

EVALUATION OF THE CORRELATION BETWEEN RESISTANCE TO FUSARIUM WILT DISEASE AND FIBER TRAITS IN SOME COTTON GENOTYPES

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Abstract

Field trials were carried out at Sids Agricultural Research Station in 2015 and 2016 growing seasons. In 2015, 18 cotton genotypes were self-pollinated. In 2016, the genotypes were grown in a randomized complete block design with three replications. A random sample of four guarded plants of each genotype was chosen from each plot to determine some technological traits. The tested technological traits were fiber length at 2.5% (mm), fiber length uniformity ratio (%), and fiber strength (g/tex). The genotypes were screened under greenhouse conditions in 2017 against a mixture of 50 isolates (race3) of the wilt fungus. Healthy survival rate (HSR) was used as a criterion to evaluate the reaction of tested genotypes to Fusarium wilt. Nine (50%) of the tested genotypes were very highly resistant. Within this group, HSR ranged from 91.67 to 100% such as genotypes 1,3,4 and 5 with no significant differences. The significant correlations between some of the technological traits and some of the wilt symptoms were sensitive to changing environmental conditions, that is, the significant correlation in one year was nonsignificant in the other year. Grouping the genotypes by cluster analysis based on the profiles of their fiber traits was not related to their reaction class (resistance level). The results of the present study demonstrated that resistance to Fusarium wilt symptoms of fusarium wilt may positively or negatively affect the technological traits depending on the trait under consideration and the prevailing environmental conditions during cotton growing season.

INTRODUCTION

Fusarium wilt of cotton is a serious fungal disease responsible for significant losses throughout the world. The causal organism *Fusarium oxysporum* Schecht. f.sp. *vasinfectum* (ATK) Snyder and Hans.(FOV), invades the host through the taproots behind the root tip. The combined effect of fungal metabolites and the production of lipoidal substances by the host in response to infection may lead to occlusion of the vascular tissue, resulting in wilt of the cotton plant (Hillocks,1984). The pathogen can survive for several decades in soil and cannot be eradicated from infested fields. The pathogen can infect cotton at all stage of growth and produces symptoms, which include seedling death, wilting, vascular discoloration and plant death (Watkins,1981). Apart from Egypt, it is commonly associated with nematode

infection (McFadden *et al.*, 2004)] particularly in acidic ,sandy soil. In Egypt,where cotton is grown in alkaline clay soil, there is no evidence for the involvement of nematodes in fusarium wilt disease (Aly *et al.*,2000).

Currently, up to eight races of FOV, most of which are geographically separated, are recognized worldwide. The basis for determining races of FOV depends on their virulence to a differential set of cotton (*Gossypium*) lines and species and up to five non- cotton hosts (Watkins, 1981). The Egyptian race (race3) of FOV has long been known in the Nile valley, where it remains as one of the most damaging pathogens on Egyptian cotton (*Gossypium barbadense* L.). This race also attacks *G.barbadense* in the former soviet Union(Watkins,1981).and Israel (Netzar *et al.*, 1885). FOV caused serious losses in the commercial Egyptian Cottons (*G.brbadense* L.) in the fifties(Barky *et al.*,1958)Since then, an extensive cotton breeding programs were conducted to develop cultivars resistant to the disease.

Breeding materials submitted by cotton breeders (Cotton Research Institute) have been screened for resistance under greenhouse conditions in soil highly infested with FOV. This test has been conducted annually for the past 60 years in the greenhouses of Cotton and Fiber Crops Diseases Research Dept, PPRI, ARC.The program has been successful in developing highly resistant cultivars (Aly *et al.*,2000).

Fusarium wilt remains a potential threat to cotton production in Egypt because FOV is still well established in the Egyptian soil (Aly *et al.*, 2000). Thus, increasing the probability that new biotypes of this race may arise to confound cotton breeders.

Cotton fiber is defined by a suite of traits, which have a major impact on fiber selling price. Several fiber quality parameters such as fiber length, length uniformity, strength, and elongation are genetically controlled, but other traits like micronaire, though genetically controlled, are impacted to a greater degree by environmental conditions (Baxevanos *et al.*, 2013).

Outside Egypt, few attempts have been made to evaluate the correlation between incidence of Fusarium wilt and agronomic and technological traits. For example, in China, Wu *et al.* (2004) found that incidence level of Fusarium wilt was negatively correlated with fiber strength, macronaire value, and the fiber span length, and reached significant and highly significant level. In USA, Ulloa *et al.* (2006) reported that foliar damage and vascular discoloration caused by FOV were negatively correlated with node number and plant height. In China, Guo *et al.* (2013) found that oil content of cottonseed was weakly and negatively correlated with Fusarium wilt resistance.

In Egypt, as far as we know, only one attempt has been made by Aly *et.al.* (2015) to study the correlation between incidence of Fusarium wilt and each of agronomic and

technological traits. The lack of significant correlation between wilt incidence and each of agronomic and technological traits in this study, suggested that breeding for Fusarium wilt resistance in cotton may not negatively affect the quality of agronomic or technological traits.

The objectives of the present study were to evaluate a collection of cotton genotypes for Fusarium wilt resistance and to evaluate the correlation between wilt symptoms on these genotypes and their technological traits.

MATERIALS AND METHODS

Cotton genotypes.

The genotypes used in the present study were randomly selected from the collection of germplasm available at the Department of Cotton Breeding, Cotton Research Institute (Table 1).

Field trials:

Field trials were carried out at Sids Agricultural Research Station in 2015 and 2016 growing seasons. In 2015 growing season, cotton genotypes were self-pollinated. In 2016 growing season, they were grown in a randomized complete blocks with three replications. Each plot consisted of two rows, each was four meter long, 60 cm apart and interhill spacing was 70 cm. Seedlings were thinned to one seedling per hill. The recommended cultural practices were adopted throughout the growing season, A random sample of four guarded plants of each genotype was chosen from each plot to determine the following technological traits:

1. Fiber length at 2.5% (mm): The upper half mean length. was measured by fibrograph according to ASTM:D 1447-83 (1984).
2. Fiber length uniformity ratio (%): The expression of the ratio of upper- half fiber length and the mean length. It was determined according to Sundaram (1979).
3. Micronaire reading : The measurement of fiber fineness and maturity. It was determined according to ASTM:D 1448-59 (1984).
4. Fiber strength (g/ tex): The necessary force to break a beard of fiber that are clamped between two sets of jaws. It was determined according to ASTM:D 1448-59 (1984).

All fiber tests were carried out in the laboratories of Cotton Research Institute, Agricultural Research Center, Giza at constant relative humidity of 65 ± 2 % and temperature of 70 ± 2 °f.

Table1. Cotton genotypes used in the present study.

Genotype no.	Pedigree
1	karashinky
2	Australian
3	Giza 90 X Australian
4	Giza 83 X Australian
5	Giza 80 X Australian
6	Dandera X Australian
7	TNB
8	BBB
9	{{ Giza 83 X Giza 80) X Giza 89}X (Giza 83 X Deltapine 703)
10	{{ Giza 83 X Giza 80) X Giza 89}X Australian
11	Giza 90 X CB58
12	Giza 83(Radiated) X karashinky
13	Giza 83(Radiated) X Australian
14	(Dandera X Australian) X Giza 91
15	(Giza 90 X Australian) X {{ Giza 83 X Giza 80) X Giza 89}
16	(Giza 83 X Australian) X Giza 90
17	(Giza 80 X Australian) X Giza 83
18	Giza 72 X {{ Giza 83 X Giza 80)X Giza 89}}

Evaluation of cotton germplasm against Fusarium wilt race 3 under greenhouse conditions.

This study was conducted in the greenhouses of Cotton and Fiber Crops Diseases Research Dept, PPRI through 2017. The experimental design used in this study was a completely randomized with three replications(pots)for each genotype.

The fungal inoculum used in the greenhouse test was a mixture of equal parts (w/w) of 50 isolates of FOV race 3. These isolates were obtained from the fungal collection of Cotton Pathology Dept, PPRI, Giza. Autoclaved clay loam soil was infested with a mixture of the isolates at a rate of 10g/kg soil Substrate for growth of each selected isolate was prepared in 500-ml glass bottles, where each bottle contained 50g of sorghum grains and 40 ml of tap water. The inocula were made from one- week old culture on PDA, and allowed to colonize sorghum for 3 weeks. Infested soil was dispensed in 10-cm diameter clay pots, which were planted with 10 seeds per pot. The greenhouse was equipped with a heating system assuring that the minimum temperature in the greenhouse was maintained at 28⁰c; however, due to the lack of cooling system, the maximum temperature was out of control fluctuating from 30 to 35 ⁰c depending on the prevailing temperature during the day (the test was conducted in January and February, 2017).

Assessment of Fusarium wilt incidence

Percentages of infected seedlings were recorded 45 days from planting date. The infected seedlings included the dead and the surviving seedling, which showed external or internal symptoms. The external symptoms usually began at the margin of cotyledons as yellowing along the veins (vein clearing), eventually, the entire cotyledons turned yellow and dropped from the seedlings. Seedlings that remained apparently healthy 45 days after planting were cut diagonally across the root and stem to examine the internal symptoms. If discoloration of xylem vessels was observed, they were considered infected. If seedlings were free of such a discoloration, they were considered healthy. Thus, the seedlings of each genotype were placed in two distinct classes: healthy if they were free of any external or internal symptoms, or infected if the seedlings died or survived showing any external or internal symptoms. (Aly *et al.*, 2007 and Abd-Elsalam *et al.*, 2009).

Statistical analysis of the data.

Data were subjected to analysis of variance and Least significant difference (LSD) was calculated to compare between genotype means. Linear correlation coefficients were calculated to measure the degree of association among wilt symptoms on the genotypes. and to evaluate the degree of association between wilt symptoms and fiber traits. The tested genotypes were clustered by the average linkage technique (unweighted pair-group method) based on the profiles of their technological traits. Statistical analysis was performed with the software package SPSS6.0.

RESULTS

Some families within each of the tested genotypes showed variable symptom expression (Table 2) due to the fact that these genotypes were not pure regarding fusarium wilt resistance. However, with the exception of genotypes 7, 10, and 11, the majority of the families of each genotype were completely free of any internal or external symptoms (healthy survival).

The highest correlations among symptom expressions were observed between healthy survivals (HS) and each of dead seedlings (DS) ($r=0.905$, $p=0.000$) and cotyledon yellowing (CY) ($r=0.862$, $p=0.00$) (Table 3).

Healthy survival rate (HSR) was used as a criterion to evaluate the reactions of the tested genotypes to Fusarium wilt (Table 4). Nine (50%) of the tested genotypes were VHR. Within this group, HSR ranged from 91.67 to 100. with no significant differences.

The significant correlations between some of the technological traits (Table 5 and 6) and some wilt symptoms (Table 7) were sensitive to changing environmental

conditions, that is, the significant correlation in one year was nonsignificant in the other year. For example, FLUR significantly correlated with each of DS, CY and HS in 2015, while it did not show significant correlation with any of these parameters in 2016. Another example, is the significant correlation between FL and each of DS, CY, and HS in 2016, which was nonsignificant in 2015. It is worth noting that HS positively correlated with FLUR in 2015 and with FL in 2016. On the other hand, HS showed negative correlation with MR in 2015.

A phenogram based on dissimilarity distance (DD) generated from cluster analysis of fiber traits profiles of the tested genotypes, is presented in Fig.1. The smaller the DD, the more closely the genotypes were related in their trait profiles. Five groups of similar genotypes were identified by cluster analysis. The first group included five genotypes, while each of the second, third, and fourth group included four genotypes. The fifth group, which was unrelated to the previously mentioned four groups, included only genotype 8. Within each of the first four groups, the genotypes showed variable reaction classes to Fusarium wilt. Therefore, grouping the genotypes by cluster analysis based on their trait profiles was not related to their reaction class to fusarium resistance.

Table 2. Symptoms used in evaluating the reactions of 18 cotton genotypes to Fusarium wilt (race3) under greenhouse conditions in 2017.

Genotype no. ^a	Symptoms ^b (%)			
	DS	CY	VD	HS
1	0.00 ^c	0.00	0.00	100.00
2	2.50	0.00	0.00	97.50
3	0.00	0.00	0.00	100.00
4	0.00	0.00	0.00	100.00
5	0.00	0.00	0.00	100.00
6	0.00	5.00	0.00	95.00
7	72.28	27.72	0.00	0.00
8	5.00	0.00	0.00	95.00
9	14.44	4.73	0.00	80.84
10	39.45	60.55	0.00	0.00
11	47.50	19.17	0.00	23.33
12	0.00	0.00	16.67	83.33
13	0.00	0.00	8.33	91.67
14	0.00	0.00	35.00	65.00
15	0.00	0.00	8.33	91.67
16	0.00	0.00	16.67	83.33
17	0.00	0.00	33.13	66.87
18	0.00	0.00	14.17	85.83
LSD(P≤0.05)	18.22	14.41	21.54	38.40

^aPedigrees of the genotypes are shown in Table 1.

^b Symptoms are dead seedlings (DS), Cotyledonary yellowing (CY), Vascular discoloration (VD), and Healthy survival(HS).

^cMean of five replicates.

Table 3. Correlation coefficient among symptoms used in evaluating the reaction of 18 cotton Genotype to Fusarium wilt (race3) under greenhouse conditions in 2017.

symptoms	symptoms		
	X1	X2	X3
Dead seedlings (X1)			
Cotyledonary yellowing (X2)	0.670 ^a (0.000) ^b		
Vascular discoloration(X3)	-0.325(0.187)	-0.284(0.253)	
Healthy survival (X4)	-0.905(0.000)	-0.862(0.000)	0.003(0.990)

^aLinear correlation coefficient.

^bprobability level.

Table 4. Reaction classes of 18 experimental cotton genotypes to Fusarium wilt (race3) under greenhouse conditions in 2017.

Genotype ^a no.	Healthy survival (%) ^b	Reaction class ^c
1	100.00 ^d	VHR
2	97.00	VHR
3	100.00	VHR
4	100.00	VHR
5	100.00	VHR
6	95.00	VHR
7	0.00	VHS
8	95.00	VHR
9	80.00	HR
10	0.00	VHS
11	23.33	HS
12	83.33	HR
13	91.67	VHR
14	65.00	R
15	91.67	VHR
16	83.33	HR
17	66.87	R
18	85.83	HR
LSD(P≤0.05)	38.40	

^aPedigrees of the genotypes are shown in Table 1.

^bSeedlings, which were completely free from any external or internal symptoms.

^cReaction class was determined based on the percentage of healthy seedlings according to the flowing scale for survival

Very highly susceptible (VHS) = 0-10

highly susceptible (HS)= 11-30

Susceptible (S)= 31- 50

Resistant (R) = 51-70

Highly resistant (HR) = 71- 90

Very Highly resistant (V H R) = 91 – 100

^dMean of five replicates

Table 5. fiber traits of genotypes^a used in the present study(2015)

Genotype	Fiber length	Fiber length at	Fiber strength	Micronaire reading
no.	uniformity ratio(%)	2.5% (mm)	(g/ tex)	
1	83.3	30.5	8.8	3.6
2	84.6	32.4	9.1	4.1
3	84.7	31.2	9.2	3.9
4	84.4	31.6	9.2	3.8
5	83.6	31.5	8.8	4.1
6	84.4	29.7	8.7	4.3
7	83.0	30.5	8.8	4.2
8	83.9	32.8	9.5	3.4
9	83.9	31.2	8.8	4.4
10	83.1	30.9	9.7	4.7
11	83.9	29.9	9.0	4.8
12	83.9	31.2	8.9	3.8
13	83.6	31.3	9.1	3.9
14	84.8	31.3	9.1	4.1
15	84.4	32.1	9.1	3.5
16	84.0	30.6	9.0	4.4
17	83.0	30.5	9.1	4.7
18	83.8	32.2	9.6	4.1

^a The significance of the differences between genotype means of fiber traits was not evaluated because this was beyond the scope of the present study, which mainly focused on the correlation between fiber traits and resistance to Fusarium wilt. Therefore data of table 5 were used for calculating linear correlation coefficient, which measured the degree of association between fiber traits and Fusarium wilt resistance.

Table 6. fiber traits of genotypes^a used in the present study (2016)

Genotype	Fiber length	Fiber length at	Fiber strength	Micronaire reading
no.	Flur uniformity ratio(%)	2.5% (mm)	(g/ tex)	
1	83.2	29.8	9.2	3.5
2	82.4	31.2	9.0	3.5
3	82.9	31.1	8.8	3.5
4	83.1	30.8	9.0	3.4
5	84.3	31.3	8.9	3.8
6	82.7	30.4	8.9	3.8
7	82.7	28.5	8.9	3.5
8	84.0	34.3	9.4	3.2
9	83.7	29.8	9.4	4.0
10	82.8	29.5	9.2	3.6
11	83.9	30.5	9.5	4.5
12	82.1	30.1	8.9	3.6
13	82.1	30.1	8.9	3.6
14	84.4	32.5	9.0	3.9
15	84.0	31.5	9.0	4.2
16	83.1	31.4	9.3	3.7
17	82.6	30.9	9.1	3.5
18	83.8	32.2	9.6	4.1

^a The significance of the differences between genotype means of fiber traits was not evaluated because this was beyond the scope of the present study, which mainly focused on the correlation between fiber traits and resistance to Fusarium wilt. Therefore data of table 6 were used for calculating linear correlation coefficient, which measured the degree of association between fiber traits and Fusarium wilt resistance.

Table 7. Correlation between fiber traits and wilt symptoms of 18 experimental Cotton genotypes.

year	fiberl traits ^a	wilt Symptoms ^b (%)			
		DS	CY	VD	HS
2015	FLUR	-0.473 ^c (0.047) ^b	-0.477 (0.045)	0.026(0.919)	0.512(0.030)
	FL	-0.373 (0.128)	-0.311 (0.209)	-0.035 (0.890)	0.420(0.083)
	FS	-0.021 (0.935)	0.330(0.181)	0.077(0.760)	-0.163 (0.519)
	MR	0.450 (0.061)	0.514(0.029)	0.167(0.509)	-0.612 (0.007)
2016	FLUR	-0.042 (0.870)	-0.129 (0.610)	0.045(0.859)	0.054(0.831)
	FL	-0.526 (0.025)	-0.482 (0.043)	0.276(0.267)	0.467(0.051)
	FS	0.141 (0.576)	0.115(0.648)	-0.008 (0.974)	-0.169 (0.503)
	MR	0.156 (0.536)	0.044(0.864)	0.087(0.730)	-0.192 (0.445)

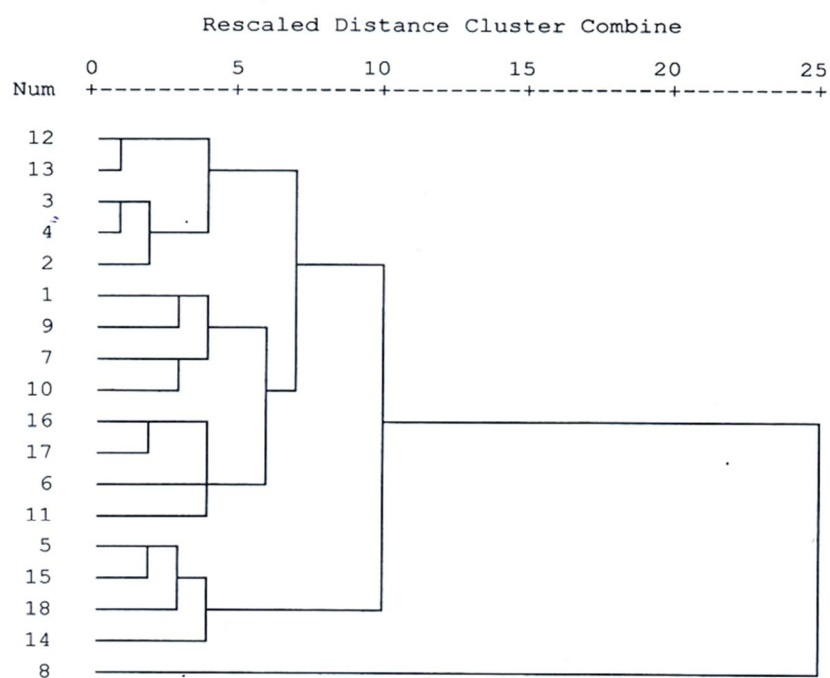
^aFiber traits are Fiber length uniformity ratio (FLUR) ,Fiber length at 2.5% (FL),

Fiber strength(FS), and Micronaire reading (MR).

^bWilt symptoms are Dead seedlings(DS),Cotyledonary yellowing (CY), Vascular discoloration (VD), and Healthy survival(HS).

^cLinear correlation coefficient.

^dProbability level.



DISCUSSION

In the present study, genotypes were screened against a mixture of 50 FOV isolates compiled from almost all cotton growing areas in Egypt. The use of such a large number of isolates is a strategy to maximize the probability that resistant genotypes identified under greenhouse conditions will maintain their resistance levels under field conditions at distinct geographic locations. On the contrary, if genotypes were screened against a limited number of isolates, they may not perform as expected throughout all growing regions due to potential presence of isolates differing in their virulence profile from those used in the greenhouse test.

A distinctive characteristic of Fusarium wilt is the olive brown discoloration of the root and stem xylem. However, there is no consensus regarding the diagnostic importance of this vascular discoloration for evaluation of the host germplasm reaction to Fusarium wilt. For example, Armstrong and Armstrong (1978) stated that vascular discoloration is a questionable standard for judging susceptibility to wilt in seedling tests. Zink *et al.* (1983) found no clear relationship between the severity of external symptoms in surviving muskmelon seedlings and the extent and degree of internal vascular discoloration. On the other hand, Salgado *et al.* (1994) used vascular discoloration as a criterion for judging susceptibility of tepary bean (*Phaseolus acutifolius* Gray) seedlings to Fusarium wilt. Osman (1996) found a highly significant correlation ($r=0.98, p \leq 0.01$) between external wilt symptoms and vascular discoloration of cotton seedlings (cultivar Giza74). In the present study, we used more rigorous criteria for disease rating. According to these criteria, the seedlings were considered susceptible if they showed internal discoloration even though they were free of external symptoms. Thus, the seedlings were considered resistant only if they were completely free of any internal and external symptoms. In our study, cotton genotypes were screened under very favorable conditions for FOV infection and development. The soil was sterile, temperature was optimal most of the time, and the inoculum density was relatively high. Under these conditions, it is unlikely that any susceptible genotypes would have escaped from infection. However, one should keep in mind that evaluation in the greenhouse precludes identifying genotypes that may possess useful levels of field resistance to wilt. The soil infestation method, which we used for seedling inoculation, had several advantages. Assays were simple, did not damage the seedlings and provided discriminating and reproducible disease reactions. Since no cotton wilt nurseries have been established in Egypt, greenhouse tests will continue to be the only reliable method for screening cotton breeding materials for Fusarium wilt resistance. The current absence of Fusarium wilt in commercial cotton

field using cultivars derived from our testing program demonstrates the reliability of these screening procedures, which we have adopted in testing cotton genotypes for Fusarium -wilt resistance. The most successful strategy to manage Fusarium wilt is the use of resistant cultivars (Doan and Davis,2014). Therefore, the present work identifies new and useful sources of resistance that might be employed in breeding programs aiming to develop cotton cultivars with resistance to FOV race 3 isolates. Such as genotypes nos1,3,4 and 5.

It is well known that the type and degree of correlation between characters may facilitate or complicate selection process in breeding programs. Selection for character may result in an improvement or deterioration in other characters according to the type and degree of correlation. Hence, it was desirable to assess the type and degree of association between resistance to Fusarium wilt (symptoms of Fusarium wilt) and some major fiber traits. The results of the present study demonstrated that resistance to Fusarium wilt symptoms of fusarium wilt may positively or negatively affect technological traits depending on the trait under consideration and the prevailing environmental conditions during cotton growing season.

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تقييم الارتباط بين المقاومة لمرض ذبول الفيوزاريوم والصفات التكنولوجية في بعض التراكيب الوراثية للقطن

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٢. معهد بحوث القطن ، مركز البحوث الزراعية ، الجيزة ، مصر

أجريت تجربة حقلية بمحطة البحوث الزراعية بسدس خلال موسمي ٢٠١٥ و ٢٠١٦ .
خلال موسم ٢٠١٥ أجري تلقيح ذاتي لعدد ١٨ تركيباً وراثياً من القطن المصري خلال موسم
٢٠١٦ زرعت هذه التراكيب الوراثية في تصميم يتكون من ثلاثة قطاعات كاملة العشوائية.أختبرت
أربعة نباتات ممثلة لكل تركيب وراثي بطريقة عشوائية من كل قطعة تجريبية. إستعملت النباتات
المتحصل عليها لقياس بعض صفات الالياف (طول التيلة عند نسبة ٢,٥% ودرجة انتظام الطول و
قراءة الميكرونير والمتانة). في عام ٢٠١٧ قيمت التراكيب الوراثية تحت ظروف الصوبة - من
حيث المقاومة أو القابلية للإصابة بمرض ذبول الفيوزاريوم ، باستعمال خليط يتكون من ٥٠ عزلة
للسلالة رقم ٣ من فطر الذبول.إستعملت النسبة المئوية للبادرات السليمة الباقية علي قيد الحياة
كمعيار لتقييم أداء التراكيب الوراثية المختبرة، أظهرت تسعة من التراكيب الوراثية المختبرة (٥٠%)
درجة عالية جدا من المقاومة للمرض إذا تراوحت نسبة البادرات السليمة الباقية علي قيد الحياة داخل
هذه المجموعة من ٩١,٦٧% إلي ١٠٠%. ومثال ذلك التراكيب الوراثية ١، ٣، ٤ و ٥. داخل هذا
النطاق الضيق لم نلاحظ فروق معنوية بين التراكيب الوراثية. أظهرت الدراسة وجود ارتباط معنوي
بين بعض الصفات التكنولوجية وبين بعض أعراض الذبول إلا أن هذا الارتباط أظهر حساسية
للظروف البيئية المتغيرة وعلي ذلك فإن الارتباط المعنوي في سنة أظهر عدم معنوية في السنة
الآخري. بإستعمال التحليل العنقودي تم تصنيف التراكيب الوراثية إلي مجموعات بناء علي ما بينها
من تباين في أنماط صفات الالياف إلا أن المجموعات المتحصل عليها لم ترتبط بمستوي المقاومة
للمرض. تدل نتائج الدراسة الحالية علي أن مستوي المقاومة لمرض ذبول الفيوزاريوم قد يؤثر سلبا
أو ايجابيا علي تحسين صفات الالياف وإن كان ذلك يتوقف علي الصفة التكنولوجية موضع الدراسة
ونوع الظروف البيئية خلال موسم نمو القطن.

