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INHERITANCE OF FATTY ACID COMPOSITION IN F_1 GENERATION OF SUNFLOWERS

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Summary

We tested four genetically distant inbreds of good combining ability for important agronomic characters and their F_1 combinations from diallel crossings. The following conclusions may be drawn:

- The inheritance of higher fatty acids varied in F_1 generation. The cases of superdominance, dominance, intermediacy, and negative heterosis were found.

- Analyses of variance of the combining ability showed that the non-additive component, i.e., dominance and epistasis were important for the inheritance of the content of oleic (18:1) and linoleic (18:2) acid.

- The tested inbreds had different GCA and SCA values.

The components of genetic variance indicate a larger importance of dominant genic action for the expression of oleic and linoleic acids. The frequency of dominant alleles for oleic acid (u=78) and linoleic acid (u=80) was much higher than the frequency of recessive alleles. The dominant and recessive alleles were thus unevenly distributed in the tested inbreds.

The average degree of dominance ($\sqrt{H1/D}$) for oleic and linoleic acids was higher than one, showing that these acids were inherited superdominantly, if all combinations were taken into account. The average degree of dominance for the other higher fatty acids also showed superdominance with the exception of 16:1 and 16:0 which showed partial dominance.

The regression analysis confirmed a higher importance of the non-additive over the additive genic action in the inheritance of oleic and linoleic acids in sunflower oil.

In the inbred RHA-56 dominant genes for the expression of linoleic and oleic acids were prevalent, in the inbred Ha-17 the recessive genes. The other two inbreds had equally distributed dominant and recessive genes.

Introduction

When developing sunflower hybrids on the basis of male sterility, attention should be paid that the hybrids have not only high oil contents in seed but also

a certain quality of oil. The biological value of oil is estimated on the basis of the content of higher fatty acids as well as the content of liposoluble vitamins. Not underestimating the value of other fatty acids and other important components, it has become generally accepted rule to estimate the biological value oil on the basis of the content of essential fatty acids and vitamin E. Regarding oil content, it is important to know the contents of oleic (18:1) and linoleic (18:2) acids as well as their ratio.

Sunflower breeders must incorporate into a hybrid model the desirable oil quality, particularly the total content of higher fatty acids and their ratio. In order to accomplish this task it is necessary to know the mode of inheritance of the content of higher fatty acids in F_1 generation, since the effect of heterosis in sunflowers is used through SC hybrids.

There are numerous literature data on the variability of higher fatty acids in different sunflower genotypes. There are also numerous literature data on the variability of higher fatty acids in sunflower oil in dependence of various environmental factors. Data on the mode of inheritance of higher fatty acids in sunflowers are scarce, although similar data are numerous for other crops, particularly for corn, rapeseed, safflower, etc.

The objective of our study was to determine the mode of inheritance of higher fatty acids in F_1 generations of different sunflower genotypes. Particular attention was paid to the mode of inheritance of linoleic (18:2) and oleic (18:1) acids, and to the components of generic variability.

Material and Method

Four homozygous inbreds from different varietal populations were used in this study: RHA-18 (restorer derived from RHA-265), RHA-56 (restorer originating from Mayak), Ha-9 (inbred developed from the cultivar VNIIMK 1931), and Ha-17, (inbred developed from the cultivar Armavirsky 3497). These inbreds had high GCA and SCA values for important agronomic characters (seed yield, oil content in seed, disease resistance, etc.). The inbreds had the following oil contents in seed: RHA-18 = 43.50%, RHA-56 = 48.30%, Ha-9 = 50.46%, and Ha-17 = 49.67%.

Diallel crossings, excluding the reciprocal ones, were conducted in 1977. The plants used as mothers were male sterilized by the solution of gibberellic acid (3 cm. cub. of H_2O + 0.5 mg of gibberellic acid per plant at the beginning of the stage of budding).

All hybrid combinations in F_1 generation were comparatively tested with parental lines in controlled conditions in greenhouse during winter 1977/78. F_1 combinations were isolated and interlineally pollinated. Oil content in seed was determined by an NMR-analyser, IJS-2-71, the content of higher fatty acids by a Hewlett Packard gas chromatographer.

In order to obtain more complete information on the components of genetic variance and the effect of genes on certain higher fatty acids, we analyzed the diallel crosses for combining ability. The analyses were conducted by the method of Griffing (1956), Method II, Model I.

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

Although we analyzed all higher fatty acids, the volume of the complete results compelled us to present in this paper only the results of the two most important acids: linoleic (18:2) and oleic (18:1) as well as the average degree of dominance for the other higher fatty acids.

Results and Discussion

Our results show that the tested inbreds differed regarding the contents of linoleic (18:2) and oleic (18:1) acids. Differences were also found in the contents of the other higher fatty acids.

TABLE 1. Content of Linoleic (18:2) and oleic (18:1) acids in inbreds and their hybrid combinations and GCA and SCA values.

		18:1			18:2		
No.	Inbreds and Hybrids	Content of acid in oil %	GCA	SCA	Content of acid in oil %	GCA	SCA
1	RHA-18	26.67	1.68**	-	59.41	-1.65	-
2	RHA-56	22.77	-1.68	-	64.88	1.54**	-
3	Ha-9	21.83	0.21	-	65.16	-0.28	-
4	Ha-17	24.36	-0.21	-	63.57	0.50**	-
5	RHA-18xRHA-56	21.86	-	-1.84	64.01	-	0.63*
6	RHA-18xHa-9	27.28	-	1.75**	60.41	-	-1.14
7	RHA-18xHa-17	23.80	-	-1.25	64.26	-	1.91**
8	RHA-56xHa-9	22.38	-	0.20	64.45	-	0.3
9	RHA-56xHa-17	18.34	-	-3.43	68.48	-	-1.08
10	Ha-9xHa-17	26.16	-	2.50**	60.57	-	-3.14
	LSD 5%	0.44	0.21	0.35	0.64	0.25	0.50
	1%	0.60	0.29	0.48	0.07	0.34	0.68

The hybrid combinations of F_1 generation had different contents of linoleic and oleic acid. The mode of inheritance of the content of oleic acid in sunflower differed in F_1 generation from combination to combination -- there were cases of superdominance (Ha-9 x Ha-17), dominance, intermediacy, and negative heterosis. Similar character of inheritance in F_1 generation was also found for the linoleic acid.

The analysis of variance of combining ability showed that the non-additive component, i.e., dominance and epistasis were important for the inheritance of the contents of oleic and linoleic acids in sunflower oil in F_1 generation. The ratio GCA/SCA was smaller than one. It may be thus concluded that the non-additive genic action was considerably more important in the inheritance of higher fatty acids than the additive action.

Ha-9 x Ha-17 and RHA-18 x Ha-9 had the highest SCA values for the oleic acid, RHA-18 x Ha-17 and RHA-18 x RHA-56 for the linoleic acid. It is characteristic that high GCA and SCA values for oleic and linoleic acids did not coincide but were found in different inbreds and hybrid combinations.

These results show that the crosses with high SCA value usually include one parent with a high GCA value and another parent with a low GCA value. Therefore, the combining ability of an inbred pertains only to a concrete combination; in combination with another inbred, it does not have to be the poorer combiner for the character in question.

The additive component for oleic (D=6.56) and linoleic (D=14.63) acids was considerably smaller than the components of variance owing to the dominant genic action (H_1 and H_2). It shows that the major part of the genetic variance belongs to the component of dominance, which agrees with the results of the analyses of combining ability.

TABLE 2. Components of genetic variability.

No.	Component	Higher fatty acids 18:2	Higher fatty acids 18:1
1	D	14.63	6.56
2	H_1	31.6	28.38
3	H_2	20.06	19.56
4	E	0.046	0.023
5	F	18.28	4.34
6	$\frac{H_2}{4H_1}$	0.159	0.172
7	$\sqrt{\frac{H_1}{D}}$	1.47	2.07
8	u	0.80	0.78
9	v	0.20	0.22
10	K_D/K_R	2.47	1.37

A positive value of F (interaction of additive x dominant effect) for oleic and linoleic acids indicates that there was a larger number of dominant alelles in relation to the recessive ones in the expression of these acids. It was also confirmed by the calculation of the frequency of alelles. The frequency of dominant alelles for oleic (u = 78) and linoleic (u = 80) acids was considerably higher than the frequency of the recessive ones. (Table 2.)

The value $H_2/4H_1$ shows that the dominant and recessive alelles for the tested fatty acids were not evenly distributed among the tested inbreds. Likewise, the ratio for the total number of dominant versus recessive alelles (Kd/Kr) shows that the dominant alelles were prevalent in all parents.

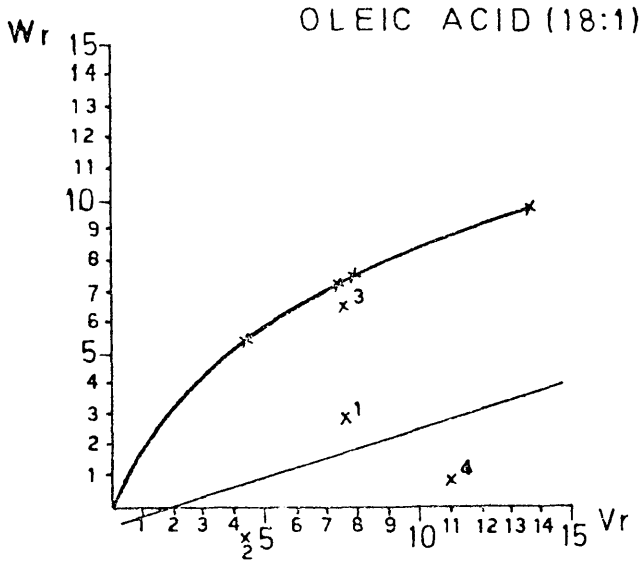
The average degree of dominance ($\sqrt{H_1/D}$) for oleic and linoleic acids was higher than one, showing that these acids were inherited superdominantly, if all combinations are taken into account. The average degree of dominance for the higher fatty acids also showed superdominance, with exception of 16:0 and 16:1 which show partial dominance.

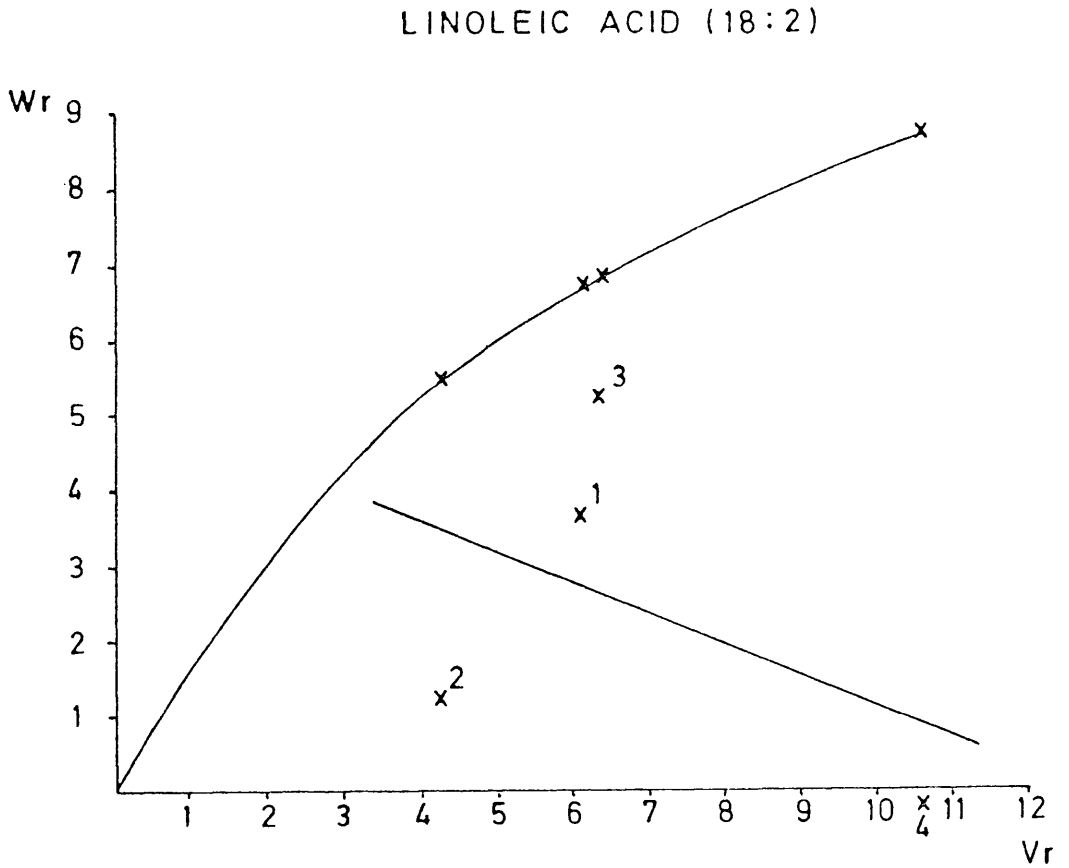
TABLE 3. Average degree of dominance for higher fatty acids in F_1 generation.

Component	Higher fatty acids									
	14:0	16:0	16:1	17:0	18:0	18:1	18:2	18:3	20:0	22:0
$\sqrt{\frac{H_1}{D}}$	1.73	0.94	0.54	1.03	1.52	2.07	1.47	3.65	6.5	1.04

The regression analyses confirmed a higher importance of the non-additive over the additive genic action in the inheritance of oleic and linoleic acid in sunflower oil. For linoleic acid (18:2) particularly, the average of the expected regression line with Wr showed superdominance, except in the regression analysis VrWr. The distribution of the points along the expected regression line indicates the genetic divergence of the tested inbreds. In the inbred RHA-56, dominant genes for the expression of linoleic and oleic acids were prevalent, in the inbred Ha-17 the recessive genes. The other two inbreds had equally distributed dominant and recessive genes.

Graph.1: REGRESSION ANALYSIS Vr Wr





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