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Short Communication

# Study of variability in the population of sunflower (*Helianthus annuus* L.)

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A precise knowledge of gene effects and genetic component of variance play an important role in selection of a particular breeding methodology. In view of this, the present study was undertaken to estimate the genetic components of variance in an improved population of sunflower (*Helianthus annuus* L.) and to suggest suitable breeding strategy based on these estimates.

An improved population $S1_B$ was used as experimental material for the development of progenies following NCM II design. $S1_B$ population was developed following recurrent S1 family selection from the base population developed by the Project Co-ordinating unit (Sunflower) University of Agricultural Sciences, Bangalore by crossing *inter se* six component lines namely 234B, 207B, PCSP, Morden, Accession 456 and Accession 1260. The material ($S1_B$ population) was planted at the Crop Research Centre of G. B. Pant University of Agriculture and Technology, Pantnagar on 7th November 2000 to initiate the development of progenies A total of eight plants was selected from $S1_B$ population. Among eight selected plants, four plants were kept as males and four as females. The selected plants were bagged with muslin cloth bags. The head of each female plant was divided into four equal parts by pulling out the disc florets. Each part was separated from the other by placing the cardboard strip to make little incision with the help of a knife. The pollen from each male plant was collected separately and used to pollinate each part of female such that each female was crossed with all the four male plants. The group of such eight plants constituted a set. Five such sets were formed in $S1_B$ population. In this way, eighty progenies were developed. Eighty progenies developed from $S1_B$ population was planted on 4th January 2002 in a randomized complete block design with three replications. In each of three blocks, there were eighty plots and each plot consisted of one row of 3-meter length. In all three blocks, the row to row and plant to plant spacing was 60 and 20 cm, respectively. Observations were recorded on eleven traits (Table 1) out of which, day to first flowering, days to 50% flowering, days to maturity and oil content were recorded on plot basis while rest of characters were recorded on ten random plants. Data for individual characters were subjected to analysis as proposed by Comstock and Robinson [1] NCM II design.

The analysis of variance (Table 1) showing the different sources of variation indicated that mean squares due to males were significant for all the traits except days to first flowering and days to 50% flowering. This indicated presence of genetic variation among selected males for all the traits except these two traits. Significant mean squares for females in sets were observed for all the traits, which also indicated the presence of significant genetic variation among females. The mean sum of squares for m × f were significant for all the traits except final plant height. This indicated presence of dominance genetic variance for all the traits except final plant height. The mean sum of squares due to females were higher than mean sum of squares due to males for all the traits except leaf length and seed yield per plant. This indicated presence of maternal effect for all the traits except for leaf length and seed yield per plant.

The progenies exhibited significant variance due to females for all the trait except head diameter, leaf length, leaf width and seed yield per plant, while the variance due to males were significant for only 100-seed weight, seed yield per plant and oil content. Estimates of variance due to interactions (males × females) were significant for all the traits except flowering time plant height and final plant height (Table 2).

The estimates of dominance genetic variance were higher in magnitude for all the traits except final plant height, 100-seed weight, seed yield per plant and oil content, which showed preponderance of dominance genetic variance. Both additive and dominance genetic

**Table 1.** Analysis of variance for different traits in $S1_B$ population of sunflower following NCM II design

| Source of variation | df | Mean sum of squares: Days to first flowering | Days to 50% flowering | Flowering time plant height (cm) | Head diameter (cm) | Leaf length (cm) | Leaf width (cm) | Days to maturity | Final plant height (cm) | 100-seed weight (g) | Seed yield/ plant (g) | Oil content (%) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Sets | 4 | 858.66 | 778.00 | 2015.96 | 25.34 | 84.48 | 309.30 | 240.88 | 1718.83 | 1.54 | 116.10 | 42.09 |
| Replication in sets | 10 | 11.93 | 7.80 | 98.57 | 17.44 | 7.08 | 14.39 | 8.18 | 109.07 | 14.41 | 11.81 | 16.71 |
| Males in sets | 15 | 73.82 | 73.71 | 261.84* | 15.80* | 32.48** | 48.28** | 82.42** | 273.44** | 8.68** | 308.07** | 38.78** |
| Females in sets | 15 | 259.40** | 206.60** | 775.49** | 16.07* | 29.49* | 53.91** | 165.22** | 761.04** | 8.91** | 170.41** | 39.31** |
| Males × females in sets | 45 | 44.04** | 42.94** | 115.44* | 6.82** | 14.59** | 21.01** | 33.30** | 96.16 | 1.55** | 61.08** | 8.25** |
| Error | 150 | 3.12 | 2.52 | 73.20 | 0.67 | 0.27 | 0.41 | 3.10 | 73.95 | 0.38 | 4.14 | 3.27 |

**Table 2.** Estimates of variance components and other allied parameters in $S1_B$ population of sunflower

| Characters | Male variance | Female variance | Male × female variance | Additive genetic variance | Dominance genetic variance | Dominance ratio | Heritability in narrow sense |
|---|---|---|---|---|---|---|---|
| Days to 1st flowering | 2.481±2.24 | 17.946*±7.45 | 13.643**±3.03 | 9.926±8.97 | 54.571**±12.12 | 2.345 | 0.147 |
| Days to50% flowering | 2.564±2.23 | 13.638*±5.95 | 13.474**±2.95 | 10.257±8.93 | 53.895**±11.82 | 2.292 | 0.154 |
| Flowering time plant height | 12.201±7.74 | 55.004*±22.25 | 14.080±8.42 | 48.802±30.97 | 56.320±33.67 | 1.074 | 0.274 |
| Head diameter | 0.748±0.46 | 0.770±0.47 | 2.050**±0.47 | 2.993±1.87 | 8.200**±1.88 | 1.655 | 0.252 |
| Leaf length | 1.491±0.96 | 1.242±0.88 | 4.771**±1.00 | 5.966±3.87 | 19.086**±4.01 | 1.789 | 0.236 |
| Leaf width | 2.272±1.43 | 2.742±1.58 | 6.867**±1.44 | 9.089±5.71 | 27.467**±5.78 | 1.738 | 0.246 |
| Days to maturity | 4.093±2.42 | 10.993*±4.76 | 10.067**±2.29 | 16.373±9.70 | 40.272**±9.17 | 1.568 | 0.274 |
| Final plant height | 14.744±7.98 | 55.407*±21.82 | 7.041±7.19 | 59.096±31.95 | 29.605±28.76 | 0.708 | 0.363 |
| 100 Seed weight | 0.595*±0.25 | 0.613*±0.26 | 0.390**±0.11 | 2.379*±2.00 | 1.560**±0.43 | 0.810 | 0.551 |
| Seed yield/plant | 20.582*±8.80 | 9.110±4.98 | 18.981**±4.20 | 82.328*±35.47 | 75.924**±16.81 | 0.960 | 0.507 |
| Oil content | 2.545*±1.12 | 2.588*±1.13 | 1.660**±0.58 | 10.178*±4.47 | 6.640**±2.32 | 0.807 | 0.507 |

*,**Significant at 1 and 5 per cent level respectively

variances were significant for three traits *viz.*, 100-seed weight, seed yield per plant and oil content. Similar results were obtained in earlier studies [2-7] but the method of analysis was different. The estimate of dominance ratio was more than one for days to first flowering, days to 50% flowering, flowering time plant height, head diameter, leaf length, leaf width and days to maturity indicated overdominance while for final plant height, 100-seed weight, seed yield per plant and oil content partial dominance was important in the determination of these traits .The estimates of narrow sense heritability were low for days to first flowering, days to 50% flowering, moderate for flowering time plant height, head diameter, leaf length, leaf width, days to maturity and high for final plant height, 100-seed weight, seed yield per plant and oil content.

Both seed yield per plant and oil content showed significant additive and dominance genetic variance in the population. This is expected as the base population was improved following S1 recurrent selection. In order to fully exploit the additive genetic variance governing these economic traits, it is suggested to advance the derived population for few more cyclic selection.

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