



Research Note

Genetic analysis of F_2 and transgressive segregants for seed yield in safflower (*Carthamus tinctorius* L.)

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Abstract:

The wide range of F_2 variability for seed yield, number of capitula per plant and number of seeds per capitulum in 24 crosses of line x tester set indicated potential of the crosses to throw large number of variable segregants. Maximum number of positive transgressive segregants was found in TSF-1 x SFS 9920, TSF-1 x SSF 658, TSF-2 x ASD-07-10, Sagarmuthyalu x SFS 9920 and Manjira x SSF 698 crosses. F_1 *per se* performance, relative heterosis, D^2 and GCA effects of parents were found to be good indicators for predicting the phenotypic variance and genetic advance for seed yield in F_2 . Average GCA effects of parents had moderate degree of influence on the mean of 10% top yielding plants in F_2 .

Keywords: Safflower, transgressive segregants

Yield is the ultimate product of action and interaction of number of yield components which are governed by large number of genes. Genetic analysis of segregation pattern and transgressive segregation in F_2 is helpful for determining prepotency of different crosses, achieving efficiency in early generation selection and reducing population size in later generation. Establishment of any kind of relationship of parental and F_1 genetic parameters with F_2 segregation potential is helpful for early rejection of inferior crosses in F_1 itself. Safflower crop has great commercial value, but the information on segregation potential and genetic parameters are limited. Hence, the present investigation is an attempt to estimate various genetic parameters with respect to variability and transgressive segregation and to determine the relationship with parents and F_1 hybrids, if any.

The materials for the present investigation comprised of 10 safflower parents (4 lines, Manjira, Sagarmuthyalu, TSF-1 and TSF-2 and 6 testers GMU 1946, ASD-07-09, ASD-07-10, SSF 658, SSF 698 and SFS 9920) and their 24 cross combinations in F_1 and F_2 generations derived through a line x tester mating design. The 10 parents and 24 F_1 s are raised in 3 row plots in rabi season. The F_2 s were raised in 10 row plots. All the experimental material were grown in a randomized block design with three replications with a wide spacing of 45 x 20 cm at Agricultural Research Station, Tandur. Observations

were recorded on ten randomly selected competitive plants in parents and F_1 s and 30 plants in F_2 s for eight quantitative characters in each replication. The mean values pooled over the two seasons in parents and F_1 s were used for estimation of genetic divergence among parental lines following Mahalanobis multivariate D^2 analysis as described by Rao (1960), combining ability estimates as per model given by Kempthorne (1957) and relative heterosis as per standard procedure. The average variance of F_1 and its respective parents was taken as environmental variance V_E and the F_2 genetic variance for a cross was obtained by subtracting V_E from the F_2 phenotypic variance (VF_2). The segregation pattern and the breeding potential of the crosses were analyzed in terms of the frequency of positive transgressive segregants (FPTS), percent positive transgressive segregants (%PTS), mean of positive transgressive segregants (MPTS), average positive transgression over better parent mean (APT), mean of 10% top yielding plants (MTP) and predicted genetic advance under selection (GA) for seed yield in F_2 . The relationship of F_2 segregation parameters (VF_2 , FPTS, APT, MTP and GA) for seed yield with genetic parameters of parents and F_1 s such as parental diversity (D^2), mean seed yield in F_1 (SY), relative heterosis (RH), average GCA effects (Av. GCA) and SCA effects in F_1 was measured by regression analysis.

Variance parameters in F_2 : The analysis of variance (Table 1) revealed that within parent and F_1 variances were due to environmental factors and within F_2 variances were of genetical origin, i.e., due to segregation. The parameters of variability and GA in F_2 for seed yield per plant and number of seeds per capitulum indicated wide range of variability, there by offering ample scope for selection (). All the lines used for the study are stabilized homogenous varieties and the testers are resistant to *Fusarium* wilt caused by *Fusarium oxysporum* fp.carthami.

Transgressive segregation for yield: Comparison of limits of variance in F_2 s with those of respective parental range indicated the presence of transgressive segregation for 17 out of 24 crosses. The FPTS ranged from 3 in TSF-2 x SFS 9920 to 19 in TSF-1 x SFS 9920 with 10 crosses having 10 or more than 10. The MPTS ranged from 10.14 in the cross Manjira x SSF 658 to 19.48 in TSF-2 x SSF 9920 with all the 24 crosses more than 10 grams per plant. The APT of the crosses measured as differences of the MPTS and the better parent mean ranged from 3.74 in the cross Manjira x GMU 1946 to 8.81 in the cross Manjira x SSF 698 with 11 crosses having more than 7 grams. The range of MPT was 8.64 in the cross Manjira x SSF 658 to 16.44 in the cross TSF-2 x SFS 9920 with 12 crosses having MTP of more than 13 g per plant. On simultaneous consideration of parameters of transgression (FPTS, MPTS and APT) along with MTP and GA, 10 crosses were found to have potential for improvement of seed yield (Table 2). Similar results were reported by Ghorpade et al (2001) and Patil et al, (2004).

Relationship of segregation potential of crosses with parents and F_1 hybrids: The regression analysis to assess the relationship of the F_2 segregation potential of crosses with parental and F_1 genetic parameters (Table 3) indicated maximum influence of F_1 per se performance on F_2 variance ($b=0.05$, $R^2=35.6$) and F_2 GA ($b=0.434$, $R^2=47.56$) for seed yield. This finding supports the previous reports suggesting F_1 per se performance as a good indicator of superior crosses in the later generations (Dikshit and Swain, 2001). The two parameters RH ($b=0.004$, $R^2=45.09$) and SCA effects ($b=0.002$, $R^2=23.12$) in F_1 had shown some degree of influence on F_2 phenotypic variance. The average GCA effects of parents assessed in F_1 showed the maximum degree of influence on F_2 phenotypic variance ($b=0.004$, $R^2=47.77$) and F_2 GA ($b=1.83$, $R^2=42.17$) for seed yield. The average GCA had moderate degree of influence on MTP ($b=0.47$, $R^2=39.57$). This finding

Table: 1 Range of parameters of variability, heritability (broad sense) and predicted genetic advance under selection for three characters in F_2 of a 4x6 line x tester set

revealed that GCA effects of parents involved in the cross combinations could be considered as good indicator to predict the potentiality of crosses in F_2 generation. The regression of F_2 parameters on parental diversity as measured by D^2 indicated significant relationship between F_2 segregation potential and parental diversity. The contribution of lines and testers towards the parental variance is genetic in nature. Similarly, significant relationship was found between other F_2 segregation parameters with parental and F_1 genetic parameters.

The present investigation suggested that F_1 per se performance, relative heterosis, D^2 and GCA effects of the parents may be used as good indicators for predicting segregation potential of the crosses in F_2 generation, so that, more attention could be diverted to handle a few superior crosses with large population to increase the frequency of transgressive or desirable segregants.

References:

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| Parameter | Seed yield/plant(g) | Capitula/plant | Seeds per capitulum |
|----------------|---------------------|----------------|---------------------|
| PCV (%) | 24-64 | 12-36 | 19-32 |
| GCV (%) | 18-45 | 10-25 | 12-28 |
| h^2_{bs} (%) | 41-89 | 15-32 | 19-40 |
| GA (g/plant) | 26-54 | 10-19 | 16-35 |

Table: 2 Transgressive parameters (FPTs, % PTS, MPT, APT, MTP &GA) of 24 crosses for yield in F2 of 4 x 6 line x tester set in safflower

| Cross | F2 range | F2 mean (g) | Better parent value (g) | FPTS | % PTS | MPTS (g) | APT (g) | MTP (g) | GA (g) |
|---------------------------|-----------|-------------|-------------------------|------|-------|----------|---------|---------|--------|
| Manjira x GMU 1946 | 5.2-12.1 | 9.34 | 8.69 | 10 | 4.6 | 12.43 | 3.74 | 11.01 | 28.3 |
| Manjira x ASD-07-09 | 4.3 -10.5 | 8.96 | 8.25 | 4 | 4.3 | 13.46 | 5.21 | 11.52 | 26.5 |
| Manjira x ASD-07-10 | 5.6 – 8.6 | 7.84 | 7.26 | 5 | 3.4 | 11.92 | 4.66 | 9.47 | 32.5 |
| Manjira x SSF 658 | 3.4 -7.5 | 6.34 | 6.12 | 8 | 3.5 | 10.14 | 4.02 | 8.64 | 34.6 |
| Manjira x SSF 698 | 5.3 -10.5 | 9.63 | 8.45 | 12 | 5.8 | 17.26 | 8.81 | 12.52 | 29.5 |
| Manjira x SFS 9920 | 7.2-12.6 | 11.97 | 11.25 | 6 | 6.3 | 19.18 | 7.93 | 14.38 | 32.1 |
| Sagarmuthyalu x GMU 1946 | 6.8-9.4 | 8.62 | 8.49 | 4 | 6.9 | 15.20 | 6.71 | 13.48 | 27.1 |
| Sagarmuthyalu x ASD-07-09 | 5.8-9.7 | 8.25 | 8.01 | 7 | 4.8 | 14.12 | 6.11 | 11.62 | 26.5 |
| Sagarmuthyalu x ASD-07-10 | 4.5-10.6 | 8.56 | 7.98 | 9 | 5.3 | 15.09 | 7.11 | 12.58 | 28.4 |
| Sagarmuthyalu x SSF 658 | 5.8-13.4 | 11.61 | 11.23 | 11 | 5.1 | 17.16 | 5.93 | 13.32 | 29.1 |
| Sagarmuthyalu x SSF 698 | 5.7-10.2 | 9.56 | 8.45 | 10 | 4.3 | 15.23 | 6.78 | 12.10 | 27.8 |
| Sagarmuthyalu x SFS 9920 | 6.4-10.5 | 8.72 | 7.94 | 16 | 4.9 | 14.10 | 6.16 | 11.97 | 26.4 |
| TSF-1 x GMU 1946 | 5.6-12.4 | 10.34 | 10.24 | 8 | 6.1 | 17.26 | 7.02 | 13.63 | 33.2 |
| TSF-1 x ASD-07-09 | 4.9-10.4 | 9.43 | 8.56 | 2 | 5.1 | 15.81 | 7.25 | 12.48 | 37.5 |
| TSF-1 x ASD-07-10 | 5.9-12.6 | 11.02 | 10.78 | 10 | 7.5 | 18.05 | 7.27 | 16.03 | 36.4 |
| TSF-1 x SSF 658 | 5.7-12.8 | 10.98 | 10.45 | 17 | 5.7 | 16.00 | 5.55 | 14.23 | 31.9 |
| TSF-1 x SSF 698 | 6.8-13.5 | 12.41 | 12.02 | 6 | 4.1 | 18.18 | 6.16 | 13.67 | 34.7 |
| TSF-1 x SFS 9920 | 5.9-9.4 | 8.49 | 8.04 | 19 | 3.6 | 13.26 | 5.22 | 9.889 | 29.7 |
| TSF-2 x GMU 1946 | 5.4-10.4 | 9.30 | 9.12 | 4 | 4.7 | 16.14 | 7.02 | 12.12 | 29.6 |
| TSF-2 x ASD-07-09 | 4.8-10.7 | 8.84 | 8.54 | 10 | 6.0 | 15.04 | 6.5 | 13.47 | 30.5 |
| TSF-2 x ASD-07-10 | 5.7-13.5 | 10.40 | 10.27 | 16 | 7.1 | 18.12 | 7.85 | 15.66 | 32.4 |
| TSF-2 x SSF 658 | 4.8-10.9 | 9.83 | 8.95 | 8 | 5.2 | 16.11 | 7.16 | 13.41 | 30.1 |
| TSF-2 x SSF 698 | 4.3-12.5 | 10.24 | 9.94 | 5 | 6.8 | 18.02 | 8.08 | 14.68 | 28.7 |
| TSF-2 x SFS 9920 | 6.4-13.8 | 12.31 | 11.58 | 3 | 7.4 | 19.48 | 7.9 | 16.44 | 29.4 |



Table: 3 Regression of F₂ variability parameters for yield on F₁ mean seed yield (SY), parental diversity (D²), relative heterosis (RH), average GCA and SCA effects for yield in F₁ of 4 x 6 line x tester set in safflower

| Regression | a | b | R² (%) |
|-----------------------------------|----------|----------|--------------------------|
| VF ₂ on SY | 2.54 | 0.053* | 35.68 |
| VF ₂ on D ² | 3.66 | 0.064* | 28.05 |
| VF ₂ on RH | 3.24 | -0.041* | 45.09 |
| VF ₂ on Av.GCA | 3.82 | 0.045* | 47.77 |
| VF ₂ on SCA | 2.67 | -0.024* | 23.12 |
| FPTS on SY | 10.035 | -0.132 | 21.42 |
| FPTS on D ² | 5.992 | 0.123 | 51.46 |
| FPTS on RH | 8.504 | 0.006 | 32.12 |
| FPTS on Av.GCA | 8.792 | 1.322 | 26.45 |
| FPTS on SCA | 8.772 | -1.086 | 4.89 |
| APT on SY | 2.576 | 0.404 | 21.15 |
| APT on D ² | 0.122 | 0.285 | 54.45 |
| APT on RH | 6.898 | -0.010 | 42.58 |
| APT on Av.GCA | 6.507 | 0.042 | 24.34 |
| APT on SCA | 6.504 | 0.083 | 12.14 |
| MTP on SY | 3.102 | 1.003 | 15.35 |
| MTP on D ² | 0.619 | 0.547 | 26.78 |
| MTP on RH | 12.816 | 0.000 | 28.20 |
| MTP on Av.GCA | 12.861 | 0.475* | 39.57 |
| MTP on SCA | 12.837 | 0.442 | 8.81 |
| GA on SY | 26.320 | 0.434* | 47.56 |
| GA on D ² | 22.564 | 0.357 | 35.19 |
| GA on RH | 30.672 | -0.003 | 36.48 |
| GA on Av.GCA | 30.919 | 1.835* | 42.17 |
| GA on SCA | 30.537 | -0.005 | 12.57 |