (43.73) (Table 2). Thus genotypes of clusters VI and IX may be utilized in breeding program for improvement of seed yield of safflower. Similar results have been reported by earlier researchers (Ghongade and Navale, 1995; Shivani and Sreelakshmi, 2013). Cluster IX recorded earliness for maturity and these genotypes can be utilized for breeding short duration varieties that escape drought. Genotypes from cluster VI and IX can be utilized for development of varieties with short duration along with high seed yield. $D^2$ statistic indicates the characters contributing to divergence (Table 3). Maximum contribution towards genetic divergence is by test weight (34.97%) followed by days to 50% flowering (15.91%). These characters together recorded for more than 50% of the total divergence in the forty seven safflower genotypes studied.

Previous studies have reported that seed yield contributed maximum for genetic divergence (Shivani and Sreelakshmi, 2011, 2013). The four three principal components explained 72% variability with PC2 explaining a maximum variability of 28% (Table 4).

Analysis of variance (data not presented) revealed that significant differences exist among the genotypes for all the characters studied. Genetic parameters like genotypic and phenotypic variability, genotypic and phenotypic coefficient of variation, heritability and genetic advance as percent of mean are presented in Table 5. High coefficients of variation were observed for seed yield followed by 100-seed weight. Phenotypic coefficient of variation was relatively high in comparison to corresponding genotypic coefficient of variation for all the characters studied, indicating environmental influence on these traits. The range of PCV observed was from 3.021 to 43.531 for the characters which indicate the extent of phenotypic variability in the population. PCV was moderate for characters like 100 seed weight (22.449%), number of capitula/plant (15.918%) and number of seeds/capitulum (20.561%). Characters like days to 50% flowering (4.576%) and days to maturity (3.021%) exhibited low PCV. Genotypic coefficient of variation which indicates the extent of genetic variability ranged from 2.804% to 39.724%. Maximum GCV was observed for seed yield (39.724%), followed by 100-seed weight (21.559%) and number of seeds/capitulum (19.292%) providing an opportunity for genetic improvement. Genetic coefficient of variation along with heritability indicates the efficiency of selection (Burton, 1952). Broad sense heritability estimates was highest for 100-seed weight (92.2%) followed by number of seeds/capitulum (88.0%) and days to 50% flowering and days to maturity (86.1%). In the present study 100-seed weight and number of seeds/capitulum have shown high magnitude of heritability in broad sense suggesting that these characters were least affected by environmental variation. Hence selection based on these characters may be more effective for improvement of seed yield in safflower. The estimated genetic advance was high for seed yield (74.6%) and moderate for 100-seed weight (42.6%) and number of seeds/capitulum (37.2%). Genetic advance as percentage of mean was moderate for seed yield/plant, plant height, height of branching from base and 100-seed weight, whereas it was low for the remaining traits (Anjani, 2005).

Phenotypic correlations estimated among the six traits recorded in forty seven genotypes indicated inherent association between any two variables. Seed yield was positively and significantly correlated with 100-seed weight (0.52) and number of capitula/plant (0.45). Positive and significant correlations between seed yield/plant and number of seeds per head have been reported earlier (Ekshing et al., 1994 and Rafiei (2002). Rafiei (2002) found negative but Abulhasani (2003) reported a positive correlation between seed yield and 100-seed weight. A positive correlation of number of capitula/plant and 100-seed weight with seed yield/plant was also reported by Parameshwarappa (1981), Malleshappa (2000) and Bidgoli et al., (2006). In the present study number of seeds/ capitulum was also positively correlated with seed yield although it was not significant. Days to maturity was significantly correlated with days to 50% flowering. This indicated that genotypes which flowered earlier matured earlier. Similar results have been published by earlier researchers in safflower (Rafiei, 2002 and Abulhasani, 2003). Number of seeds/capitulum was negatively correlated with 100-seed weight. Genotypes with bold seeds had less number of seeds/capitulum (Table 6).

In the present investigation path coefficient analysis was carried out to estimate the direct and indirect contribution of various traits to seed yield. 100-seed weight (0.8013) exhibited maximum direct effect followed by number of seeds/capitulum (0.3955) and number of effective capitula/plant (0.3518) (Table 7). These traits are principal components of seed yield and may aid in increasing the seed yield of safflower. The direct effect of number of capitula/plant was more pronounced followed by test weight, plant height and capitulum diameter on seed yield/plant (Malleshappa et al., 1989 and Pandya et al., 1996). The component characters namely number of capitula/plant and 100-seed weight are very important characters for seed yield because they have shown positive and significant correlation with seed yield. Both these characters also had positive and strong direct effects on seed yield. Results of correlation and path analysis suggest that all the characters having positive association with grain yield are also directly contributing to seed yield and hence of selection of genotypes may be reliably done based on these characters.

### Table 1. Average Inter and intra cluster distances ($D^2$) of four clusters of safflower genotypes

| Cluster | I | II | III | IV | V | VI | VII | VIII | IX | X |
|---|---|---|---|---|---|---|---|---|---|---|
| **I** | 2.93 | 3.62 | 3.63 | 4.06 | 4.03 | 3.83 | 4.54 | 3.97 | 4.46 | 6.29 |
| **II** | 3.62 | 0.0 | 1.96 | 1.39 | 1.40 | 5.11 | 3.20 | 2.72 | 3.60 | 4.22 |
| **III** | 3.63 | 1.96 | 0.0 | 1.48 | 2.71 | 4.91 | 2.46 | 4.05 | 4.31 | 3.84 |
| **IV** | 4.06 | 1.39 | 1.48 | 0.0 | 1.91 | 5.29 | 2.19 | 3.77 | 3.57 | 3.81 |
| **V** | 4.03 | 1.40 | 2.71 | 1.91 | 0.0 | 5.49 | 3.85 | 2.35 | 3.19 | 3.84 |
| **VI** | 3.83 | 5.11 | 4.91 | 5.29 | 5.49 | 0.0 | 4.67 | 6.04 | 5.79 | 8.27 |
| **VII** | 4.54 | 3.20 | 2.46 | 2.19 | 3.85 | 4.67 | 0.0 | 5.61 | 4.54 | 5.50 |
| **VIII** | 3.97 | 2.72 | 4.05 | 3.77 | 2.35 | 6.04 | 5.61 | 0.0 | 3.45 | 4.79 |
| **IX** | 4.46 | 3.60 | 4.31 | 3.57 | 3.19 | 5.79 | 4.54 | 3.45 | 0.0 | 5.28 |
| **X** | 6.29 | 4.22 | 3.84 | 3.81 | 3.84 | 8.27 | 5.50 | 4.79 | 5.28 | 0.0 |

### Table 2. Cluster means of four clusters for six characters in safflower genotypes

| Cluster | Days to 50% flowering | Days to maturity | No. of effective capitula/ plant | No. of seeds/ capitulum | 100-seed weight | Seed yield (kg/ha) |
|---|---|---|---|---|---|---|
| **I** | 76.95 | 116.95 | 23.76 | 26.99 | 3.56 | 955.01 |
| **II** | 83.00 | 123.00 | 15.07 | 32.13 | 2.92 | 449.40 |
| **III** | 83.00 | 123.00 | 22.93 | 25.43 | 2.52 | 261.73 |
| **IV** | 83.00 | 123.00 | 19.47 | 30.40 | 2.15 | 390.13 |
| **V** | 83.00 | 123.00 | 20.33 | 39.27 | 2.66 | 874.07 |
| **VI** | 81.33 | 121.33 | 29.73 | 22.13 | 3.72 | 1159.27 |
| **VII** | 83.00 | 123.00 | 21.80 | 21.87 | 1.70 | 267.40 |
| **VIII** | 78.00 | 118.00 | 17.20 | 42.97 | 3.67 | 953.07 |
| **IX** | 72.33 | 112.33 | 24.50 | 43.73 | 2.17 | 914.83 |
| **X** | 83.00 | 123.00 | 28.87 | 40.12 | 1.70 | 254.70 |

### Table 3. Percent contribution of characters towards genetic diversity

| Characters | Contribution % | Times Ranked 1st |
|---|---|---|
| Days to 50% flowering | 15.91 | 172 |
| Days to maturity | 0.0 | 0 |
| No. of effective capitula/plant | 3.79 | 41 |
| No. of seeds/capitula | 14.15 | 153 |
| 100-seed weight | 34.97 | 378 |
| Seed yield/plant | 9.99 | 108 |

### Table 4. Eigen values and proportion of total variance represented by four principal components of safflower genotypes

| | PC1 | PC2 | PC3 | PC 4 |
|---|---|---|---|---|
| Eigen Value (root) | | | | |
| Percent Var. Exp | 12.5 | 28.08 | 17.87 | 14.23 |
| Cumulative Var. Exp | 12.5 | 40.58 | 58.45 | 72.69 |
| Days to 50% flowering | -0.24479 | 0.49062 | 0.34823 | -0.35172 |
| Days to maturity | 0.33403 | -0.45369 | -0.35425 | 0.36548 |
| No. of effective capitula/plant | 0.41941 | -0.26271 | -0.28474 | -0.33083 |
| No. of seeds/capitula | -0.11941 | 0.40871 | -0.36611 | 0.30932 |
| 100-seed weight | 0.30556 | -0.38511 | 0.54734 | 0.27229 |
| Seed yield (kg/ha) | 0.54298 | -0.32163 | 0.35735 | -0.21377 |

*PC= Principal Component

### Table 5. Estimation of GCV, PCV, $h^2_b$ and Genetic Advance of characters of safflower genotypes

| **Characters** | **Variance** | | **Coefficient of variation** | | **$h^2_b$ (%)** | **GA (5%)** | **GA as % of Mean (5%)** |
|---|---|---|---|---|---|---|---|
| | Genotypic | Phenotypic | GCV (%) | PCV (%) | | | |
| Days to 50% flowering | 10.895 | 12.652 | 4.246 | 4.576 | 0.861 | 6.310 | 8.117 |
| Days to maturity | 10.895 | 12.652 | 2.804 | 3.021 | 0.861 | 6.310 | 5.359 |
| No. of effective capitula/plant | 8.725 | 13.954 | 12.587 | 15.918 | 0.625 | 4.812 | 20.503 |
| No. of seeds/capitula | 29.516 | 33.525 | 19.292 | 20.561 | 0.880 | 10.501 | 37.291 |
| 100-seed weight (g) | 0.527 | 0.572 | 21.559 | 22.449 | 0.922 | 1.437 | 42.653 |
| Seed yield (kg/ha) | 124901.9 | 149991.7 | 39.724 | 43.531 | 0.833 | 664.359 | 74.674 |

### Table 6. Estimates of phenotypic correlation coefficients for yield related traits of safflower genotypes

| Characters | Days to 50% flowering | Days to maturity | No. of effective capitula/plant | No. of seeds/ capitula | 100-seed weight | Seed yield (kg/ha) |
|---|---|---|---|---|---|---|
| Days to 50% flowering | | 1.0000 | -0.4436 | -0.0190 | -0.2180 | -0.4350 |
| Days to maturity | | | -0.4436 | -0.0190 | -0.2180 | -0.4350 |
| No. of effective capitula/plant | | | | -0.0439 | 0.0184 | 0.4506*** |
| No. of seeds/capitula | | | | | -0.5194 | 0.0078 |
| 100-seed weight | | | | | | 0.5200*** |

| Characters | Days to 50% flowering | Days to maturity | No. of effective capitula/plant | No. of seeds/ capitula | 100-seed weight | Seed yield (kg/ha) |
|---|---|---|---|---|---|---|
| Days to 50% flowering | | 1.0000 | -0.4436 | -0.0190 | -0.2180 | -0.4350 |
| Days to maturity | | | -0.4436 | -0.0190 | -0.2180 | -0.4350 |
| No. of effective capitula/plant | | | | -0.0439 | 0.0184 | 0.4506*** |
| No. of seeds/capitula | | | | | -0.5194 | 0.0078 |
| 100-seed weight | | | | | | 0.5200*** |

*** Significant at P= 0.001

### Table 7. Phenotypic path coefficient showing direct and indirect effect of characters on seed yield in safflower

| Character | Days to 50% flowering | Days to maturity | No. of effective capitula/ plant | No. of seeds/ capitula | 100-seed weight | Phenotypic correlation with seed yield/plant |
|---|---|---|---|---|---|---|
| Days to 50% flowering | **0.0772** | 0.0772 | -0.0343 | -0.0015 | -0.0168 | -0.4350 |
| Days to maturity | 0.0000 | **0.0000** | 0.0000 | 0.0000 | 0.0000 | -0.4350 |
| No. of effective capitula/plant | -0.1561 | -0.1561 | **0.3518** | -0.0154 | 0.0065 | 0.4506*** |
| No. of seeds/capitula | -0.0075 | -0.0075 | -0.0174 | **0.3955** | -0.2054 | 0.0078 |
| 100-seed weight | -0.1747 | -0.1747 | 0.0147 | -0.4162 | **0.8013** | 0.5200*** |

Figures in bold letters indicate the direct effects, Residual effect = 0.4802

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SNCVL Pushpavalli, T. Rajeshwar Reddy, G. Kumar, C. Sudhakar
Agricultural Research Station, Tandur-501 141, Prof. Jayashankar
Telangana State Agricultural University.