

INHERITANCE OF INCREASED OLEIC ACID CONTENT IN SUNFLOWER SEED OIL

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SUMMARY

The inheritance of increased (mid) oleic acid content about 62% of an inbred line, LG27, was studied in the crosses with high oleic HA89OL (89%), high oleic LG26OL (86%) and low oleic LG28 (22%).

Fatty acid composition of single seeds was determined by gas chromatography of methyl esters.

The crosses of high x increased oleic and high x low oleic genotypes revealed the genetic control on oleic acid content with multiple allelism. Three alleles of one gene - dominant *Ol*, recessive *ol*¹ and recessive *ol* lead in homozygote to the high, increased and low oleic phenotypes, respectively.

Genetic segregations in F₂ and BC of the cross of increased x low oleic lines did not show clear-cut phenotypic classes. No maternal inheritance was observed.

Key words: inheritance, oleic acid, sunflower

INTRODUCTION

There is a wide range of phenotypic variability in oleic acid content of cultivated sunflower seed oil. This varies from 10 to 95%.

A normal phenotype can be divided into low (10-30%), common (30-50%) and increased or mid (50-70%) oleic ones. Due to the strong negative correlation between oleic and linoleic percentage, a low oleic phenotype is considered a high linoleic.

Oleic acid content within a normal phenotype is known to be essentially influenced by temperature during the seed development. Each 1°C - increase of temperature leads to about 2% - increase of oleic acid content.

A mutant high oleic phenotype (Soldatov, 1976) consists of high oleic (70-90%) and very high oleic (90-95%) classes. This is relatively temperature-stable.

The research on the inheritance of low oleic (Simpson *et al.*, 1989) and increased oleic traits (Fernandez-Martinez *et al.*, 1987) has not found any particu-

lar genes. The main difficulty was the lack of clear-cut fatty acid classes in segregating progenies.

The high oleic mutation (derived from Pervenetz variety) is controlled by single dominant *Ol* gene in several crosses. There is a number of deviations from monogenic segregation in different genetic backgrounds. The main observation was the lack of mutant phenotypes in hybrid progenies.

To explain the above deviations the next hypothesis have been introduced - one recessive modifier *ml* of *Ol* gene (Miller *et al.*, 1987), three complementary genes *Ol*₁, *Ol*₂ and *Ol*₃ (Fernandez-Martinez *et al.*, 1989) and incomplete penetrance with genetically unstable expression of *Ol* gene (Demurin *et al.*, 1996).

The last hypothesis has been developed from the special genetic program to coordinate different explanations for the inheritance of *Ol* mutation.

Another point of our interest within the program was to understand the mode of inheritance of increased oleic acid content. The data are presented in this paper.

MATERIAL AND METHOD

The research was carried out at the Institute of Field and Vegetable Crops, Novi Sad, Yugoslavia.

Four inbred lines with the same period of flowering were used - high oleic HA89OL (Spain) and LG26OL (Russia), increased oleic LG27 (Russia) and low oleic LG28 (Russia).

The *F*₁ was obtained in summer field 1994, the *F*₂ and BC - in greenhouse 1994 and 1995. Head by head crosses were performed. The seeds from a middle zone of head were harvested.

Fatty acid composition of single seeds was determined by gas chromatography of methyl esters.

RESULTS AND DISCUSSION

Parents and *F*₁. The mean values and limits of single seed variation in oleic acid content of high, increased and low oleic parent lines were clear-cut (Table 1). The range of trait variability per head of high oleic HA89OL and LG26OL was about 3 times smaller than LG27 and LG28. It supports the data that the *OlOl* homozygote is relatively stable in respect to the environment modifications.

Reciprocal crosses of high x increased oleic and high x low oleic showed the dominance of mutant high oleic character in *F*₁ (Table 2). *F*₁ seeds of the cross of increased (LG27) x low (LG28) oleic were intermediate.

Table 1: Fatty acid composition of single seeds of parent lines (field, 1994)

Line	Fatty acid content (%)				Oleic acid content (%)		
	16:0	18:0	18:1	18:2	min	max	range
HA89OL	5	4	89	2	87	90	3
LG26OL	6	5	86	3	83	87	4
LG27	5	5	62	28	54	66	12
LG28	10	2	22	66	17	27	10

Table 2: Oleic acid content of single seeds in F₁ (field, 1994)

Cross	Seed number	Oleic acid content (%)			Range
		mean	min	max	
LG27 x HA89OL	10	87	86	90	4
LG27 x LG26OL	10	90	90	90	0
HA89OL x LG27	10	89	88	90	2
HA89AOL x LG27	10	89	85	90	5
LG28 x HA89OL	10	86	82	90	8
LG28 x LG26OL	10	85	79	90	11
HA89OL x LG28	10	87	85	88	3
HA89AOL x LG28	10	89	88	91	3
LG27 x LG28	10	46	45	47	2
LG28 x LG27	10	34	32	39	7

F₂ and BC. In greenhouse 1994 the HA89OL averaged 91%, LG27 - 67% and LG28 - 46% of oleic acid as parent phenotype (Table 3). Nevertheless no overlapping was observed.

Table 3: Oleic acid content of single seeds in F₂ and BC (greenhouse, 1994)

Genotype	Oleic acid content (%) mean (min-max)			Range
	high	increased	low	
P				
HA89OL	91 (90-92)	-	-	2
LG27	-	67 (63-71)	-	8
LG28	-	-	46 (42-51)	9
F ₂				
LG27 x HA89OL	93 (88-95)	69 (66-74)	-	29
LG27 x LG26OL	91 (84-93)	71 (65-74)	-	28
HA89OL x LG27	91 (88-94)	60 (52-66)	-	42
BC				
(HA89OL x LG27) x LG27	93 (92-95)	75 (71-78)	-	24
F ₂				
LG28 x HA89OL	92 (85-94)	-	38 (26-49)	68
LG28 x LG26OL	92 (85-93)	-	50 (40-58)	53
HA89OL x LG28	90 (85-93)	-	48 (42-52)	51
BC				
(HA89OL x LG28) x LG28	89 (75-93)	-	49 (39-57)	54

Parent range per head was from 2 to 9%. The F_2 and BC range per head varied from 24 to 68% due to segregation in the two parent phenotypic classes found (Table 3). There was "high / increased oleic" and "high / low oleic" types of segregation. The χ^2 - test showed these types to fitt 3:1 (F_2) and 1:1 (BC) ratios (Table 4).

Table 4: Segregation of single seeds for oleic acid classes in F_2 and BC (greenhouse, 1994)

Cross	Seed number in class			χ^2 for ratio		P
	high	increased	low	3:1	1:1	
F ₂						
LG27 x HA89OL	42	8	0	2.16	-	0.2-0.3
LG27 x LG26OL	34	16	0	1.31	-	0.2-0.3
HA89OL x LG27	36	14	0	0.24	-	0.5-0.7
BC						
(HA89OL x LG27) x LG27	21	27	0	-	1.28	0.2-0.3
F ₂						
LG28 x HA89OL	39	0	11	0.24	-	0.5-0.7
LG28 x LG26OL	39	0	11	0.24	-	0.5-0.7
HA89OL x LG28	32	0	18	3.23	-	0.05-0.1
BC						
(HA89OL x LG28) x LG28	22	0	28	-	0.72	0.3-0.5

This mode of inheritance can be explained with three alleles of one gene - Ol , ol^1 and ol for high, increased and low oleic content, respectively. Genetic control by multiple allelism with additive action for acid content is known in safflower seed oil (Ladd *et al.*, 1971).

Table 5: Variability of oleic acid content of single seeds in F_2 and BC in the cross of increased and low oleic lines (greenhouse, 1995)

Genotype	Seed number	Oleic acid content (%) mean (min-max)	Range
P			
LG27	10	52 (42-57)	10
LG28	10	20 (19-21)	2
F_2			
LG27 x LG28	50	35 (28-48)	20
LG28 x LG27	50	31 (23-45)	22
BC			
LG27 x (LG27 x LG28)	50	53 (40-65)	25
LG27 x (LG28 x LG27)	50	46 (33-59)	26
LG28 x (LG28 x LG27)	50	25 (16-30)	14
LG28 x (LG28 x LG27)	50	26 (19-32)	13

In order to understand the inheritance of increased oleic trait in the cross with low oleic line, the F_2 and BC were obtained in greenhouse 1995 (Table 5).

Parent phenotypes of LG27 and LG28 were 52% and 20% of oleic acid content, respectively.

The F_2 and BC showed genetic variability with no clear phenotypic classes. The same kind of inheritance of increased oleic acid content of wild sunflower line AO-6 in the cross with common oleic line P-21 was previously reported (Fernandez-Martinez *et al.*, 1987).

Both small range of the trait variability within single head F_2 and BC seed populations (13-26%) and essential environment influence on homozygote parent genotypes of LG27 and LG28 (about 10% in different conditions) have not allowed to observed phenotypic segregation and to apply χ^2 - test.

Observation on means of the F_1 , F_2 and BC showed increased oleic acid content not to be maternely inherited. Maternal effect is still unproved. Additional research is needed for correct statistical analysis.

Table 6: Proposed description of the genetic collection for oleic acid content

Line	Genotype	Phenotype, oleic acid content (%)	Oleic class
HA89OL	<i>Ol Ol</i>	89	high
LG26OL	<i>Ol Ol</i>	86	high
LG27	<i>ol¹ ol¹</i>	62	increased (mid)
LG28	<i>ol ol</i>	22	low

Nevertheless crossing with a high oleic mutation helped to escape the above difficulties and to identify *ol¹* allele. The genetic collection of inbred lines for oleic acid character is presented in Table 6.

CONCLUSIONS

Increased oleic acid content about 60% is controlled by recessive allele, designated *ol¹*, of *Ol* gene. Thus the multiple allelism of the gene includes dominant *Ol* (high oleic) and both recessive *ol¹* (increased oleic) and *ol* (low oleic) alleles.

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HERENCIA DEL CONTENIDO AUMENTADO DEL ACIDO OLEICO EN EL ACEITE DE GIRASOL

RESUMEN

La herencia del contenido del ácido oleico ha sido estudiado en las líneas inbred con el contenido (medio) aumentado del ácido oleico, LG27 (cerca de 62%) cruzada con la línea altamente oleica HA89OL (89%), la línea altamente oleica LG26OL (86%) y la línea bajo oleica LG28 (22%).

El contenido de ácidos grasos en granos singulares era determinado por cromatografía por el gas metiléster.

Con el cruce de genotipos con el contenido alto y aumentado del ácido oleico y de genotipos con el contenido alto y bajo fué constatado que el contenido del ácido oleico era bajo el control genético de varios alelos. Tres alelos de un gen - dominante *Ol*, recesivo *ol*¹ y recesivo *ol* - hacen formar los fenotipos homocigóticos con el contenido del ácido oleico alto, aumentado y bajo.

Las separaciones genéticas en las generaciones F₂ y BC del cruce de genotipos con el contenido del ácido oleico aumentado y bajo no han señalado las categorías de fenotipos claramente separadas. No fué constatada tampoco la presencia de la herencia materna.

HÉRITAGE D'UN CONTENU AUGMENTÉ D'ACIDE OLÉIQUE DANS L'HUILE DE TOURNESOL

RÉSUMÉ

L'héritage du contenu d'acide oléique a été étudié dans les lignes inbred avec contenu augmenté (moyen) d'acide oléique, LG27 (environ 62%) dans les croisements avec les lignes à haut niveau d'acide oléique HA89OL (89%), LG26OL (86%) et à bas niveau oléique LG28 (22%).

La composition en acides gras de certaines graines a été déterminée par la chromatographie gazeuse d'esters méthyliques.

Le croisement de génotypes à contenu élevé avec des génotypes à contenu augmenté d'acide oléique et le croisement de génotypes à contenu élevé avec des génotypes à contenu moindre a révélé que le contenu d'acide oléique se trouve sous le contrôle génétique de plusieurs allèles. Trois allèles d'un gène - dominant *Ol*, récessif *ol*¹, récessif *ol* mènent à la création de phénotypes homozygotes à contenu élevé, augmenté et moindre d'acide oléique.

Les divisions génétiques dans les générations F₂ et BC par le croisement de génotypes à contenu augmenté avec des génotypes à contenu moindre n'a pas montré de catégories de phénotypes clairement distinctes. On n'a pas observé d'héritage maternel.