GENETIC COLLECTION OF OLEIC ACID CONTENT IN SUNFLOWER SEED OIL

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Received: November 15, 2011 Accepted: December 10, 2011

SUMMARY

Development of genetic collection is considered to be an essential part of genetic resources of cultivated sunflower. The VNIIMK genetic collection of identified alleles determining oleic acid content in the seed oil consists of about 50 constant inbred lines. Fourteen of them are in a core collection. The general range of this trait varies from 20 to 92%. These inbred lines correspond to four main phenotypic classes: low, conventional, mid and high oleic. The normal line RIL100 was shown to contain a high oleic mutation *Ol* in hypostatic condition. The mid oleic LG27 averagely 67% does not contain the high oleic mutation in genetic background. The high oleic LG 26 with relatively low content of oleic acid, about 86%, possesses resistance to suppressor's actions.

Key words: fatty acid composition, mutation, gene, suppressor

INTRODUCTION

The genetic collection of identified alleles determining a character is the permanent result of screening for genetic variability, inheritance analysis and allelic test with environment influence control (Fernandez-Martinez *et al.*, 2009; Seiler and Jan, 2010; Vear, 2010). The clear correspondence between genotype and phenotype is believed to be a goal.

Oleic acid content belongs to the main characteristics of the seed oil quality. There were many attempts to carry out the genetic research with this trait. The most of them were dedicated to a high oleic mutation of variety Pervenets, obtained by Soldatov (1976). There are data of another mutant line with 80% of oleic acid content from Bulgaria (Ivanov, P. and Ivanov, I., 1982) and a mutant genotype with up to 90% of oleic acid content from Italy (Andrich *et al.*, 1992). Nevertheless, Pervenets was exclusively used as a donor of the high oleic trait in breeding programs worldwide.

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Research on genetic control of a high oleic mutation led to the hypotheses of one dominant gene *Ol* (Fick, 1984; Urie, 1985), major gene *Ol* and gene-modifier *ml* (Miller *et al.*, 1987), recessive gene *ol* and dominant *Ml* (Fernandez *et al.*, 1999), three complementary genes *Ol1*, *Ol2* and *Ol3* (Fernandez-Martinez *et al.*, 1989), five genes *Ol1*, *Ol2*, *Ol3*, *Ol4* and *Ol5* (Velasco *et al.*, 2000), gene *Ol* with incomplete penetrance determined by genotypic epistatic factors of reversion (Demurin *et al.*, 1996; Demurin, 2003), high oleic locus oleHOS and suppressor locus Sup (Lacombe *et al.*, 2001; Berville, 2010). All of these hypotheses focus on explanation of the lack of mutant seeds from a monogenic number expected in the progenies of cross-breeding mutant with normal lines.

This paper describes the results of research which have been obtained since 1982 at VNIIMK in order to develop the genetic collection of sunflower for oleic acid content in the seed oil.

MATERIALS AND METHODS

Constant inbred lines of the genetic collection were involved in the research. It includes both lines developed at VNIIMK and the lines from other institutions. The next designations of the lines are used: VK (VNIIMK, Krasnodar) and LG (line genetic) – from VNIIMK; K – from VIR; HA and RHA – from USDA; RIL (recombinant inbred line) – from INRA.

The plants were grown, self-pollinated or crossed in the field plots of VNIIMK, Krasnodar during summer time at 70×35 cm population density. Greenhouse chambers were used in winter annually.

Fatty acid composition of the oil from the seeds was determined by gas chromatography of methyl esters.

RESULTS AND DISCUSSION

There are about 50 constant inbred lines of sunflower in the VNIIMK collection regarding oleic acid content in the seed oil. The general range of this trait varies from 20 to 92% in Krasnodar weather conditions at 45° northern latitude with average temperature of 27°C in July. At that time seed maturation usually begins. The range can be divided into four main phenotypic classes: low, conventional, mid (increased) and high oleic (Figure 1). Two gaps surrounding a mid oleic class have no inbred lines with corresponding phenotypes.



Figure 1: Oleic acid classes of homozygous genotypes (%)

A low oleic class from 20 to 30% includes two lines. LG 28 is originated from selfed progenies of the old VNIIMK open pollinated variety of Kruglik A-41. Another one of RHA 413 was developed in the USDA, ND, Fargo.

A conventional oleic class from 30 to 55% can be divided into common and maximum subclasses. The first is abundant with dozens of lines. The most interesting representative of that is RIL 100 (83HR4 × RHA 345) which was created in the frame of a research program of INRA, France. RIL 100 possesses a normal phenotype of oleic content, while the molecular marker shows an existence of the high oleic mutation. French geneticists have tried to explain this phenomenon by probable action of a suppressor (Berville, 2010). We have carried out an inheritance analysis in Krasnodar, VNIIMK with the cross-breeding of LG 28 × RIL 100. Parents and F_1 were normal in oleic acid content of 27, 40 and 32% respectively. The F_2 seeds segregated in two classes of 111 normal: 9 high oleic. The high oleic mutant segregants in the F_2 from the cross of phenotypic normal lines are a crucial evidence of suppression over *Ol* mutation obtained for the first time with classical hybridological approach. The dominant epistatic action of the suppressor as a major gene might be proposed on the data obtained.

There are two lines possessing from 45 to 55% of oleic content near a maximum border of the conventional class. It is interesting to note that these K 1587 and VK 678 belong to early maturing genotypes (Table 1). As a result the sunflower genes of early flowering can indirectly influence fatty acid composition in the way of increasing oleic content in the oil due to the higher temperature during seed maturation.

Phenotype				Poriod from omorganica	
class	average oleic acid content, %	Line	Genotype	to flowering, days	
	91	VK 508	0101	51	
High oleic	89	VK 876	0101	55	
	86	LG 26	OIOI + Sup-resistance	50	
Mid oleic	69	VK 805	OIOI p1p1p2p2	50	
	67	LG 27	olol + additive genes	53	
Conventional	53	K 1587	olol SupSup	47	
	45	VK 678	olol	48	
	41	RIL 100	OIOI SupSup	53	
	40	K 235	olol SupSup	48	
	40	K 824	olol SupSup	55	
	35	VK 580	olol	50	
	34	RHA 416	olol SupSup	51	
Low oleic	29	HA 413	olol	53	
	27	LG 28	olol	61	

Table 1: Core genetic collection for oleic acid content in sunflower seed oil

A mid oleic class from 65 to 70% contains only one line without the high oleic mutation Ol in its genotype (Table 1). LG 27 is originated from selfed progenies of the K 2210 accession of VIR. This trait is controlled by additive genes with strong maternal influence in the F_1 (unpublished data) though in the cross-breeding with a high oleic line it seemed to be recessive monogenic (Demurin *et al.*, 2000). Another possibility to get the mid oleic phenotype was realized in VK 805 with a partial epistatic effect of a high palmitic mutation over a high oleic one in a combined homozygote genotype (Table 2). That phenomenon was firstly described by Fernandez-Martinez *et al.* (1997). Moreover, several mid-range oleic acid genetic stocks released by Miller and Vick (2002) are based on the high oleic mutation background.

Lino	Fatty acid composition, %						
LINE	C16:0	C16:1	C18:0	C18:1	C18:2		
VK 805 <i>Ol, p</i>	18.5	5.5	1.4	69.0	5.6		
VK 580 wild type	5.7	trace	3.0	35.1	56.2		
LSD ₀₅	1.1	-	0.5	2.0	1.5		

Table 2: Mid oleic phenotype of high palmitic/ high oleic mutations combined

A high oleic class from 84 to 92% consists of two subclasses. LG 26 is located within the first one with minimum oleic content (Table 1). This line shows resistance to suppressor with complete dominance of Ol mutation in the F_1 and monogenic inheritance in the F_2 when LG 26 was crossed with suppressor-carrying lines (unpublished data). VK 876 and VK 508 have maximum level of oleic acid content up to 91%.

CONCLUSIONS

The VNIIMK genetic collection of identified alleles determining oleic acid content in sunflower seed oil consists of about 50 constant inbred lines (14 of them in a core collection). The general range of this trait varies from 20 to 92%. These inbred lines correspond to four main phenotypic classes: low, conventional, mid and high oleic.

ACKNOWLEDGEMENTS

This work was supported by grant 09-04-96588 from the Russian Foundation of Basic Research (RFBR); grant 11-04-96522 and grant 11-04-96524 from VNIIMK in the frame of regional competition of RFBR.

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