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The Determination of Tolerances of Some Cotton Genotypes Against Wilt Disease (*Verticillium dahliae* Kleb.) Under The Ecological Conditions of Diyarbakir

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ABSTRACT

Verticillium wilt disease in cotton is a soil-borne disease that causes significant yield losses, and it is therefore important to identify disease-resistant genotypes. Current study was carried out in the experimental field of the Faculty of Agriculture, Dicle University (Diyarbakir) in the year 2020 to determine the tolerance levels of some cotton genotypes which contain different characteristics to wilt disease (*Verticillium dahliae* Kleb.). The experiment area has been naturally infected with *Verticillium* wilt pathogens. A total of 124 cotton genotypes, including four controls (DP-499, Edessa, ST-468, ES-1), were arranged in five blocks according to the Augmented Design. The indices of stem cross-section and the leaf-disease severity were found significant. The leaf-disease severity varied between 0.12-3.09 at 50-60 % at boll opening period, whilst stem cross-section values ranged between 0.36-2.30. Moreover, a positive correlation was found between the indices. In conclusion, G7, G12, G21, G22, G23, G41, G51, G55, and G101 were determined as tolerant genotypes to *Verticillium* wilt in terms of examining two parameters.

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Introduction

Cotton is an important strategic and fiber product, which has significant value worldwide. It is cultivated to provide raw materials for the textile industry, and it is also known as "White Gold". Cotton belongs to the genus *Gossypium* and consists of about 50 species. In general, four types of cotton are cultivated around the world. These are *G. arboreum*, *G. herbaceum*, *G. hirsutum*, and *G. Barbadense* species. The *G. arboreum* and *G. herbaceum* species have diploid (2n = 26) chromosomes and are commonly called Old World Cotton, whereas the *G. hirsutum* and *G. barbadense* species are tetraploid (2n = 4x = 52) chromosomes and are known as New World Cottons (Sangwan et al., 2019). Among these four cultivated species, *G. hirsutum* is commonly cultivated in more than 90% of the cotton-growing areas of the world. And it stated that it is grown on about 3% of the cultivated land worldwide, within an area of 31.8 million hectares, in about 70 countries (Pundir et al., 2020). In terms of cultivation area, the top five cotton producing countries are India, China, the USA, Brazil, and Pakistan, respectively. It has been determined that Türkiye is ranked as the 6th cotton producer in world cotton production (ICAC, 2020). A total of 2,200,000 tons of cotton wool with a yield of 460 kg/da were produced during the 2019–2020 cotton producing season on 478 thousand hectares of cotton-growing land. In the Southeastern Anatolia region, cotton cultivation was carried out on a total of 2,889,140 decares of land, and it was determined that there was approximately 1,312,703 tons of cotton wool with a yield of 454 kg per decare. Cotton production is highest in the cities of Diyarbakir and Şanliurfa. In Türkiye, 37% of cotton is grown in the Şanliurfa region, while 11% is grown in Diyarbakir (TUIK, 2020).

Recently, there has been a serious decrease in cotton production in our country and around the world. The main reasons for this decrease in amount are biotic and abiotic stress factors. Widely, the wilt disease caused by *Verticillium dahliae Kleb*. fungus is one of the most destructive biotic stress factors in cotton production. It is known that this wilt disease causes the annual loss of 1.5 million cotton bales worldwide (Bell, 2001). It has been reported that *Verticillium* wilt disease caused the loss of approximately 148,000 bales in the 2010 cutton production season in the USA and 480 million bales in the world between 1990 and 2014 (Blasingame and Patel, 2005; Lawrence et al., 2016). In Türkiye, this disease is present in almost every field where cotton is grown. Therefore, serious economic losses are increasing day by day (Göre, 2007). It has been stated that this disease is common in the Aegean and Mediterranean regions (Esentepe, 1979). Along with these regions, it has been identified that *Verticillium* wilt disease is becoming more widespread day by day and causing high yield reductions in the Southeastern Anatolia region. Especially, the incidence of *Verticillium* wilt disease was 16.27% and the prevalence rate was 79.28% in provinces of Mardin, Diyarbakır, Şanlıurfa, Siirt, Batman and Adıyaman. In various studies conducted in these cities, it has been determined that this disease spread rate of 86% is too high (Sağır et al., 1991). Initially, *Verticillium* wilt disease enters slowly from the root to the tissue, settles in the xylem, starts to develop here and causes obstruction by precipitation in the veins of the stem. First the disease causes chlorosis and necrosis on the leaves, and then it causes the wilt. It prevents the transfer of pathogens, water, and other mineral substances from the roots to the leaves and tissues. This disease, starting from the lower leaves, induces wilting, drying, decreased photosynthesis, changes in yield and fiber quality characteristics, and shedding in combs and flowers. The necessity of developing important strategies against cotton wilt disease has emerged. In this direction, it will be inevitable to develop and improve more resistant varieties from genetic resources consisting of local cultivars, varieties that are not used continuously, wild relatives, and lines with unqualified genetic characteristics (Yu et al., 2012).

In cotton breeding programs, it is very important to develop resistant varieties to combat *Verticillium* wilt disease. During breeding programs, an experimental design should be used, which is referred to in the case of a shortage of materials and is often used to test breeders' advanced materials. If there are not enough seeds to set up a normal trial, the Augmented experimental design is used specifically. In this experimental design, control varieties are repeated in each block and other materials are used only once in each block (Petersen, 1994; Karaman et al., 2021).Due to the general ongoing rise in the global population, cotton and other natural fibers and foodstuffs are becoming more and more essential, and the demand for them is unavoidable. Accordingly, the genotype resistant to *Verticillium* wilt disease has been determined. One of the objectives of the study is to contribute to future cotton breeding programs and the development of the most resistant and tolerant varieties to wilt disease.

Materials and Method

Material

The cotton genotypes used in this study were obtained from the Nazilli Cotton Research Institute Directorate and a total of 128 genotypes were used, including 110 cotton genotypes with different characteristics and 18 cotton pure lines (Table 1).

The plants were grown in the experimental area of Diyarbakır that belongs to Dicle University-Faculty of Agriculture, Department of Field Crops during the 2020 growing season. This experimental field is known to be naturally infected and previous grown cotton crops suffered from *Verticillium* wilt disease. The research was designed in a total of 5 blocks according to the augmented experimental design. In this study, 124 cotton genotypes were compared with 4 registered cultivars (control). In addition, cultivars used as controls (DP-499, Edesa, St-468, and Es-1) were replicated in each block. The other cotton genotypes used in the experiment were grown sequentially in blocks without replication. The experimental area was established with a spacing of 2.5 meters between the blocks. The trial plot was 6 meters long and consisted of 2 rows. The cotton genotypes were planted in plots of 70 cm x 20 cm. The seeds of the 128 cotton genotypes used in this research study were sown on May, 15th 2020. During the sowing process, 6 kg of pure nitrogen (N) and 6 kg of pure phosphorus (P2O5) were utilized as base fertilizers per decare. The overall fertilizer application was 9.6 kg of nitrogen (N) per decare on July 4, 2020.

According to the data of the Diyarbakır Meteorology Regional Directorate, it was noted that the average temperatures in July and September, covering the cotton growing season, deviated from the averages of long years. However, it has been shown that the maximum temperature data is below the average data of long years. The relative humidity (%) was found to be above the average values of long years in April and May (Table 2).

Samples were taken at certain depths (0-30, 30-60 and 60-90 cm) in order to identify the soil properties of the area where the experiment was conducted (Çetin and Üzen, 2018). It was stated that the soil properties of the field of experiment did not have drainage and salinity problems. The lime and potassium ratio were high but slightly alkaline. It was determined that the organic matter and phosphorus content in this field was low and the clay content was higher (65%) in the soil texture, so it was classified as clayey (Table 3).

Method

Evaluations of Disease Severity

Evaluation of wilt disease in the leaves, the yellowing and necrosis of the leaves according to the 0-4 Verticillium wilt disease scale of the plants in each plot (Bejarano-Alcazar et al., 1995).The disease severity index was calculated by looking at the leaves (Figure 1) and the values were estimated (Table 4).

In terms of leaf disease severity index (DSI), a total of 20 plants were selected in each plot. The obtained data from these plants was determined with the help of the following formula. It was calculated by leaving 1 degree level between the severity rates by using the leaf disease severity index data in the determined 50-60% boll opening period.

Table 1. Species and Origin of Cotton Genotypes Used in this Study

No	Genotype	Species	Origin	No.	Genotype	Species	Origin
G1	Acala44	*G. Hirsutum* L.	USA	G65	Maydos yerlisi	*G. Herbaceum* L.	Türkiye
G2	Agala sindou	*G. Hirsutum* L.	Greece	G66	Nata	*G. Hirsutum* L.	Türkiye
G3	Ağdaş3	*G. Hirsutum* L.	Türkiye	G67	Nazilli143	*G. Hirsutum* L.	Türkiye
G4	Aktaş3	*G. Hirsutum* L.	Azerbaijan	G68	Nazilli303	*G. Hirsutum* L.	Türkiye
G5	AlbaAcala70	*G. Hirsutum* L.	USA	G69	Nazilli342	*G. Hirsutum* L.	Türkiye
G6	Aleppo-1	*G. Hirsutum* L.	Syria	G70	Nazilli663	*G. Hirsutum* L.	Türkiye
G7	Aşkabat100	*G. Barbadense* L.	Turkmenistan	G71	Nazilli84	*G. Hirsutum* L.	Türkiye
G8	Austral	*G. Hirsutum* L.	Australia	G72	Nazilli87	*G. Hirsutum* L.	Türkiye
G9	Aydın110	*G. Hirsutum* L.	Türkiye	G73	Nazilli954	*G. Hirsutum* L.	Türkiye
G10	Azerbaycan3038	*G. Hirsutum* L.	Azerbaijan	G74	New mexican acala	*G. Hirsutum* L.	USA
G11	Babylon	*G. Hirsutum* L.	Türkiye	G75	Nova	*G. Hirsutum* L.	Greece
G12	Bahar14	*G. Barbadense* L.	Turkmenistan	G76	Oğlakçı	*G. Hirsutum* L.	Türkiye
G13	Barut2005	*G. Hirsutum* L.	USA	G77	Özaltın404	*G. Hirsutum* L.	Türkiye
G14	Bulgar3279	*G. Hirsutum* L.	Bulgaria	G78	Özbek105	*G. Hirsutum* L.	Uzbekistan
G15	Candia	*G. Hirsutum* L.	Australia	G79	Paumg21	*G. Hirsutum* L.	USA
G16	Carisma	*G. Hirsutum* L.	Türkiye	G80	Penta	*G. Hirsutum* L.	USA
G17	Carmen	*G. Hirsutum* L.	Australia	G81	Poyraz	*G. Hirsutum* L.	Türkiye
G18	Cascot2910	*G. Hirsutum* L.	USA	G82	Rantos	*G. Hirsutum* L.	Greece
G19	Ceyhan520	*G. Hirsutum* L.	Türkiye	G83	Sealand542	*G. Hirsutum* L.	USA
G20	Coker310	*G. Hirsutum* L.	USA	G84	Samon	*G. Hirsutum* L.	USA
G21	Condor	*G. Hirsutum* L	USA	G85	Sayar314	*G. Hirsutum* L.	Türkiye
G22	Corina	*G. Hirsutum* L.	Spain	G86	Selçuk bey	*G. Hirsutum* L.	Türkiye
G23	Crinkle leaf (green)	*G. Hirsutum* L.	USA	G87	Silcot3	*G. Hirsutum* L.	USA
G24	Crumpled	*G. Hirsutum* L	USA	G88	Sorbon	*G. Hirsutum* L.	Tajikistan
G25	Çukurova1518	*G. Hirsutum* L.	Türkiye	G89	Stardel	*G. Hirsutum* L.	N/A
G26	Çoşkun1	*G. Hirsutum* L.	Türkiye	G90	Stoneville 62	*G. Hirsutum* L.	USA
G27	Darmi	*G. Hirsutum* L	Bulgaria	G91	Şahin 2000	*G. Hirsutum* L.	Türkiye
G28	Dawn	*G. Hirsutum* L	ABD	G92	Taşkent uzbek	*G. Hirsutum* L.	Uzbekistan
G29	Delcerro	*G. Hirsutum* L.	Australia	G93	Veramine	*G. Hirsutum* L.	Iran
G30	Delta diomond	*G. Hirsutum* L.	USA	G94	Veret	*G. Hirsutum* L.	USA
G31	Deltapine12	*G. Hirsutum* L.	USA	G95	Volkan	*G. Hirsutum* L.	Türkiye
G32	Dicle2002	*G. Hirsutum* L.	Türkiye	G96	Vurcano	*G. Hirsutum* L.	ABD
G33	Ege69	*G. Hirsutum* L.	Türkiye	G97	Ziroatkar64	*G. Hirsutum* L.	Türkiye
G34	Ege7913	*G. Hirsutum* L.	Türkiye	G98	BA440	*G. Hirsutum* L.	Türkiye
G35	Erşan92	*G. Hirsutum* L.	Türkiye	G99	BA119	*G. Hirsutum* L.	USA
G36	Ed76	*G. Hirsutum* L.	Türkiye	G100	PG2018	*G. Hirsutum* L.	Türkiye
G37	Fiberma819	*G. Hirsutum* L.	USA	G101	Carla	*G. Hirsutum* L.	Türkiye
G38	Frego	*G. Hirsutum* L.	Australia	G102	Bomba	*G. Hirsutum* L.	Türkiye
G39	Gacot79	*G. Hirsutum* L.	USA	G103	SC2009	*G. Hirsutum* L.	Türkiye
G40	Garant	*G. Hirsutum* L.	Australia	G104	SC2079	*G. Hirsutum* L.	Türkiye
G41	Gedera5	*G. Hirsutum* L.	Türkiye	G105	Sezener	*G. Hirsutum* L.	Türkiye
G42	Giza7	*G. Hirsutum* L.	Egypt	G106	Experia	*G. Hirsutum* L.	Türkiye
G43	Gloria	*G. Hirsutum* L.	Australia	G107	Karan 1	Pure Line	Türkiye
G44	Golda	*G. Hirsutum* L.	USA	G108	Karan 2	Pure Line	Türkiye
G45	Gossypolsüz86	*G. Hirsutum* L.	Türkiye	G109	Karan 3	Pure Line	Türkiye
G46	Gossypolsüz Nazilli	*G. Hirsutum* L.	Türkiye	G110	Karan 4	Pure Line	Türkiye
G47	Gumbo	*G. Hirsutum* L.	USA	G111	Karan 6	Pure Line	Türkiye
G48	Gürelbey	*G. Hirsutum* L.	Türkiye	G112	Karan 7	Pure Line	Türkiye
G49	Haridost	*G. Hirsutum* L.	Pakistan	G113	Karan 8	Pure Line	Türkiye
G50	Helius	*G. Hirsutum* L	Bulgaria	G114	Karan 9	Pure Line	Türkiye
G51	Hopicala – vert	*G. Hirsutum* L.	USA	G115	Karan 10	Pure Line	Türkiye
G52	İmpala	*G. Hirsutum* L.	Greece	G116	Karan 11	Pure Line	Türkiye
G53	İpek607	*G. Hirsutum* L.	Türkiye	G117	Karan 12	Pure Line	Türkiye
G54	Julıa	*G. Hirsutum* L.	Australia	G118	Karan 13	Pure Line	Türkiye
G55	Karnak55	*G. Hirsutum* L.	USA	G119	Karan 14	Pure Line	Türkiye
G56	Korina	*G. Hirsutum* L.	USA	G120	Karan 16	Pure Line	Türkiye
G57	Kurak2	*G. Hirsutum* L.	Türkiye	G121	Karan 19	Pure Line	Türkiye
G58	Lider	*G. Hirsutum* L.	Türkiye	G122	Karan 22	Pure Line	Türkiye
G59	Lima	*G. Hirsutum* L.	Türkiye	G123	Karan 23	Pure Line	Türkiye
G60	Lodos	*G. Hirsutum* L.	Türkiye	G124	Karan 27	Pure Line	Türkiye
G61	Lydia	*G. Hirsutum* L.	Türkiye	K1	St468	*G. Hirsutum* L.	USA
G62	Maraş92	*G. Hirsutum* L.	Türkiye	K2	Es-1	*G. Hirsutum* L.	Türkiye
G63	Marcel leaf (brow)	*G. Hirsutum* L.	USA	K3	Edessa	*G. Hirsutum* L.	Türkiye
G64	Marvi	*G. Hirsutum* L.	Pakistan	K4	Dp-499	*G. Hirsutum* L.	USA

K: Contol varieties, G: Genotype, N/A: not available

Table 2. Climate Data for 2020 Cotton Growing Season in Diyarbakir Province

Months	Average Temperature (ºC)		Maximum Temperature (ºC)		Total Precipitation (mm)		Relative Humidity (%)	
	2020	LYA	2020	LYA	2020	LYA	2020	LYA
April	13.7	13.6	24.8	35.5	109.9	69.7	71.2	64.0
May	19.1	19.4	34.7	39.6	63.2	44.0	57.6	56.7
June	26.0	26.8	39.5	41.8	0.9	9.0	34.7	36.1
July	31.3	30.9	42.4	46.3	0.5	1.1	26.5	26.7
August	31.0	30.1	41.0	45.5	0.0	0.9	23.9	26.5
September	27.1	25.4	41.2	41.6	0.3	5.3	25.9	31.4
October	16.5	17.6	32.9	35.8	33.9	33.0	29.5	48.0
Total	164.7	163.8	256.5	286.9	208.8	163.2	269.3	290
Average	23.53	23.4	36.64	40.99	29.83	23.31	38.47	41.43

* Diyarbakir Regional Directorate of Meteorology LYA: Long Years Average

Table 3. Properties of Soil for this Experiment

Depth (cm)	pH	K (ppm)	P (ppm)	Lime (%)	EC (dS/m)	Soil texture (%)			
						Sand	Silt	Clay	Soil constituency
0-30	7.66	559	8.9	9.9	0.49	18.1	18.6	63.7	C
30-60	7.75	424	2.2	11.0	0.37	15.8	18.7	66	C
60-90	7.77	422	2.2	12.1	0.42	17.8	18.7	63.7	C

K: Potasyum, Si: Silt, P: Phosphorus, EC: Electrical Conductivity

Table 4. Scale Values of Wilt Disease

Disease Scale Value (0-4)	Disease Symptom
0	No symptoms on the plant (Plants are healthy).
1	On the leaves of the plant, there are symptoms at the beginning stage, very little yellowing and unclear symptoms (1-33%).
2	Yellowing of the leaves, interveinal necrosis and leaf fall (34-66%).
3	Local necrosis between the leaf veins of the plant, defoliation and shriveling of all parts of the plant (i.e. going towards death) (67-97%).
4	Dying and death plant (98-100%)

Monitored levels “0, 1, 2, 3, 4” scale data of leaf disease severity index, “a, b, c, d, e” represents the number of plants included in each scale value, and “M” represents the total number of plants. For each scale value, “M” represents the total number of plants. As the determined leaf disease index data goes towards 0, it shows that the leaf becomes more resistant/tolerant to the disease severity index. However, when there is a trend towards 4 in the data, there is an increase in the sensitivity in terms of the leaf disease severity index (Karman, 1971).

$$\text{Leaf Disease Severity Index}=\frac{a_0+b_1+c_2+d_3+e_4}{M} \qquad (1)$$

Determination of Disease Severity Index in Stem Section

After the cotton plant harvesting, the plants within 0.5 cm were removed from each block of the experiment, taking into account the edge effect from the beginning and end of each plot. Then the cotton plants were cut at a height of 5 cm from the soil level and at an angle of 45 degree from the root collar. By looking at the discoloration of the wood tissue of the cut plants, the 0-3 disease scale was calculated according to Buchenauer (1976) (Figure 2) (Table 5).

A total of 20 plants were selected in each plot, and the evaluation of wilt disease in the stem section was performed. The data obtained from these plants were identified using the following formula, which was calculated by leaving 1 degree level between the disease severity indexes. The calculated levels “0, 1, 2, 3” indicate the scale data according to the stem section disease severity index; “a, b, c, d” indicates the number of plants included in each scale value; and “M” indicates the total number of plants processed. As the stem section disease severity index data goes to 0, the stem section shows that it is more resistant/tolerant to the disease severity index. However, if the data is directed towards 3, it has been determined that the trunk section is more sensitive than the disease severity index (Karman, 1971).

Statistical Analysis

The disease severity index data observed in regards to various cotton genotypes in the experimental area were subjected to variance and correlation analysis according to the augmented trial design by the means of the JMP (13.0) pro package software, and the data that were different were analyzed by the Tukey test (according to P≤0.01 or P≤0.05) grouped into various levels. In addition, the DARwin (version 6) package software was used for the visual presentation of the relationships and grouping between genotypes.

$$\text{DSI}=\frac{a_0+b_1+c_2+d_3}{M} \qquad (1)$$

DSI: Disease Severity Index of Cross-Sections in Stem

Figure 1. Disease severity values on leaves

0% 1-33% 34-67% 68-100%

Figure 2. Disease severity indices in stem section

Table 5. Disease Scale Values on Stem Section

Disease Scale Value (0-3)	Disease Symptom
0	No browning (discoloration) in wood (xylem) tissue
1	The browning and black spots (discoloration) 1-33% in the wood (xylem) tissue of the plant
2	The 34-67% of browning and black spots (discoloration) in the wood (xylem) tissue of the plant
3	Browning and darkening 68-100% (discoloration) in the plant wood (xylem) tissue

Table 6. Variance Analysis of Mean Squares

Variance Sources	DF	Leaves during the boll opening period of 50-60% (DSI)	Stem cross-section (DSI)
Model	131	0.29	0.12
Blok	4	0.02	0.03
Genotype	127	0.27**	0.12**
Error	12	0.05	0.02
LSD (0.05)		0.02	0.01
CV (%)		14.46	10.01

** $P<0.01$, DF: Degrees of Freedom, DSI: Disease Severity index, CV: Coefficient of Variation

Findings and Discussion

Due to the variance analysis results of some cotton genotypes, there was statistically significant differences at the $P<0.01$ level between genotypes in terms of stem section and leaf disease severity index of 50-60% at boll opening period between genotypes (Table 6). According to the results of this study, the genotype differences were grouped based on the analyzed characteristics using the Tukey test. Furthermore, owing to the stem section and leaf disease severity index data obtained in this study, it was determined that 12 cotton genotypes were better than the resistant/tolerant control variety (Table 7a, b).

Disease Severity Index Values (50-60%) in the Stem Section and Leaf at Boll Opening Period

In this study, stem section and leaf disease severity indices were found to be significant among cotton genotypes ($P\leq0.01$) (Table 6).

Table 7a. Examined Traits Results and Formed Groups

No.	G. Name	Leaves during the boll opening period of 50-60% (DSI)	Stem cross-section (DSI)
G1	Acala44	0,95b-m	2,13ab
G2	AgalaSindou	1,24a-m	1,55a-l
G3	Ağdaş3	1,37a-m	0,93d-m
G4	Aktaş 3	1,29a-m	1,37a-m
G5	AlbaAcala 70	0,70b-m	1,40a-m
G6	Aleppo-1	1,77a-m	1,77a-h
G7	Aşkabat 100	0,12l-m	0,36m
G8	Austral	1,63a-m	1,59a-l
G9	Aydın 110	1,74a-m	2,04a-c
G10	Azerbaycan 3038	1,46a-m	1,34a-m
G11	Babylon	1,39a-m	1,67a-k
G12	Bahar 14	0,54d-m	0,98d-m
G13	Barut 2005	1,79a-m	1,25a-m
G14	Bulgar 3279	1,21a-m	1,52a-l
G15	Candia	1,47a-m	0,74d-m
G16	Carisma	2,09a-k	1,27a-m
G17	Carmen	1,57a-m	1,26a-m
G18	Cascot 2910	1,12b-m	0,79d-m
G19	Ceyhan 520	2,05a-k	1,14b-m
G20	Coker 310	1,19a-m	1,23a-m
G21	Condor	0,60d-m	0,80d-m
G22	Corina	0,37g-m	0,94d-m
G23	CrinkleLeaf (Green)	0,24ı-m	0,60j-m
G24	Crumpled	0,84b-m	1,30a-m
G25	Çukurova 1518	0,61d-m	1,16a-m
G26	Çoşkun1	1,17a-m	0,66g-m
G27	Darmi	1,22a-m	1,63a-l
G28	Dawn	1,12b-m	1,10b-m
G29	Delcerro	1,11b-m	1,04b-m
G30	Delta Diomond	1,13b-m	1,07b-m
G31	Deltapine 12	2,07a-m	1,37a-m
G32	Dicle 2002	2,08a-m	1,46a-m
G33	Ege 69	2,12a-j	2,30a
G34	Ege 7913	1,69a-m	1,03b-m
G35	Erşan 92	1,92a-m	1,32a-m
G36	Ed 76	2,03a-m	1,00b-m
G37	Fibermax 819	1,50a-m	0,61ı-m
G38	Frego	1,30a-m	1,15b-m
G39	Gacot 79	2,17a-j	1,53a-l
G40	Garant	2,47a-d	1,74a-j
G41	Gedera 5	0,56e-m	0,74d-m
G42	Giza 7	1,36a-m	1,12b-m
G43	Gloria	0,80b-m	0,76d-m
G44	Golda	0,92b-m	0,95c-m
G45	Gossypolsüz 86	1,52a-m	1,34a-m
G46	Gossypolsüz Nazilli	1,38a-m	1,14b-m
G47	Gumbo	1,52a-m	0,94c-m
G48	Gürelbey	1,06b-m	0,78d-m
G49	Haridost	1,86a-m	0,87d-m
G50	Helius	1,55a-m	1,34a-m
G51	Hopicala – vert	0,17k	1,16a-m
G52	İmpala (Etna)	1,35a-m	1,47a-m
G53	İpek 607	0,96b-m	1,20a-m
G54	Julıa	1,28a-m	1,00b-m
G55	Karnak 55	0,23j-m	0,80d-m
G56	Korina	1,92a-m	1,65a-l
G57	Kurak-2	1,34a-m	1,43a-m
G58	Lider	1,82a-m	1,25a-m
G59	Lima	1,34a-m	1,31a-m
G60	Lodos	1,34a-m	0,74d-m
G61	Lydia	1,15a-m	1,27a-m
G62	Maraş 92	2,01a-l	1,65a-k
G63	MarcelLeaf (Brown)	1,41a-m	1,59a-l
G64	Marvi	2,33a-f	1,51a-m
G65	Maydos Yerlisi	1,66a-m	1,42a-m
G66	Nata	1,54a-b	0,95c-m
G67	Nazilli 143	1,20a-m	1,18a-m
G68	Nazilli 303	1,64a-m	0,98b-m
G69	Nazilli 342	1,36a-m	1,43a-m

Table 7b. Examined Traits Results and Formed Groups

No.	G. Name	Leaves during the boll opening period of 50-60% (DSI)	Stem cross-section (DSI)
G70	Nazilli 663	1,11b-m	1,40a-m
G71	Nazilli 84	0,86b-m	1,00b-m
G72	Nazilli 87	1,82a-m	1,36a-m
G73	Nazilli 954	0,88b-m	0,84d-m
G74	New Mexican Acala	0,69b-m	0,61h-m
G75	Nova	1,07b-m	0,96c-m
G76	Oğlakçı	1,89a-m	1,52a-m
G77	Özaltın 404	2,10a-k	1,40a-m
G78	Özbek 105	1,66a-m	1,39a-m
G79	Paumg-21	2,10a-k	1,22a-m
G80	Penta (G)	2,41a-e	1,39a-m
G81	Poyraz	1,82a-m	1,24a-m
G82	Rantos	1,30a-m	1,45a-m
G83	Sealand 542	2,56a-c	1,68a-j
G84	Samon	2,35a-e	1,45a-m
G85	Sayar 314	1,85a-m	1,16a-m
G86	Selçuk Bey	1,95a-m	1,54a-l
G87	Silcot-3	1,82a-m	1,24a-m
G88	Sorbon	2,11a-k	1,42a-m
G89	Stardel	2,29a-g	1,66a-j
G90	Stoneville 62	1,90a-m	1,61a-l
G91	Şahin 2000	2,60a-c	1,58a-l
G92	Taşkent Uzbek	2,10a-k	1,31a-m
G93	Veramine	1,98a-m	1,83a-e
G94	Veret	1,66a-m	0,56k-m
G95	Volkan	1,55a-m	0,77f-m
G96	Vurcano	1,27a-m	1,26a-m
G97	Ziroatkar-64	1,72a-m	0,81d-m
G98	BA-440	1,35a-m	0,92c-m
G99	BA119	0,99b-m	0,94c-m
G100	PG 2018	1,60a-m	0,93c-m
G101	Carla	0,39f-m	0,97c-m
G102	Bomba	1,49a-m	1,56a-l
G103	SC-2009	1,47a-m	1,42a-m
G104	SC-2079	0,79c-m	1,22a-m
G105	Sezener	1,30b-m	1,57a-l
G106	Experia	1,76a-m	1,88a-f
G107	Karan1	2,07a-m	1,70a-k
G108	Karan2	3,09a	1,77a-h
G109	Karan3	1,99a-m	1,77a-h
G110	Karan4	2,24a-g	1,75a-j
G111	Karan6	1,87a-m	1,87a-f
G112	Karan7	1,39a-m	1,71a-k
G113	Karan8	1,47a-m	1,52a-m
G114	Karan9	2,59ab	1,46a-m
G115	Karan10	1,58a-m	1,78a-g
G116	Karan11	1,47a-m	1,75a-j
G117	Karan12	1,59a-m	1,38a-m
G118	Karan13	2,04a-m	1,56a-l
G119	Karan14	1,75a-m	1,54a-l
G120	Karan16	1,96a-m	1,43a-m
G121	Karan19	1,09b-m	1,31a-m
G122	Karan22	1,72a-m	1,77a-g
G123	Karan23	1,24b-m	1,22a-m
G124	Karan27	1,71a-m	1,12b-m
St-468	K1	1,36b-m	1,01e-m
Es-1	K2	1,69a-ı	1,42b-k
Edessa	K3	1,52b-m	1,38b-k
Dp-499	K4	0,75h-m	0,79l-m
Small		1,50	1,28
Min.		0,12	0,36
Max.		3,09	2,30
The Most Durable Control Type More Resistant Genotype Number		12	12

Resistant cotton genotypes are indicated in bold. K: Control, DSI: Disease Severity index , G: Genotype

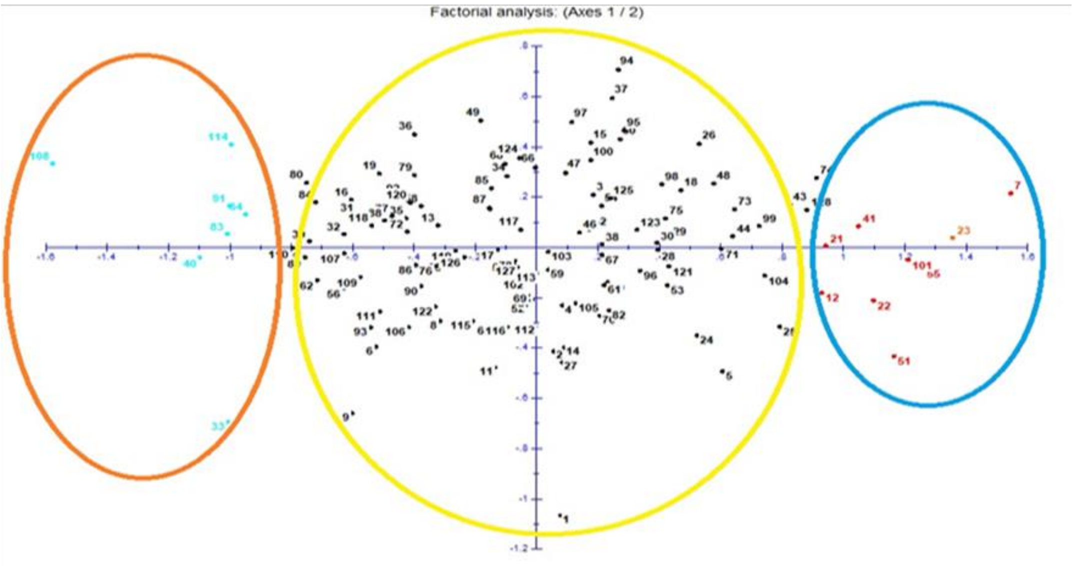

Figure 3. DARwin diagram showing genotype groups

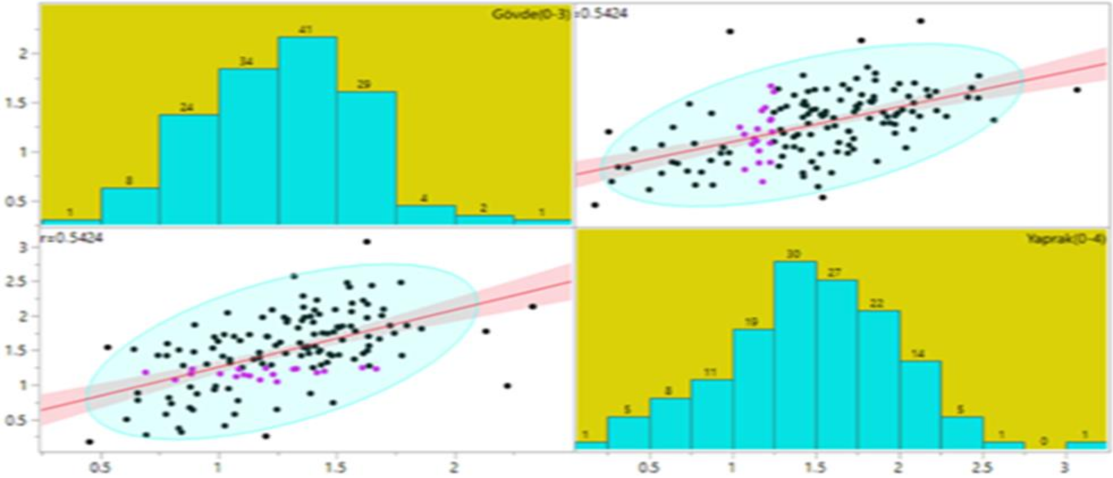

Figure 4. Correlation of disease index values of the evaluated traits

Table 8. Correlation Coefficients and Significance Levels Between the Evaluated Traits

Traits	DSI during boll opening period of 50-60% in the leaf	DSI in stem cross-section
DSI during boll opening period of 50-60% in the leaf	-	
DSI in stem cross-section	0.5424**	-

** P<0.01

Additionally, depending on the disease severity index of the stem section, the genotypes that were grouped into the “m” group (1.52-0.36) are the most resistant/tolerant genotypes to wilt disease (*Verticillium dahliae* Kleb.) and the most susceptible genotypes were in the “a” group (2.30-1.16) (Danıştı, 2001; Lüders et al., 2008; Göre et al., 2009; Karademir et al., 2010). The leaf disease severity index was founf to be the most resistant/tolerant genotypes in the “m” group (2.08-0.12) during the boll opening period of 50-60%, while the most susceptible was observed in the “a” group (3.09-1.15). Afterward, it was demonstrated that 12 cotton genotypes were better than the control, particularly Dp-499, which is the most resistant/tolerant to wilt disease, in terms of stem section and leaf disease severity index. In the other studies, it has been reported that the difference between cotton genotypes was significantly observed in regards to the stem section and disease severity index values (Erdoğan et al., 2015; Göre et al., 2017; Yaşar, 2022). Additionally, we identified the genotypes G7, G12, G21, G22, G23, G41, G51, G55, and G101 when evaluating the traits of the used genotypes that are resistant in accordance with the stem cross-section and leaf disease severity index at 50–60% at boll opening phase. While G35, G40, G64, G83, G91, G108 and G114 genotypes were found to be the most sensitive in terms of these two evaluated traits. The Darwin’s diagram shows the grouping of genotypes for the examined traits and it visually confirms the results (Figure 3).

Correlation Analysis

Table 8 highlights the relationships between the characteristics analyzed related to *Verticillium* wilt disease as well as the correlation between the stem cross-section and the leaf disease severity index, which was found to be positive (r = 0.5424) and statistically significant at the 1% level (Figure 4).

Moreover, similar research studies have been carried out to determine the reactions of different cotton genotypes of various origins to wilt disease and it was stated that there was a highly positive and significant correlation (r= 0.972) between the disease severity index data determined from the leaf and stem sections of the studied cotton genotypes (Akışcan and Tok, 2019). According to the severity index for leaf disease during the 50%–60% boll opening period and the stem section, there was a positive correlation (r= 0.5616) at a moderate level (Baran and Temiz, 2021). In the study carried out in field and greenhouse conditions, they found that the traits they examined were highly positive and highly correlated (r = 0.966) between stem section and leaf disease severity index values in all genotypes (Khaskheli, 2013). However, Zhou (2014) conducted field tests during the cotton growing season in 2013. In this study, the data obtained in terms of the characteristics analyzed in 3 different experimental studies were insignificant and very low (r = 0.03) in the first trial area. A significant and low (r = 0.39) correlation was reported in the second experimental area. Furthermore, in the third experimental field, they found a moderately positive correlation (r = 0.58) at the significance level. The findings of this study were in accordance with the values obtained by Akışcan et al. (2019); Baran et al. (2021) and Khaskheli et al. (2013), but were higher than the values of Zhou et al. (2014).

Conclusion

From this study, carried out in Diyarbakır's ecological conditions, findings shows that there are some resistant cotton genotypes which are important in terms of the evaluated traits. It was stated that there was a positive and significant correlation (r = 0.5424) between the stem section and the leaf disease severity index. The result concludes that in terms of all characteristics investigated in this study, significant differences were detected between cotton genotypes ($P<0.01$). Compared with control varieties; the 12 cotton genotypes were identified as the most resistant/tolerant genotypes due to the stem section and leaf disease severity index. Besides, the tolerance of resistant/tolerant genotypes to *Verticillium* was established to be much more resistant than Dp-499, which is the most resistant genotype among the control varieties to disease used in the study. The results of this study suggest that these genotypes should be used as parents in future cotton breeding programs.

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References

Akışcan Y, Tok FM. 2019. Investigation of resistance to verticillium wilt in some cotton genotypes of different origins. KSU Journal of Agriculture and Nature 22 (Additional Issue 2): 354-360. Doi: 10.18016/ ksutarimdoga.vi.544323.

Baran N, Temiz MG. 2021. Determination of resistance of different cotton genotypes against verticillium wilt (verticillium dahliae Kleb.) in Diyarbakır ecological conditions according to augmented trial design. ISPEC Journal of Agricultural Sciences, 5(3): 627-640.

Bejarano-Alcazar J., Melero-Vera J.M., Blanco-Lopez M.A., Jımenez-Diaz R.M. 1995. Influence of ınoculum density of defoliating and nondefoliating pathotypes of *verticillium dahliae* on epidemics of *verticillium* wilt of cotton in southern spain. Phytopathology, 85:1474-1481.

Bell, A. A. (2001). *Verticillium* Wilt 28-31. Eds, TL Kirkpatrick and CS Rothrock "Compendium of Cotton Diseases" Second ed. APS Pres VIII, 77.

Blasingame D, Patel MV. 2005. Cotton disease lossestimate committee report. In Proceedings of the Beltwide Cotton Conference, January 2005, Louisiana, LA, USA, 4–7, pp. 102–103.

Buchenauer H., D. Erwin C. 1976. Effect of the plant growth retardant pydanon on *verticillium* wilt of cotton and tomato. Phytopathology, 49:68-72.

Çetin Ö., Üzen N. 2018. The effect of surface and subsurface drip irrigation on soil moisture change and soil water tension. Harran Journal of Agricultural and Food Sciences, 22(4):461-470. Doi: 10.29050/harranziraat.442314

Danıştı L. 2001. Researches on the Response of Some Cotton Varieties to Wilt Disease (V. dahliae Kleb.) and their ecology and density and damage degree. Regional Plant Protection AE research works serial No.32, İzmir.

Erdoğan O, Bolek Y, Dündar H, Bardak A. 2015. Screenıng of cotton genotypes for resıstance to *verticillium dahliae* kleb. under greenhouse and field condıtıons. *Romanian Agricultural Research*, No. 32, Print Issn 1222-4227; Online Issn 2067-5720.

Esentepe M. 1979. Investigations on the factor, distribution, density, damage degree and ecology of wilt disease in cotton in Adana and Antalya provinces. Regional Plant Protection AE Research Works Serial No.32. Izmir.

Göre ME. 2007. Vegetative Compatibility and Pathogenicity of *Verticillium dahliae* İsolates From The Aegean Region of Türkiye. Phytoparasitica, 35, 222-231.

Göre ME, Caner ÖK., Altın N, Aydın MH., Erdoğan O, Filizer F, Büyükdöğerlioğlu A. 2009. Evaluation of cotton cultivars for resistance to pathotypes of *verticillium* dahliae. *Crop Protection*. 28:215–219. Doi: https :// doi .org /10. 10 16 /j.cropro.2008.10.004

Göre ME, Erdoğan O, Altın N. 2017. Searching for resistance sources to *verticillium* wilt of cotton in seedlings from Gossypium Spp. Tropical Plant Pathology, 42: 28–31. Doi: 10.1007/s40858-016-0120-6

ICAC, 2020. International Cotton Advisory committee. ICAC. Available from https:// icac.gen10.net/statistics (Accessed 19 August 2021).

Karademir E, Karademir Ç, Ekinci R., Baran B, Sağır A. 2010. Assessment of tolerance level of some cotton (*Gossypium hirsutum* L.) varieties against *Verticillium* wilt (*Verticillium dahliae* Kleb.). Not. Bot. Hort. Agrobot. Cluj, 38(1):196-202. Doi: https://doi.org/10.15835/nbha3814574

Karaman M, Başaran M., Erdemci İ, Okan M. 2021. Evaluation of bread wheat genotypes (*Triticum aestivum* l.) based on augmented trial design in terms of some agricultural characteristics under precipitation-based conditions in Diyarbakır. MSU Science and Technology Journal, 9:1 833-842.

Karman M. 1971. General information in Plant Protection research, Ministry of Agriculture Professional Books Series, Bornova, 279, İzmir/Türkiye.

Khaskheli MI, Sun JL, He SP, Du XM. 2013. Screening of cotton germplasm for resistance to *Verticillium dahlia Kleb*. under greenhouse and field conditions. Eur J Plant Pathol., 137:259-272. Doi: 10.1007/s10658-013-0235-2

Lawrence K, Hagan A, Olsen M, Faske T, Hutmacher R, Mueller J, Wright D, Kemerait R, Overstreet C, Price P. 2016.Cotton disease loss estimate committee report, 2015. In Proceedings of the Beltwide Cotton Conference, Memphis, 20–23 June 2016, TN, USA, Volume 1, pp. 113–115.

Lüders RR., Galbieri R., Fuzatto MG, Cia E. 2008. Inheritance of resistance to *Verticillium* wilt in cotton. Crop Breeding and Applied Biotechnology, 8: 265-270.

Petersen RG. 1994. Agricultural field experiments: design and analysis. New York: Marcel Dekker Inc. ISBN 0-8247-8912-1

Pundir SR, Sangwan O, Rathi M, Kumar S. 2020. "Study of genetic parameters and clustering on basis of morpho bio traits of cotton genotypes (*Gosyypium arboreum* L.)" Breeding P, Haryana C.C.S, Volume 34, no. 0972, pp. 183–191.

Sağır A, Tatlı F, Gürkan B. 1991. Researches on diseases seen in cotton cultivation areas in Southeastern Anatolia Region. Diyarbakır Agricultural Control Research Project No: KKGA-B-2115/04-F-018 1. and 2. year report.

Sangwan S, Sangwan O, Pundir SR., Jangid K. 2019. "Characterization of elite Asiatic cotton (*Gossypium arboreum*) lines on the basis of DUS traits," vol. 33, no. 0972, pp. 214–220.

TUIK, 2020. Türkiye İstatistik Kurumu. TÜİK. Available from https://biruni.tuik.gov.tr/bitkilapp/bitkisel.zul (Accessed 18September 2021).

Yaşar M. 2022. Evaluation of some new cotton genotypes against verticillum disease (*Verticillum dahliae* Kleb.). ISPEC Tarım Bilimleri Dergisi, 6(1): 110-117.

Yu JZ, Fang DD, Kohel RJ, Ulloa M, Hinze LL, Percy RG, Zhang J, Chee P, Scheffler BE, Jones DC. 2012. Development of a core set of ssr markers for the characterization of gossypium germplasm. Euphytica, 187, 203- 213. Doi: 10.1007/s10681-012-0643-y

Zhou H, Fang H, Sanogo S, Hughs SE, Jones DC, Zhang J. 2014. Evaluation of Verticillium wilt resistance in commercial cultivars and advanced breeding lines of cotton. Euphytica, 196:437-448. Doi: 10.1007/s10681-013-1045-5