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GENETIC ANALYSIS FOR OIL PERCENTAGE, PROTEIN PERCENTAGE AND SEED YIELD IN SUNFLOWER (*HELIANTHUS ANNUUS* L.)

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A 4 x 4 diallel cross was made to generate information on type of gene action and to evolve superior genotypes carrying desirable characteristics. Oil percentage indicated additive type of gene action with partial dominance. Genotype Romania had maximum dominant genes due to its closest position at array points and sunflower genotype KNI had maximum recessive genes for this character. Protein percentage and seed yield per plant showed overdominance type of gene action. Romania and Suncom 90 got maximum dominant genes while Suncom 110 and Romania appeared to have maximum recessive genes for protein percentage and seed yield per plant respectively. Among actual diallel values, arry mean of Suncom 90 were high for oil percentage, protein percentage and seed yield per plant which appeared to be the best general combiner. The cross combinations of Suncom 110, KN1 and Romania with Suncom 90 showed the best specific combining ability with that array for oil percentage, protein percentage and seed yield per plant respectively.

Key words: *Helianthus annuus*, Combining ability, Diallel crosses.

Introduction

The genus *Helianthus* belongs to family Asteraceae. Sunflower (*Helianthus annuus* L.) is an important oil seed crop. Little information is available on genetic mechanisms involved in the inheritance of oil and protein content and seed yield per plant. The diallel analysis technique [1-3] provides a handy technique to study the nature of gene action in quantitatively inherited characters in early generations. The present studies were, therefore initiated to ascertain the genetic mechanism and mode of transmission of traits like oil, protein content and seed yield. Manjunath [4] and Sherief *et al.* [5] revealed an overdominance type of gene action for protein percentage and seed yield. The results for oil percentage (additive dominance) are in agreement with the research findings of Dua and Yakava [6] and Kadkol *et al.* [7]. Fick [8] observed dominance type of gene action for oil percentage in sunflower.

The useful information so derived will not only provide an insight into the inheritance pattern of these characters but will also help in deriving proper breeding strategies and selection procedures to tailor new varieties for various production situations in the country.

Materials and Methods

The research work dealing with genetic analysis was conducted at the experimental farm of Plant Breeding and Genetics, University of Agriculture, Faisalabad during 1988-89. Four sunflower cultivars *viz*; Suncom 90, Suncom 110, Romania and KN1, genetically divergent, were selected as parents for hybridization. These cultivars were crossed in all possible combinations (excluded reciprocals) in pots (30 x 30 cm) in the greenhouse during the autumn of 1988.

A list of diallel set of crosses made is as follows:-

(1) Suncom 90 x Suncom 110; (2) Suncom 90 x Romania; (3) Suncom 90 x KN1; (4) Suncom 110 x Romania; (5) Suncom 110 x KN1; (6) Romania x KN1; (7) Suncom 90 (self); (8) Suncom 110 (self); (9) Romania (self); (10) KN1 (self).

The seeds of the genotypes thus obtained were sown in the field during 1989 in a randomized complete block design with three replications. The observational plot consisted of a row of 15 plants of each genotype. The plant to plant and row to row distance was 30 and 75 cm respectively. At maturity 10 plants were randomly selected from each row to record the data on oil percentage, protein percentage and seed yield per plant.

The data were analyzed according to Fisher's [9] analysis of variance technique. For further genetic analysis diallel cross technique was developed [1-3]. Information on gene interactions were obtained by plotting the co-variance of each array against its variance. The slope and position of regression line fitted to the array points lying within a limiting parabola ($Wr^2 = Vp \times Vr$) indicated the degree of dominance and presence or absence of gene interactions.

Results and Discussion

Oil percentage. Vr/Wr graph (Fig. 1) indicated that the regression line with a unit slope intercepted the wr-axis above the origin showing thereby additive type of gene action with little dominance. The linear regression coefficient (b) did not deviate from unity. Therefore, there was no non-allelic interaction present in this respect. From the position of array points (Fig. 1) cultivar Romania was nearer to the origin and there-

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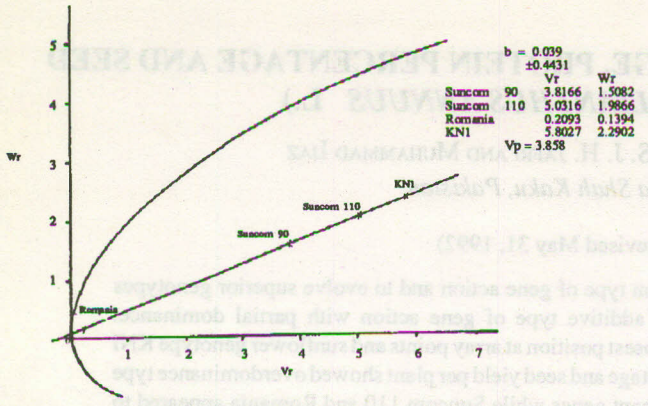

Fig. 1. Vr/Wr graph for oil percentage.

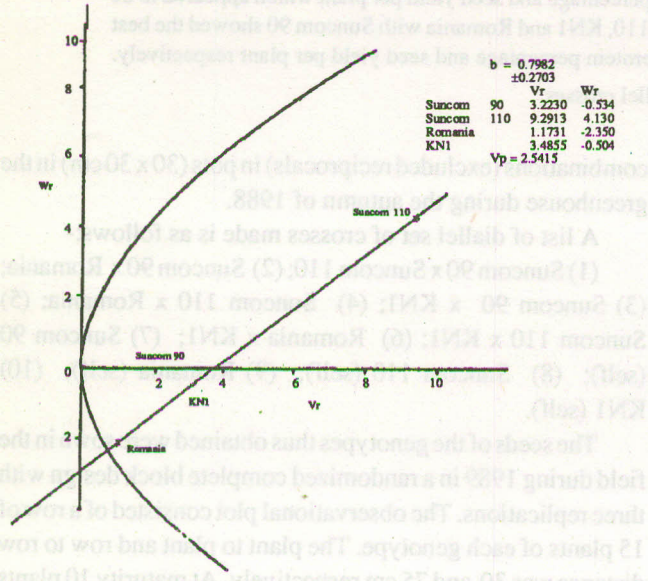

Fig. 2. Vr/Wr graph for protein percentage.

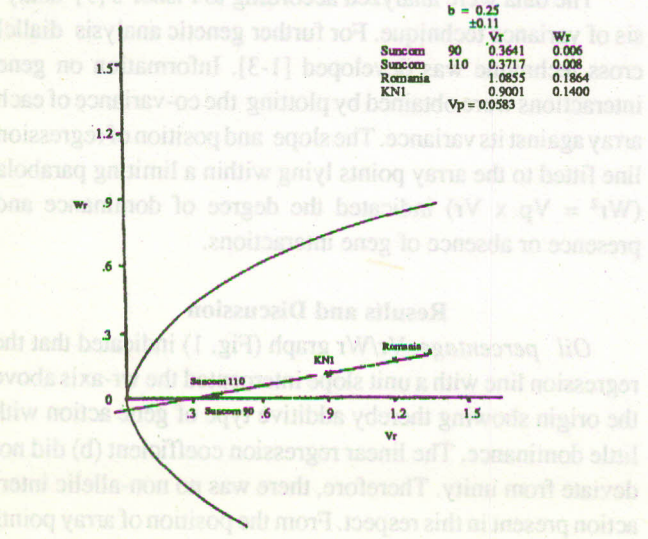

Fig. 3. Vr/Wr graph for seed yield/plant.

fore possessed maximum dominant genes while KN1 was farthest from the origin and possessed maximum recessive genes for this character. Variety Suncom 90 with an array mean of (15.01%) possessed higher general combining ability for oil percentage (Table 1). The cross combination of Suncom 90 x Suncom 110 (17.48%) showed the best specific combining ability as exhibited by comparing mean values within that array. These results are supported by early workers [7, 10-12] but differ from the works of [4,5,8]. It could be because of different genetic material tested under different ecological conditions.

Protein percentage. Vr/Wr regression line (Fig. 2) intercepted the Wr-axis on the negative side. It indicated the overdominance type of gene action. As the linear regression coefficient (b) did not deviate from unity, therefore, no non-allelic interception was present. Position of array points on the regression line revealed that cultivar Romania was nearer to the origin and possessed maximum dominant genes while Suncom 110 was farthest from the origin and had maximum recessive genes for this character. Suncom 90 had the maximum array mean (14.61%) and proved to be the best general combiner for protein percentage (Table 2). Within the array of Suncom 90, the cross between Suncom 90 and KN1 with a value of (16.0210%) appeared to be the best specific combiner. These results confirmed some early findings of Yakova [6], Manjunath [4] and Sherief *et al.* [5]. But they differ from Dua and Yadava [10] and Kadkol *et al.* [7]. This difference can be attributed to the difference in the genetic material and environment.

TABLE 1. 4 x 4 DIALLEL CROSS FOR OIL PERCENTAGE.

	Suncom 90	Suncom 110	Romania	KN1
Suncom 90	15.677	17.487	13.421	13.479
Suncom 110	17.487	15.141	12.414	13.301
Romania	13.421	12.414	13.340	13.103
KN1	13.479	13.301	13.103	18.102
Total	60.065	58.343	52.79	57.986
Array Mean	15.016	14.585	13.069	14.596

TABLE 2. 4 x 4 DIALLEL CROSS FOR PROTEIN PERCENTAGE.

	Suncom90	Suncom 110	Romania	KN1
Suncom 90	16.301	13.132	12.987	16.021
Suncom 110	13.132	18.677	13.258	11.791
Romania	12.987	13.258	15.393	13.632
KN1	16.021	11.791	16.632	15.210
Total	58.441	56.858	55.270	56.654
Array Mean	14.610	14.214	13.817	14.163

TABLE 3. 4x4 DIALLEL CROSS FOR SEED YIELD PER PLANT (gm).

	Suncom 90	Suncom 110	Romania	KN1
Suncom 90	7.766	7.311	8.688	8.300
Suncom 110	7.311	7.377	6.366	6.222
Romania	8.688	6.366	7.233	6.611
KN1	8.300	6.222	6.611	7.633
Total	32.066	27.277	28.899	28.766
Array Mean	8.016	6.819	7.224	7.191

Seed yield per plant (gm). The Vr/Wr regression line (Fig. 3) intercepted the Wr-axis on the negative side and indicated the overdominance type of gene action. As the linear regression coefficient (b) did not deviate from unity, there was no gene interaction for this character. Position of arry points on the regression line revealed that Suncom 90 was near to the origin and possessed maximum dominant genes, followed closely by Suncom 110. Romania was farthest from the origin and had the maximum recessive genes for this character. Suncom 90 had the maximum array mean (8.0166 gm), and proved to be the best general combiner for this character (Table 3). The cross combination Suncom 90 x Romania with a value of 8.688 gm had the best specific combining ability for seed yield per plant. Findings by workers like Manjunath [4] and Sherief *et al.* [5] support these results.

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