

## APPLYING OF THE COTTON WILD SPECIES *G. TRILOBUM* SKOVSTED IN THE BREEDING FOR WILT RESISTANCE AND FIBER QUALITY

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### Abstract

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The triploids ( $2n=39$ ) had been obtained by the crossing of cultivated species *G. hirsutum* L. of the variety C-4727 ( $2n=52$ ) with diploid species *G. trilobum* Skovsted ( $2n=26$ ). The hexaploid amphydiploid ( $2n=78$ ) had been synthesized by colchicizing of triploid growing point. The introgressive line L-T had been obtained by four times crossing. By crossing of line L-T with varieties and lines the lines had been created combining best characteristics of parents: resistance to verticillium, high fiber quality.

**Key words:** cotton, hybrid, introgression, wild species, fiber quality

### MATERIALS AND METHODOLOGY

The material for study served *G. hirsutum*, *G. trilobum*, number of varieties and introgressive lines of cotton. For obtaining hybrids between introgressive lines and varieties the methods of hybridization, selection and statistic analysis of experimental material had been used.

### RESULTS

The diploid species with new donor properties is a great source to achieve more genetic variability of the features and resistance to the diseases, pests, stress factors, as well. Thus, *G. trilobum* Skovsted is resistant to Verticillium wilt, to low temperatures and in the favorable conditions buds appear earlier and crops also mature earlier. Series of introgressive cotton lines with such properties were developed during the long-term studies with cotton type V in the cotton breeding laboratory.

They have been selected according to the scheme in recent years by means of hybridization of planted varieties with the wild diploid species *G. trilobum* and the others (see Appendix 1).

The baseline materials for our researches were homogeneous lines of genetically distant origin, as well as some local and foreign varieties with various maturity days, ginning outturn and wilt resistance. The aim of the present research is to check and reveal new sources of genetic variability, to develop cotton genotypes with new characteristics, such as resistance to Verticillium wilt; early maturity and other economically useful features on the basis of variability analysis and donor capacity of the homogeneous lines with genetically distant origin. The aim is also to elaborate the principles of parents selection and valuable recombinants in hybrids generations.

The most valuable assessment criteria are staple length, micronaire and strength (Lewis. 1991; Ustugin at. al.1999). The upper semi-medium length indices of all hybrids completely meet requirements of long staple (Table 1).

Thus, in parental forms staple length varies from 28,2 – 29,5 mm, and that of F<sub>1</sub> hybrids varies from 28,7 – 29,5 mm. The difference in feature expression rate depends upon crossing combination and baseline form genotype, and generally there is a slight deviation. L-T interspecific origin line has the finest staple with micronaire equal to 3,6, which is considered to be low. The F<sub>1</sub> hybrids F<sub>1</sub> (L-T x L-SG), F<sub>1</sub> (Omad x L-T) have the most fine and the highest quality staple (micronaire is 4,2 and 4,3 respectively), that is to say high quality of staple semi-dominant or dominant over the low quality, hp index is equal to 0,0 and 0,4 respectively. The Omad variety and L-T interspecific origin line has the best combination capacity among parent forms. The F<sub>1</sub> hybrid (Omad x L-T) revealed semi-domination of high micronaire. Hence, Omad variety and L-T interspecific origin line, possessing the best fiber micronaire, transfer this feature to hybrids, being the valuable genotype sources of high quality fiber.

**Table 1.** Fiber characteristics of f<sub>1</sub> complex hybrids and parental forms (2002)

No	Parental and genotype combinations	Upper semi-medium staple length			Hp	Micronaire			Hp	Strength g/tex			Hp
		F <sub>1</sub>	P <sub>1</sub>	P <sub>2</sub>		F <sub>1</sub>	P <sub>1</sub>	P <sub>2</sub>		F <sub>1</sub>	P <sub>1</sub>	P <sub>2</sub>	
1	C-2609 x L-T	29,5	29,5	29,5	0,0	4,6	4,3	3,6	1,8	35,2	30,3	30,0	5,0
2	Omad x L-T	28,9	29,5	29,5	-0,6	4,3	4,6	3,6	0,4	31,5	24,7	30,0	1,5
3	L-T x Omad	29,5	29,5	29,5	0,0	4,6	3,6	4,6	1,0	33,1	30,0	24,7	2,1
4	L-T x L-SG	29,5	29,5	28,9	0,0	4,2	3,6	4,8	0,0	31,8	30,0	35,8	-0,8
5	L-SG x L-T	29,2	28,9	29,5	0,0	4,9	4,8	3,6	1,2	24,7	35,8	30,0	-2,8
6	P-1 x L-T	29,5	28,2	29,5	0,0	4,6	5,0	3,6	0,4	33,5	30,0	31,0	6,0
7	L-T x P-1	28,9	29,5	28,2	-0,1	4,8	3,6	5,0	0,7	37,3	30,0	30,0	7,3
8	L-U x L-T	29,2	28,7	29,5	-0,2	4,5	4,5	3,6	1,0	33,1	37,0	30,0	-1,1
9	St. Namangan 77	29,5	-	-	-	4,5	-	-	-	28,3	-	-	-

Note: L-T – F<sub>1</sub>BC<sub>4</sub>(C-4727 x *G.trilobum*) x C-4727.

The table 1 data witnesses about the contrast of strength among the varieties. Such index of all the hybrids and parents satisfies the requirements accepted as standard for the fiber of medium-staple cotton varieties.

The strength, as well as other fiber properties, is inherited according the type of polymeric feature. Depending on genotype of crossed forms, hybrids often demonstrated heterosis and super-dominance or occupied intermediate position with deviation towards the best parent (complete or incomplete dominance). Hybrids with participation of the variety C-2609 variety and L-T line often demonstrated good results on fiber strength, therefore these parents can be considered as good donors on this feature.

L-T lines and Omad variety are remarkable for good quality, the best length and low micronaire among the baseline parental pairs. Long fiber is formed by hybrids where the parents are L-T lines and Omad variety. F<sub>2</sub> hybrid (L-SG x L-T) has the strongest staple (38,7 g/tex). The staple length analysis of F<sub>2</sub> hybrids in the individual selection showed significant differences between the parental forms. Omad variety, C-2609 variety and L-T line has the longest staple (on average from 33,7 to 35,5 mm) (table 2.). A big range of staple length variability surpassing indices of both parents was revealed also in F<sub>2</sub> hybrids (L-T x Omad), which has staple length variation from 29,6 to 39,5. Measured by HVI set the staple length of F<sub>2</sub> hybrids (L-SG x L-T) exceed F<sub>1</sub> hybrids level for 2,6 mm. All studied parent pairs and hybrids had a strong staple, which strength exceeds standard requirements for 3,0 – 12,9 g/tex.

Concerning the staple length, the hybrids take intermediate position between the initial parents with deviation towards long-staple form in all cases, or hybrids are inferior

to both parents.  $F_3$  (L-T x Omad) had demonstrated the longest staple among  $F_3$  hybrids (34,2 mm). Frequency of long-fiber hybrids is higher when L-T line and Omad variety participate in crossing. Variability range in  $F_3$  hybrid (P-1 x L-T) includes only 3 classes, variation ratio is 2,6 %, which is the evidence of the feature stabilization. When crossing introgressive lines among them long-staple forms appear, which have also high ginning outturn (45 – 48 % and higher), which we consider important for selection. Such results indicate to great genetic potential of introgressive lines, which realization allows to extract recombinants with high ginning outturn and staple length.

**Table 2.** Fiber length variability of  $f_2$ – $f_3$  hybrids and in parental forms of cotton (2003–2004)

No	Parents and hybrids	$F_2$			$F_3$		
		X+Sx	S	V %	X + Sx	S	V%
1	Omad	35,5 +0,4	1,2	3,5	35,3 + 0,4	1,6	4,5
2	C-2609	33,7 + 0,5	1,3	3,9	33,0 + 0,4	1,1	3,4
3	P-1	32,1 + 0,3	1,5	4,7	31,7 + 0,3	1,7	5,4
4	L-U	31,2 + 0,3	1,8	5,7	31,1 + 0,3	1,8	5,9
5	L-T	35,1 + 0,5	1,9	5,5	35,2 + 0,4	1,4	4,0
6	L-SG	32,3 + 0,4	1,6	4,9	31,6 + 0,5	2,2	6,9
7	C-2609 x L-T	32,2 + 0,4	2,2	6,7	32,7 + 0,6	2,5	7,7
8	Omad x L-T	34,0 + 0,4	1,7	5,2	32,1 + 0,6	2,7	8,4
9	L-T x Omad	34,6 + 0,5	2,5	7,4	34,2 + 0,5	2,3	6,7
10	L-T x L-SG	33,4 + 0,5	1,7	5,2	31,4 + 0,6	1,8	5,6
11	L-SG x L-T	31,0 + 0,5	1,6	5,1	30,5 + 0,4	2,1	6,9
12	P-1 x L-T	32,3 + 0,6	2,5	7,7	31,5 + 0,4	0,8	2,6
13	L-T x P-1	30,6 + 0,4	1,9	6,4	30,7 + 0,6	1,8	6,0
14	L-U x L-T	32,3 + 0,6	2,7	8,5	32,7 + 0,5	2,3	7,0
15	St. Namangan 77	33,4 ± 0,5	1,2	3,6	31,9 + 0,3	0,8	2,6

With the increasing of hybrids generations number the staple length also increases and it exceeds the standard.

Significant differences were observed on Verticillium wilt resistance in parent pairs (3,0 – 16,7%) (table 3). L-T and L-U lines should be considered as the most stable, which plants are affected by wilt only in 3,0 and 3,5 %. Affection rate of other parents varies from 12,2 to 16,7 %. Thus, parent pairs contrastingly differ in resistance and are affected by wilt in various grade, but no absolutely stable forms have been revealed.

**Table 3.** Resistance to verticillium wilt of  $f_1$  hybrids and parental forms (2002)

No	Genotype combinations	$F_1$		$P_1$		$P_2$		hp
		General rate %	High rate %	General rate %	High rate %	General rate %	High rate %	
1	C-2609 x L-T	3,8	3,8	16,7	16,7	3,0	3,0	-0,9
2	Omad x L-T	10,5	5,2	12,7	6,5	3,0	3,0	0,5
3	L-T x Omad	1,0	0,0	3,0	3,0	12,7	6,4	-1,4
4	L-T x L-SG	3,4	0,0	3,0	3,0	12,7	9,7	-0,9
5	L-SG x L-T	2,0	0,0	12,2	9,7	3,0	3,0	-1,2
6	P-1 x L-T	1,0	0,0	12,9	6,4	3,0	3,0	-1,4
7	L-T x P-1	1,0	0,0	3,0	3,0	12,9	6,4	-1,4
8	L-U x L-T	1,0	0,0	3,5	3,5	3,0	3,0	-9,0
9	St. Namangan 77	12,5	5,5	-	-	-	-	-

It is evident from the table 3, that wilt affection rate of the majority of  $F_1$  genotype combinations is very low in comparison to initial parents.

Receptivity of parental forms in  $F_1$  hybrids (Omad x L-T) semi-dominant over the stable forms, hp = 0,5. Thus, the lines with distant genetic origin being highly resistant to Verticillium wilt contribute to more drastic increase in the first generation of hybrids. In

such hybrids resistance super-dominates over receptivity. When crossing highly wilt resistant parents with less resistant ones the resistance dominates over the receptivity.

Value of dominant genes of both sides which determine the development of resistance to wilt consists in the fact, that in natural selection with few exceptions only dominant features remain. In spite of all selection peculiarity, orienting to natural conditions as to the highest standard in evaluation of adaptation in the experiment, exceptionally important task should be considered enrichment of varieties with valuable dominant features. In artificial selection a little attention is paid to the dominance. In view of the above said, economically useful features in which seed breeder interested in depends on many polymeric genes.

In case of crossing two parent forms equally possessing any desirable feature, than in the result of splitting in descendants there may be generated forms surpassing both parents in this feature. Such transgressions also present significant theoretical interest.

Thus, when crossing AAbb and aaBB parental forms as a result of recombination in F<sub>2</sub> AABB form can be obtained. Even now genetic recombination represents one of the actual questions of selection

In conditions of 2003 the majority of introgressive lines proved themselves to be more tolerant than stable varieties. The L-T line was the most resistance to Verticillium wilt, it was affected by wilt in 3,0 %. F<sub>2</sub> hybrids (L-T x Omad) and F<sub>2</sub> (L-U x L-T) were affected by wilt on average for 3,7 % and 5,9 % respectively (Table 4).

Due to the experimental researches L-T and L-U lines of interspecific and inter sub specific origin, which genotype includes features of wild diploid and polyploid species, as well as Omad variety showed big efficacy as resistance donors in crossing, providing heterosis in resistance to Verticillium disease and providing the transgression of the feature in the hybrid generations. Such lines are a valuable source for enrichment of genetic structure of the hybrid populations concerning the resistance to Verticillium wilt. Therefore, these lines and Omad variety should be involved wider into selection for resistance to Verticillium wilt, early maturity in combination with good ginning outturn.

**Table 4.** Verticillium wilt affection of inter-line and variety-line f<sub>2</sub>–f<sub>3</sub> hybrids (2003–2004)

No	Parents and hybrids	Affection rate, % F <sub>2</sub>			Affection rate, % F <sub>3</sub>		
		General	High	Low	General	High	Low
1	Omad	9,7	3,2	6,5	44,4	16,6	27,7
2	C-2609	14,3	6,4	7,9	44,7	10,4	34,3
3	P-1	6,9	3,5	3,4	22,3	6,4	15,9
4	L-U	15,4	1,4	14,0	44,3	13,4	30,9
5	L-T	3,0	2,1	0,9	31,9	12,5	19,4
6	L-SG	5,5	0	5,5	18,2	5,7	12,5
7	C-2609 x L-T	14,7	2,3	12,3	19,6	2,9	16,6
8	Omad x L-T	12,4	5,4	7,0	54,9	16,9	38,0
9	L-T x Omad	3,7	1,6	2,1	35,7	5,9	29,7
10	L-T x L-SG	14,7	0	14,7	31,4	6,6	24,7
11	L-SG x L-T	10,6	3,8	6,7	11,7	1,9	9,8
12	P-1 x L-T	17,7	3,9	13,8	38,8	7,7	31,1
13	L-T x P-1	13,3	6,6	6,6	33,8	9,8	23,9
14	L-U x L-T	5,9	3,6	2,3	25,0	7,0	18,0
15	St. Namangan 77	10,6	2,6	8,0	43,6	12,0	31,6

As in the previous years in 2004 the L-T line had rather high resistance to Verticillium wilt yielding to standard variety for 11,7 % in general affection. Less affected by wilt were F<sub>3</sub> combinations (C-2609 x L-T)–19,6 %, F<sub>3</sub> (L-SG x L-T)– 11,7%, and F<sub>3</sub> hybrids (L-U x L-T)–25,0 %. All other hybrid combinations were affected by wilt from 31,4 % to 54,9 %.

In general F<sub>3</sub> hybrids with participation of varieties tend to be higher affected than inter-line hybrids. Parental form influence can be observed in F<sub>3</sub> (Omad x L-T) hybrids,

where affection was 54,9 % against 35,7 % in reverse  $F_3$  combination (L-T x Omad).

In the generations of hybrids  $F_6$ - $F_7$ , the lines had been defined, which combined the best characteristics of the varieties and introgressive lines.

### CONCLUSIONS

The best donors of fiber quality are the line L-T and the variety Omad.

Among initial parental forms the most resistant to wilt were the lines P-1, L-T, L-SG.

From the studied combinations the highest indices on resistance had hybrids  $F_3$  (C-2609 x L-T),  $F_3$  (L-U x L-T).

Highly resistant hybrids are obtained when in crossing the line of interspecific origin L-T is used.

In the result of crossing of introgressive lines L-T, L-U with the varieties the new lines highly resistant to verticillium, in the combination with the increased output of quality fiber, had been defined.

### REFERENCES

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**Appendix 1.** A scheme of obtaining homogeneous L-T line of interspecific origin, crossing *G. hirsutum* L. cultivated species with *G. trilobum* Skovsted. diploid species.

Initial crossing: *G. hirsutum* L., C-4727 variety (2n=52) x  
*G. trilobum* Skovsted (2n=26)

F<sub>1</sub> amphigaploid F<sub>1</sub> (2n+39)

Doubling of amphigaploid chromosomes by colchicinating of germs' growing-point and obtaining of amphidiploid (2n=78)

The 1<sup>st</sup> recurrent crossing of amphidiploid with C-4727 variety. Selections of wilt resistant plants of cultivating type.

The 2<sup>nd</sup> recurrent crossing of sesquidiploid with C-4727 variety. Continuation of selections of wilt resistant, with high ginning outturn plants, evaluation of staple properties.

The 3<sup>rd</sup> recurrent crossing of hybrids with C-4727 variety. Selections for complex of features.

The 4<sup>th</sup> recurrent crossing of hybrids with C-4727 variety. Selections for complex of features.

The best long-term selections of families and lines with features, permanent evaluation of fiber properties, plants of the resistance to Verticillium wilt on the natural soils infected by *V. dahliae* Kleb.

Sum of two haploid chromosomes

The plants are sterile

Sum of two diploids chromosomes.

The plants are fruitful, wilt, resistant to late maturity.

Sesquidiploids (2n=65). The plants are fruitful, resistant to wilt, medium maturity.

The plants are fruitful, resistant to wilt with different chromosomes number (2n=52; 2n=54, 2n=58).

The plants are highly fruitful, with early maturity, resistant to wilt with chromosomes number 2n=52.

The families are highly fruitful, wilt resistant, with early maturity and higher fiber quality.

Biologically active homogeneous lines and families with ginning outturn, approaching to the planted varieties productivity. They superate initial variety and planted varieties in early maturity, wilt resistance, fiber quality, including L-T line.