

HERITABILITY ESTIMATES IN DWARF POPULATION OF SUNFLOWER (*Helianthus annuus* L.)

D.K. Mishra* and D. Roy

*Department of Genetics and Plant Breeding, G.B. Pant University of
Agriculture and Technology, Pantnagar-263 145, India*

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SUMMARY

A comparison of heritability estimates from regression and intra-class correlation analyses in full-sib and half-sib families showed that heritability estimates from regression analysis are lower than intra-class correlation estimates in both types of families. The heritability estimates from half-sib families are higher than from full-sibs for all the traits, except number of leaves per plant and 100-seed weight. A comparison of heritability estimates from offspring-parents, bOP₁, bOP₂ and bOMP showed that heritability estimates from regression of offspring-mid parent are higher than offspring-one parents. Further, leaf length showed the lowest heritability in regression analysis. The overall results showed that plant height, 100-seed weight and number of leaves per plant showed higher heritability.

Key words: sunflower, dwarf population, heritability

MATERIAL AND METHODS

The experimental materials comprised of an open pollinated dwarf population selected from U.P. Council of Agricultural Research (UPCAR) hybrid trial conducted at Crop Research Centre, G.B. Pant University of Agriculture and Technology, Pantnagar, during 1997 and raised for two generations in isolation to allow intermating. This open pollinated dwarf population was used as a base population for carrying out the selection program.

The base material was planted on October 28, 1998. The field was divided into two blocks to make half-sib and full-sib families separately. Each part comprised 16 rows of 14 m in length. At the time of flower initiation, 85 superior plants were selected in the first block and 110 in the second block on the basis of observable phenotypic traits, namely, plant height, general growth and vigor. The selected plants were bagged with muslin cloth bags. In one half of the field, pollen from these selected plants was collected, thoroughly mixed and used to pollinate selected

* Corresponding author

plants to generate half-sib families. In the other half of the field, crosses between pairs of two plants selected on the basis of phenotypic characters were made. Pollen from one selected plant was transferred to the other and *vice-versa* and thus were full-sib families developed. Observations were recorded on selected plants for plant height, head diameter, leaf length, leaf width, number of leaves per plant and 100-seed weight. At maturity, 66 heads were individually harvested from first part of the plot and seeds were collected separately. From the second part of the plot, 45 pairs (90 heads) were individually harvested and seeds of each pair were mixed and collected separately. Seeds collected from both parts were used for evaluation.

RESULT AND DISCUSSION

The selected 66 half-sib and 45 full-sib families were planted on July 10, 1999 in a randomized complete block design with three replicates. In three blocks of each full-sib and half-sib families, there were 45 and 66 plots, respectively, with each plot of one row of 4.2 m in length. The row-to-row and plant-to-plant spacings were 60 and 30 cm, respectively. The observations of half-sib and full-sib families were recorded on individual plant basis for plant height, head diameter, leaf length, leaf width, number of leaves per plant, 100-seed weight and seed yield per plant. Observations for days to first flower, days to 50 per cent flowering and days to maturity were recorded on plot basis.

Heritability estimates were calculated by the following two methods:

1. Regression method (Falconer, 1960)

$$bOP_1 = 1/2 h_n^2$$

$$bOP_2 = 1/2 h_n^2$$

$$bOMP = h_n^2$$

$$2. \text{ Intra-class correlation coefficient (t)} = \frac{\text{Between families variance}}{\text{Between families variance} + \text{Within families variance}} = \frac{\sigma^2 b}{(\sigma^2 \cdot b + \sigma^2 \cdot w)}$$

$$a) \text{ Half-sib, } t = 1/4 h_n^2$$

$$b) \text{ Full-sib, } t = 1/2 h_b^2$$

Analyses of variance for full-sib and half-sib families (Tables 1 and 2) showed the existence of significant variation for all traits under study in both types of families. Intra-class correlation coefficients in full-sib and half-sib analyses and heritability estimates from regression analysis in full-sib and half-sib cases are presented in Tables 3 and 4, respectively. Heritability estimates based on intra-class correlation coefficients in full-sib and half-sib families were higher for all traits. Between full-sib and half-sib families analyses, heritability estimates from the latter were found to be higher for all traits except number of leaves per plant and 100 seed weight. Regression analysis in both half-sib and full-sib families showed higher estimates for plant height but very lower estimates for leaf length. Heritability estimates from regression analysis were much smaller than from intra-class correlation coef-

Source of estimation of heritability	Mean of squares							Seed yield/ Plant	
	Days to first flower	Days to 50% flowering	Days to maturity	Plant height	Head diameter	Leaf length	Leaf width		No. of leaves/ plant
Regression									
bOP ₁				0.5477	0.1824	0.0945	0.2525	0.5653	0.2509
bOP ₂				0.4665	0.2319	0.1363	0.2110	0.3633	0.3324
bOMP				0.5748	0.2533	0.1725	0.3125	0.7489	0.4534
Intra-class correlation coefficient	0.5390	0.5717	0.4940	0.6978	0.2734	0.3810	0.4714	0.9170	0.9659
bOP ₁ = Regression offspring over first parent	bOP ₂ = Regression offspring over second parent								
bOMP = Regression offspring over mid parent									0.8863

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	Days to first flower	Days to 50% flowering	Days to maturity	Plant height	Head diameter	Leaf length	Leaf width	No. of leaves/plant	100-seed weight	Seed yield/Plant
Regression										
bOP _f				0.4175	0.3126	0.0796	0.0608	0.1330	0.5729	
Intra-class correlation coefficient	0.6697	0.6853	0.7156	0.7461	0.8802	0.8148	0.7252	0.5885	0.8940	0.9112
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ficients. It is not surprising as regression analysis provides a measure of narrow sense heritability, whereas intra-class correlation coefficient provides estimate of broad sense heritability. Heritability estimates from regression of offspring-mid parent (bOMP) were higher than offspring-one parent (bOP₁, bOP₂). It was in conformity with the theory that regression offspring-mid parent provides estimate of narrow sense heritability, whereas offspring-one parent provides estimates of 1/2 narrow sense heritability. Higher heritability estimates for different traits in different materials had also been reported by Saravanan *et al.* (1996), Gill *et al.* (1997), Wang *et al.* (1997) and Chikkadevaiah *et al.* (1998).

CONCLUSION

Considering the analyses of both types of families, only plant height gave higher estimates of heritability. Considering the increased variability and heritability for plant height and seed yield per plant, selection could be effective for these traits in this dwarf population and this was supported by the results of expected genetic advance (Table 5). Genetic advance was highest for seed yield per plant in both types of families and comparatively higher in the case of plant height. As the full-sib and half-sib families were developed in the same dwarf population, either type of the families yielded the same results.

Table 5: The mean and genetic advance of different traits in full-sib and half-sib families

Character	Full-sib families		Half-sib families	
	Mean $\pm$ SE	Genetic advance in % of means	Mean $\pm$ SE	Genetic advance in % of mean
Days to first flower	42.86 $\pm$ 0.980	6.4775	44.34 $\pm$ 0.863	8.0925
Days to 50% flowering	45.98 $\pm$ 0.832	5.6382	47.52 $\pm$ 0.727	6.6696
Days to maturity	68.41 $\pm$ 1.109	4.0158	69.48 $\pm$ 0.845	5.8231
Plant height	84.20 $\pm$ 3.325	17.8870	88.98 $\pm$ 2.760	16.3868
Head diameter	15.45 $\pm$ 1.058	7.8408	15.34 $\pm$ 0.445	26.2797
Leaf length	22.28 $\pm$ 1.216	9.4292	23.02 $\pm$ 0.762	22.4117
Leaf width	21.04 $\pm$ 1.196	13.1502	21.20 $\pm$ 0.904	20.9930
Number of leaves/plant	17.91 $\pm$ 0.350	22.2231	17.80 $\pm$ 0.712	13.1010
100-seed weight	5.73 $\pm$ 0.093	30.4718	5.76 $\pm$ 0.199	33.6930
Seed yield/plant	27.83 $\pm$ 1.459	49.1753	27.54 $\pm$ 1.387	54.9878

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EVALUACIÓN DE HERITABILIDAD EN LA POPULACIÓN ENANA DE GIRASOL (*Helianthus annuus* L.)**RESUMEN**

La comparación de valores de heritabilidad, evaluados a base de análisis de regresión y análisis de correlación de las familias en consanguineidad y semiconsanguineidad, mostró que los valores obtenidos por el análisis de regresión, eran más bajos que los valores obtenidos por el análisis de correlación en ambos tipos de familias. Los valores de heritabilidad para las familias en semiconsanguineidad, eran más altos para todas las características, con excepción del número de hojas por planta y peso de 100 granos. La comparación de valores de heritabilidad para la descendencia y los padres, bOP_1 , bOP_2 y $bOMP$ mostró que los valores de heritabilidad obtenidos por regresión de la descendencia y los valores medios de los padres, eran más altos que los valores de la descendencia y de uno de los padres. Aparte de ello, la longitud de la hoja ha mostrado la más baja heritabilidad en el análisis de regresión. La totalidad de los resultados mostró que para la altura de la planta, el peso de 100 granos y el número de hojas por planta, los valores de heritabilidad que se obtuvieron, eran más altos.

ÉVALUATION DE LA TRANSMISSIBILITÉ DANS UNE POPULATION NAINE DE TOURNESOL (*Helianthus annuus* L.)**RÉSUMÉ**

Une comparaison des valeurs de transmissibilité par hérédité estimées d'après l'analyse de régression et l'analyse de corrélation des familles parentales et semi-parentales a montré que les valeurs obtenues par l'analyse de régression étaient inférieures à celles obtenues par l'analyse de corrélation dans les deux types de famille. Les valeurs de transmissibilité par hérédité pour les familles semi-parentales étaient supérieures pour toutes les caractéristiques sauf pour le nombre de feuilles par plante et le poids de 100 graines. La comparaison des valeurs de transmissibilité pour les descendants et les parents bOP_3 , bOP_2 , et $bOMP$ a montré que les valeurs de transmissibilité obtenues par régression des descendants et les valeurs moyennes des parents étaient supérieures aux valeurs des descendants et d'un parent. De plus, la longueur de la feuille a montré le niveau de transmissibilité le plus faible dans l'analyse de régression. Les résultats obtenus ont démontré que la hauteur de la plante, le poids de 100 graines et le nombre de feuilles par plante montraient une plus grande transmissibilité par hérédité.