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CORRELATION BETWEEN SUSCEPTIBILITY TO FUSARIUM WILT AND AGRONOMIC AND TECHNOLOGICAL TRAITS IN SOME COTTON GENOTYPES

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ABSTRACT

Field trials were carried out at Giza Agricultural Research Station in 2012 and 2013 growing seasons. In 2012, 50 cotton genotypes were self-pollinated. In 2013, the genotypes were grown in a randomized complete block design with thre replications. A random sample of four guarded plants of each genotype was randomly chosen from each plot to determine some agronomic and technological traits. The agronomic traits were boll weight (g), seedcotton yield (g/plant), lint yield (g/plant), and lint percentage. The technological traits were fiber length at 2.5 % (mm), fiber length uniformity ratio (%), micronaire reading and fiber strength (g/tex). The genotypes were screened, under greenhouse conditions, in 2014 against a mixture of 50 isolates (race 3) of the wilt fungus. Incidence of Fusarium wilt was used as criterion to evaluate the reactions of the tested genotypes to the disease. The genotypes showed a narrow range of reactions to Fusarium wilt incidence ranging from 0 to 19.99 %. Of the tested genotypes, 54, 40 and 6 % were classified as highly resistant (wilt incidence was 0 %) resistant (wilt incidence ranged from 3.33 to 6.66 %), and susceptible (wilt incidence ranged from 13.33 to 19.99 %), respectively. Linear correlation coefficient was calculated to measure the degree of association between wilt incidence and each of agronomic and technological traits. Cluster analysis was used for grouping the genotypes based on the profiles of their agronomic and technological traits. Correlation and cluster analysis showed a lack of correlation between wilt incidence and each of agronomic and technological traits. This result suggests that breeding for Fusarium wilt resistance in cotton will not negatively affect the quality of agronomic or technological traits.

Keywords: Egyptian cotton, Fusarium wilt resistance, agronomic, and technological traits.

INTRODUCTION

Fusarium wilt of cotton is a serious fungal disease responsible for significant losses throughout the world. The causal organism *Fusarium oxysporum* Schlecht. f.sp. *vasinfectum* (ATK.) Snyd and Hans. (FOV) invades the host through the taproots behind the root tip. The combined effect of fungal metabolites and the production of lipodial 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). FOV can survive for several decades in soil and cannot be eradicated from infested fields. The pathogen can infected cotton at all stages of growth and produces symptoms, which include seedling death, wilting, vascular discolouration and plant death (Watkins, 1981).

Outside Egypt, it is commonly associated with nematode infection [root knot- Fusarium wilt complex (McFadden *et al*., 2004)], particularly in acidic, sandy soils. In Egypt, where cotton is grown in alkaline clay soils, there is no evidence for the involvement of nematodes in Fusarium wilt disease (A.A. Aly, *personal observation*).

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 5 non-cotton hosts (Watkins, 1981).

The Egyptian race (race 3) of FOV, has long been known in the Nile Valley, where it remains one of the most damaging pathogens on Egyption Cotfons (*G. barbadense* L.). This race also attacks *G. barbadense* in the former, Soviet Union (Watkins, 1981) and Israel (Netzer *et al*., 1985).

FOV caused serious losses in the commercial Egyptian cottons (*G. barbadense* L.) in the late fifties (Bakry *et al.,* 1958). Since then, an extensive cotton-breeding program was initiated to develop cultivars resistant to the disease. In this program, breeding materials submitted by cotton breeders (Cotton Research Institute) have been screened for Fusarium wilt resistance under greenhouse conditions in soil artificially infested with FOV. This test has been conducted annually for the past 60 years in the greenhouses of Cotton and Fiber Crops Dis. Res. Section, Plant Pathology Research Institute. The program has been so successful in developing highly resistant commercial cultivars that the disease no longer occurs in the commercial fields (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 races other than race 3 or 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, mainly 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 each of agronomic and technological traits. For example, in China, Wu *et al*. (2004) found that incidence grade of Fusarium wilt was negatively correlated with fiber strength, micronaire value, and the fiber span length, and reached significant and highly significant levels. In USA, Ulloa *et al*. (2006) reported that foliar damage and vascular discolouration caused by FOV were negatively correlated with node number and plant height. In China, Guo *et al*. (2013) found that oil content in cottonseed Kernels was weakly negatively correlated with Fusarium wilt resistance. Thus, the improvement of the oil content of cottonseed kernels will weakly affect disease resistance.

In Egypt, as far as we know, no attempts have been made to study the correlation between incidence of Fusarium wilt and each of agronomic and technological traits. Therefore, the objectives of the present study were to evaluate a collection of cotton germplasm against Fusarium wilt race 3 and

to evaluate the correlation between wilt incidence on the tested genotypes and their agronomic and 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, Cytology and Genetics Unit, Cotton Research Institute (Table 1).

Field traits:

Field traits were carried out at Giza Agricultural Research Station in 2012 and 2013 growing seasons. In 2012 growing season, cotton genotypes were self- pollinated. In 2013 growing season, they were grown in a randomized complete block design with three replications. Each plot consisted of two rows, the row was six meter long, 60 cm apart and interhill spacing was 20 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 traits (Said *et al*., 2013).

a. Agronomic traits:

1. Boll weight (BW): The average weight in grams of a boll calculated from a random sample of five harvested bolls / plant.
2. Seedcotton yield (SCY): The expression of seedcotton weight in grams / plant.
3. Lint yield (LY): The expression of lint weight in grams / plant.
4. Lint percentage (L %): The ratio by weight of lint to seedcotton.

Agronomic traits of the tested genotypes are shown in Table 2.

b. Technological traits:

1. Fiber length at 2.5 % (mm): The upper half mean length. It was measured by a 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 fibers that are clamped between two sets of jaws. It was determined according to ASTM: D 1448- 59 (1984).

All fiber test were carried out in the Laboratories of Cotton Research Institute, Agric. Res. Center, Giza at constant relative humidity of 65 ± 2 % and temperature of 70 ± 20ºf. Technological traits of the tested genotypes are shown in Table 3.

Table 1. Cotton genotypes used in the present study.

Genotype Number	Pedigree
1	Giza 69 / 92
2	Giza 70 / 93
3	Giza 81/ 94
4	Giza 85 / 96
5	Giza 86 / 98
6	Australian 10229 / 101
7	(Giza 81 x Giza 86) / 106
8	(Giza 85 x Giza 89) / 107
9	(Giza 86 x Giza 85 x Giza 89) / 115
10	(Pima S) 2 / 127
11	Giza 67 / 128
12	(Pima S x Giza 85) / 129
13	(Aamon x Giza 89) / 130
14	(Pima S_7 x Giza 67) / 131
15	Bahteem / 142
16	Giza 84 / 144
17	Giza 70 / 145
18	Giza 87 / 146
19	Giza 74 / 148
20	Giza 45 / 149
21	(Giza 77 x Giza 81) / 150
22	(Giza 70 x Giza 77 x Giza 87) / 153
23	(Giza 70 x Giza 84) / 155
24	(Pima S_6 x Giza 77) / 162
25	(Giza 74 x Giza 71) / 163
26	(Giza 70 x Giza 77) / 164
27	(Giza 45 x Giza 68) / 165
28	Giza 88 / 167
29	Giza 45 / 169
30	Giza 68 / 171
31	Giza 71 / 172
32	Karnak / 175
33	(Giza 86 x Giza 84) / 176
34	(Giza 45 x Giza 70) / 177
35	(Giza 77 x Giza 76) / 178
36	(Giza 77 x Giza 45) / 179
37	(Giza 81 x Giza 87) / 180
38	Pima S_6 x Giza 45) / 181
39	(Giza 77 x Giza 74)/ 182
40	Pima S_6 x Giza 70) / 183
41	Giza 84 x (Giza 45 x Giza 84) / 184
42	Giza 77 x (Giza 77 x Giza 84) / 185
43	(Giza 86 x Giza 74) x Giza 84 / 187
44	(Giza 45xGiza 77)x(Giza 51 B x Giza 70) / 189
45	(Pima S x Giza 45) x (Giza 45 x Giza 68) / 190
46	Giza 45 (Radiated) / 192
47	Giza 76 / 193
48	(Giza 77 x Giza 84) / 193
49	(Pima S_6 x Giza 87) / 199
50	(Giza 74 x Giza 71) x Giza 77 / 202

Table 2. Agronomic traits of genotypes used in the present study.

Genotype Number.	Boll weight (g)	Seedcotton yield (g / plant)	Lint yield (g / plant)	Lint percentage
1	2.80	27.83	7.73	34.15
2	2.63	25.10	8.80	34.08
3	2.08	13.93	4.80	35.88
4	2.43	13.70	4.60	34.25
5	2.33	32.05	11.35	36.35
6	2.28	9.48	3.63	37.15
7	2.30	7.53	2.85	38.15
8	2.43	11.08	4.25	38.43
9	2.58	20.55	6.73	35.65
10	2.43	30.40	10.33	34.73
11	2.88	26.40	9.53	36.58
12	2.98	19.50	6.93	35.80
13	2.80	15.25	5.63	36.93
14	2.75	16.43	6.05	37.10
15	2.65	34.00	11.43	33.15
16	2.33	8.53	2.65	31.40
17	2.45	11.70	3.55	30.60
18	2.25	10.40	3.10	30.00
19	2.80	11.23	3.63	32.33
20	2.55	22.88	7.48	32.45
21	2.33	16.80	5.48	32.48
22	2.48	65.80	6.63	31.53
23	2.43	13.33	4.55	34.25
24	2.43	12.80	4.05	31.88
25	2.73	7.60	2.53	33.70

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

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 Lab., Plant Pathology Res. Inst., Agric. Res. Center., Giza. Autoclaved clay loam soil was infested with the mixture of the isolates at a rate of 10 g / Kg of soil. Substrate for growth of each isolate was prepared in 500-ml glass bottles, each bottle contained 50 g of Sorghum grains and 40 ml of tap water. Contents of the bottle were autoclaved for 30 minutes. Isolate inoculum, taken from one-week old culture on PDA, was aseptically introduced into the bottle and allowed to colonize sorghum for 3 weeks. Infested soil was dispensed in 10-cm-diameter clay pots and these were planted with 10 seeds per pot. There were five replications (pots) for each genotype. Pots were distributed on a greenhouse bench in a randomized complete block design of five replications. The greenhouse was equipped with a heating system assuring that the minimum temperature in the greenhouse was maintained at 28º C; however, due to the lack of a cooling system, the maximum temperature was out of control fluctuating from 30 to 35ºC depending on the prevailing temperature during the day (the test was conducted in January and February, 2014).

Table 2. Cont..

Genotype Number.	Boll weight (g)	Seedcotton yield (g / plant)	Lint yield (g / plant)	Lint percentage
26	2.60	15.35	5.25	33.85
27	2.30	9.20	3.25	35.45
28	2.48	13.23	4.43	34.35
29	2.50	15.00	5.10	33.51
30	2.25	7.25	2.85	39.30
31	2.25	6.05	2.03	36.90
32	2.83	14.63	5.05	34.50
33	2.90	13.50	4.73	35.13
34	2.73	16.90	5.70	33.90
35	2.48	11.33	4.23	37.35
36	2.43	12.83	3.25	34.13
37	2.48	17.68	6.38	37.25
38	2.43	12.50	4.50	36.05
39	2.60	11.63	4.30	37.25
40	2.53	15.68	5.85	37.10
41	2.68	19.78	7.25	36.43
42	2.68	16.63	5.98	35.83
43	2.60	19.30	6.03	30.93
44	2.20	12.10	4.15	34.90
45	2.48	14.53	4.55	31.28
46	2.63	14.98	4.80	32.45
47	3.10	17.63	6.05	33.05
48	2.60	25.08	8.20	32.43
49	2.70	11.48	4.23	36.88
50	2.93	8.63	2.83	33.20

Assessment of Fusarium wilt incidence:

Percentages of infected seedlings were recorded 45 days from planting date. The infected seedlings included the dead seedlings and the surviving seedlings, 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 discolouration of xylem vessels was observed, they were considered infected. If seedlings were free of such a discolouration, 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).

Wilt incidence on the tested genotypes is shown in Table 4.

Statistical analysis of the data:

Linear correlation coefficient was calculated to measure the degree of association between wilt incidence and each of agronomic and technological traits. Genotypes were clustered by the average linked technique (unweighted pair-group method) based on the profiles of their agronomic and technological traits. Correlation and cluster analyses were performed with the software package SPSS 6.0.