

# INHERITANCE OF SEED NUMBER PER SUNFLOWER HEAD IN F<sub>1</sub> GENERATION AND COMPONENTS OF GENETIC VARIABILITY

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## INTRODUCTION

Heterosis in sunflowers is utilized through SC hybrids but it is necessary to know mode of inheritance of characters in F<sub>1</sub> generation in order to efficiently achieve the desired objective.

An advantage of hybrids over varietal populations is an increased seed yield. Thus, "when breeding for high yield, it is necessary to determine characters which correlate with the yield as to make the breeding for these characters the breeding for high yield" (Borojevic, 1972).

Seed number per plant is a character which ensures high yields. Kovacik and Skaloud (1977) found a high correlation between the yield and the number of seeds per plant. Similar results were reported by Putt (1943) and Shabana (1974).

To develop a plant with more than 1500 seeds, it is necessary to breed inbreds for a large number of flowers (Skoric, 1978).

As it is impossible to foresee the combining ability of different inbreds, diallel crossings are performed to determine best inbreds.

An analysis of diallel crosses provides data on the mode of inheritance of the character as well as on the components of genetic variability.

Rao and Singh (1977) pointed out that a large part of the total genetic variance for seed number per head belongs to the dominant component.

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A number of authors studied this problem in other crops: Singh and Anond (1971), Mihaljev (1977), M. Kraljevic-Balalic (1978) found that both additive and non-additive component play an important role in the inheritance of grain number per wheat spike. However, Borojevic (1965) stated that the grain number is inherited partially dominantly, while Patterson and Bitzer (1966) mentioned superdominance in the inheritance of grain number.

The objectives of this study were to evaluate the combining ability of different inbreds, to determine the mode of inheritance of seed number per head of F<sub>1</sub> sunflowers, as well as to determine the components of genetic variability.

## MATERIAL AND METHOD

The following six inbreds originating from different varietal populations were selected for crossing in order to analyse the inheritance of seed number per head: cms-Ha-99, M-6/4, S-59, R-251, R-387, and R-222.

Diallel crossings, excluding reciprocals, were performed during the growing season of 1977. Artificial male sterility in mother plants was induced with a solution of gibberellic acid (3 cm<sup>3</sup> H<sub>2</sub>O 0.5 mg of gibberellic acid per plant at the beginning of budding).

All parents and hybrid combinations in F<sub>1</sub> generation were tested in 1978 at the experimental field of the Institute of Field and Vegetable Crops, Novi Sad, at Rimski Šančevi. The material was planted in three replications, by the method of random blocks. The basic plot included 20 plants at harvest.

The number of seeds per head was determined at the stage of full maturity.

To evaluate the mode of inheritance, we compared the mean values of F<sub>1</sub> generation against the parents' average.

To obtain more information on the components of genetic variance and the effect of genes determining the number of seeds per head, diallel crosses were analysed for combining ability after Griffing (1956), method 2, Model I.

The analysis of the components of genetic variance and the regression analysis were performed by the methods of Jinks (1954), Hayman (1954), and Mather and Jinks (1971).

The coefficient of regression = 1 was checked after Steele and Torrie (1960) through the coefficient of regression (b) and the standard regression error (sb).

## RESULTS AND DISCUSSION

The number of seeds per head depends on the number of flowers and the conditions of fertilization and seed setting in the flowers. Due to these and a number of other factors, the number of seeds may vary considerably (Borojevic, 1965). The examined inbreds and their F<sub>1</sub> hybrid combinations had a high variability in seed number per head (Table 1).

Superdominance was expressed in the inheritance of seed number per head in all F<sub>1</sub> hybrid combinations (Table 1).

The data for the analysis of variance of combining ability showed highly significant differences for general and specific combining ability (Table 2a). As GCA is considered as an indicator of additive genetic variance and SCA as an indicator of non-additive genetic variance, i.e., dominance and epistasis (Griffing, 1956), both additive and non-additive genic action played an important role in the inheritance of seed number per head in F<sub>1</sub> generation. Nevertheless, the ratio GCA: SCA = 0.62 shows that the non-additive genic action was dominant in the inheritance of this character.

Four inbreds had positive values of GCA, two had negative values (Table 2b). The inbred cms-Ha-99 had the highest value of GCA for seed number per head, significantly higher than the other inbreds. This inbred was considered to have the best combining ability for this character. The inbreds R-222 and R-251 were poor combiners for this character.

Nine hybrid combinations had high values of SCA (Table 2c). Those were the crosses between the best general combiners, cms-Ha-99 and S-59, and poor combiners, R-222, R-251, and R-387. Hybrid combinations with high SCA effects include usually one parent with high and another with low GCA. It shows that the combining ability of an inbred pertains exclusively to a certain combination; in combination with another inbred, it does not have to be a poor combiner for a certain character.

For seed number per head, the dominant component (H<sub>1</sub> and H<sub>2</sub>) was much higher than the additive one (D), which means that the main part of genetic variance belonged to the dominant component (Table 3). These results agree with the data of Rao and Singh (1977). Furthermore, as the value of component F (representing interaction between additive and dominant effect) is positive, it means that dominant genes prevailed over the recessive ones in the expression of this character, as confirmed by the frequencies of dominant ( $U = 0.60$ ) and recessive genes ( $v = 0.40$ ) (Table 3).

TABLE 1

*Results of diallel crossings for seed number per head*

	Parent	(1) cms- Ha-99	(2) M-6/4	(3) S-59	(4) R-251	(5) R-387	(6) R-222
1	cms-Ha-99	1262	1750**	2113**	1997**	2126**	1467*
2	M-6/4		1229	1573**	1614**	1849**	1709**
3	S-59			932	2015**	1779**	1655**
4	R-251				881	1546**	1643**
5	R-387					1137	1337*
6	R-222						595

LSD — 0,05 = 177,5

0,01 = 237,5

The calculated value  $V H1/D$ , representing the average degree of dominance, was larger than one indicating superdominance in the inheritance of seed number per head if all combinations are taken into account (Table 3).

The ratio of total number of dominant vs. recessive alleles in all parents showed the prevalence of dominant alleles since the value  $Kd/Kr$  was 1.12, i.e., larger than one (Table 3).

The regression analysis, as a method of evaluation of the intensity of correlations between phenomena, has found its place in quantitative genetics. It serves for the determination of the genetic system of inheritance of quantitative characters.

The mode of inheritance of a certain character may also be defined by the point of intersection of the expected line of regression and  $Wr$  axis in the regression analysis  $VrWr$ . In the case of full dominance, the regression line intersects the origin of the coordinate system. In the cases of superdominance and partial dominance, the regression line intersects the  $Wr$  axis below and above, respectively, the coordinate origin.

The  $VrWr$  (variance, covariance) graph shows that the regression line intersects the  $Wr$  axis below the coordinate origin indicating superdominance (Figure 1), as confirmed by the indicator of the average degree of dominance ( $V H1/D = 2.87$ ), the value of which was larger than one (Table 3).

The dispersion of points along the expected regression line indicates a genetic diversity of parents. The inbred with the largest number of dominant genes has the lowest variance ( $Vr$ ) and covariance ( $Wr$ ) and its corresponding point is closer to the coordinate

TABLE 2

*a) Analysis of variance for combining ability*

Source of vari.	SV	SUM of Sq	Mean Sq	F. val.	F. tab.	
					0,05	0,01
GCA	5	590308,6	118061,7	30,59**	2,45	3,51
SCA	15	2850693,1	190046,2	49,24**	2,00	2,66
E	40		3858,9			

GCA/SCA = 0,62

*b) General combining ability values*

Parent	GCA values	Rank	LSD	
			0,05	0,01
1. cms-Ha-99	155,1**	1		
2. M-6/4	27,1	3		
3. S-59	32,8	2	62,77	83,98
4. R-251	19,9	5		
5. R-387	21,8	4		
6. R-222	216,9	6		

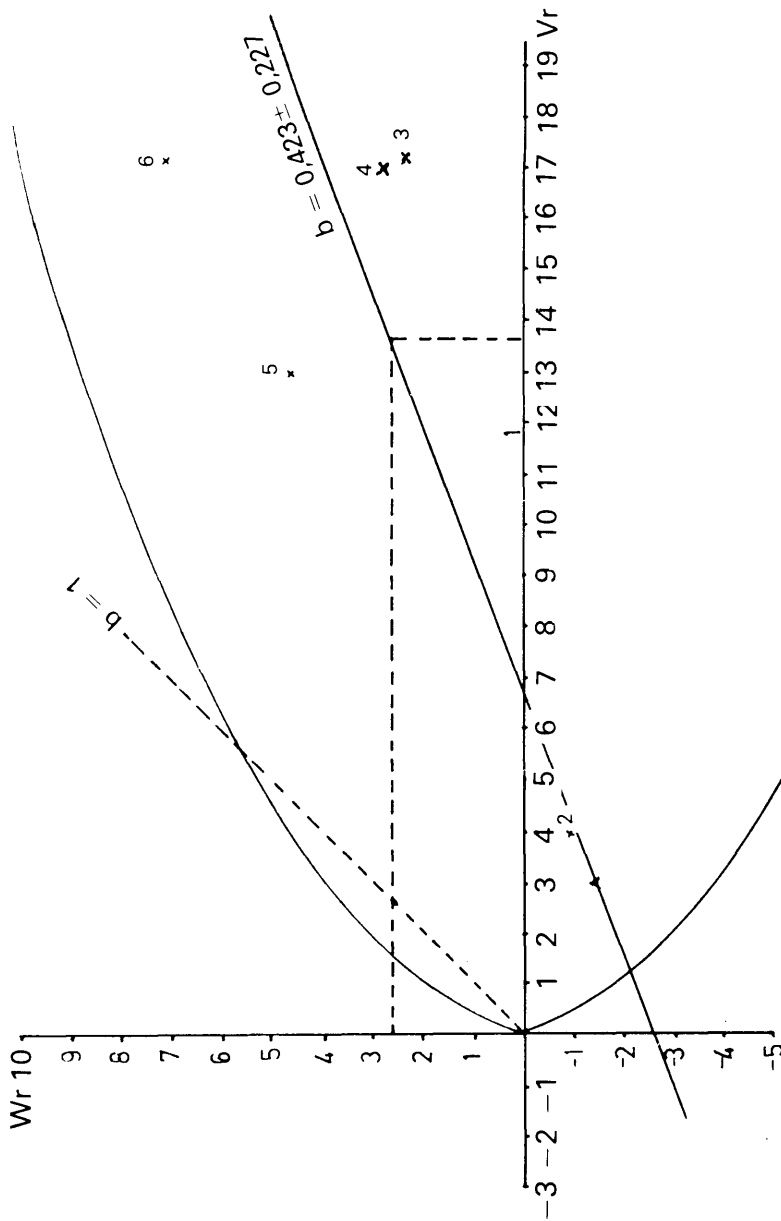
*c) Specific combining ability values*

Parent	2	3	4	5	6
	M-6/4	S-59	R-251	R-387	R-222
1. cms-Ha-99	34,32	391,0**	327,7**	415,0**	5,25
2. M-6/4		21,0	72,75	266,0**	364,7**
3. S-59			468,0**	190,2*	305,0
4. R-251				10,0	345,7**
5. R-387					2,0

LSD 0,05 = 153,7  
 0,01 = 205,7

origin. Conversely, the inbred with the largest number of recessive genes has the largest variance ( $V_r$ ) and covariance ( $W_r$ ) and its corresponding point is further away from the coordinate origin. The inbred whose point lies at the intersection of the limiting parabola and the expected regression line contains either all dominant or all recessive genes.

On the basis of the above, the inbred M-6/4 had the largest number of dominant genes for seed number per head while the inbreds S-59, R-251, and R-222 had the largest number of recessive genes for this character (Figure 1).



SL1 REGRESSION ANALYSIS Vr FOR NUMBER OF SEEDS PER HEAD

Table 3

*Components of variance for seed number per head*

Component	Value
D	60630,7
H1	501723,0
H2	480647,0
F	19825,7
E	3858,9
H2/4H1	0,239
U	0,60
V	0,40
H1/D	2,87
Kd/Kr	1,12

As there was not a single point at the intersection of the limiting parabola and the expected regression line, there were no inbreds containing all dominant or all recessive genes.

In  $WrW'$  graph, the inbred M-6/4 is found in the third square (Figure 2). According to the theory of diallel crossing (Jinks, Hayman, 1954), if some points in an  $WrW'$  graph are dispersed in the third square, they show certain superdominance. It may thus be concluded that the inbred M-6/4 is superdominant parent regarding seed number per head.

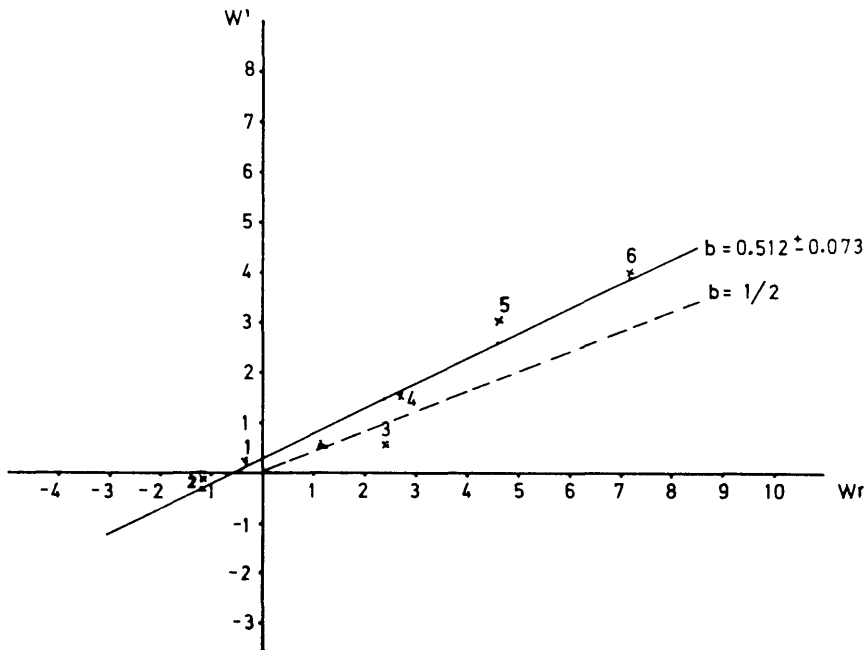
## CONCLUSIONS

Significant differences were found among the examined inbreds regarding the seed number per head.

Non-additive genic action played the main role in the inheritance of seed number per head in  $F_1$  generation of the examined inbreds.

The inbred cms-Ha-99 had a significantly higher value of GCA for seed number per head than the other inbreds. R-222 and R-251 were poor combiners for this character.

Dominant component was larger than the additive one, which agrees with the analysis of variance for combining ability.



## SL.2 REGRESSION ANALYSIS $W_r$ $W'$ FOR NUMBER OF SEEDS PER HEAD

The value of component  $F$  was positive, indicating the prevalence of dominant over recessive genes.

The frequency of dominant genes ( $U$ ) was higher than that of recessive genes ( $V$ ).

The average degree of dominance ( $V H_1/D$ ) was larger than one, indicating superdominance if all combinations are taken into account.

The expected regression line intersects the  $W_r$  axis below the coordinate origin, indicating superdominance in the inheritance of seed number per head in  $F_1$  generation.

The inbred M-6/4 had the largest number of dominant genes and inbreds S-59, R-251, and R-222 largest number of recessive genes for seed number per head.



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