



Determination of Seedling Reactions of Some Barley Cultivars, Lines, and Wild Barley (*Hordeum spontaneum*) Genotypes to *Cochliobolus* Leaf Spot Disease

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HIGHLIGHTS

- *Cochliobolus* leaf spot disease is an important disease of barley caused by the fungus *Cochliobolus sativus*.
- Under greenhouse conditions, seedling stage reactions of 36 barley cultivars, 35 advanced lines, and 21 wild barley (*Hordeum spontaneum*) genotypes were determined.
- Among barley cultivars and genotypes, six genotypes showed a low reaction, 29 genotypes showed moderate reactions and 36 genotypes showed a high reaction.
- Of the wild barley genotypes, two, 8, and 11 genotypes showed low, moderate, and high reactions respectively.

Abstract

Cochliobolus leaf spot disease, also seen in barley, is an important disease caused by the fungus, *Cochliobolus sativus*. In this study, under greenhouse conditions, seedling stage reactions of 36 barley cultivars, 35 advanced lines, and 21 wild barley (*Hordeum spontaneum*) genotypes obtained from Elazığ province of Türkiye and Güzelyurt district of the Turkish Republic of Northern Cyprus against a virulent isolate of *Cochliobolus sativus* has been determined. Among barley cultivars and genotypes, six genotypes showed a low reaction, 29 genotypes showed moderate reactions and 36 genotypes showed a high reaction. Of the wild barley genotypes, two, 8, and 11 genotypes showed low, moderate, and high reactions respectively. Barley cultivars Harman and Pınar showed low reaction responses, cultivars Akar, Bolayır, Bozlak, Burgaz, Çumra 2001, Hasat, Misket, Orza 96, Sabribey, Sinanbey, Yaprak, and Yesevi 93 exhibited intermediate reaction responses and cultivars Anka-06, Asil, Avcı 2002, Aydanhanım, Ayrancı, Başgül, Burakbey, Bülbül 89, Cacabey, Cirit, Çetin 2000, Hazar, İnce 04, Keykubat, Larende, Özdemir 05, Sayım 40, Tarm 92, Tosunpaşa, Yalın, Yüksel, and Zeynelağa showed high reaction responses. Barley cultivars exhibiting low reaction types can be used by farmers in the field, while barley lines and wild barley genotypes showing low reactions can be used in breeding studies.

Keywords: Barley; *Bipolaris sorokiniana*; *Cochliobolus sativus*; spot blotch; disease resistance

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1. Introduction

Barley (*Hordeum vulgare* L.), a member of the Poaceae family, is an annual long-day plant among the cool climate cereals. Cultivated barleys are typically categorized as 2 rowed or 6 rowed based on ear structure (Geçit 2016), and they are divided into hulled or hulless (naked) according to the separation of grains and husks after harvest (Duan et al. 2015). Barley, which can be grown without irrigation in arid and semi-arid regions, shows better growth in areas with high relative humidity, and moderate climates. *Hordeum spontaneum* C. Koch, which is accepted as the ancestor of modern barley, is two-rowed and predominantly self-pollinated (Zohary and Hopf 2000).

It is estimated that the barley cultivation areas in the world are 51.7 million ha with an increase of 1% in the cultivation areas in the 2020/21 season, and the barley production is 159.7 million tons with an increase of 1.9%. Analysis of the 2019/20 USDA datashowed that the EU has the largest barley cultivation area in the world with 21.7% in the last seven production seasons. The EU is followed by Russia, Australia, Türkiye, and Canada with 16.4%, 7.9%, 7.4%, and 5.3%. These countries constitute approximately 58.7% of the world's cultivation area (Eğilmez 2021; USDA 2022).

Approximately 55-60% of the world's barley production is used for animal feeding, 30-40% in the malt industry, 2-3% in human consumption, and 5% as seed (Ullrich 2011). Barley, which is mostly cultivated under rainfed conditions and in the arid climate zone, is a grain known for its earliness, which has an escape mechanism from drought in Türkiye (Anonymous B 2020). Barley, which ranks second in Türkiye after wheat, is produced in every agro-ecological zones of Türkiye. Barley cultivation areas and production amounts for the last ten years vary between 2.4-3.0 million hectares (ha) and 6.3-8.0 million tons, respectively (Anonymous A 2020; Eğilmez 2021; Anonymous 2021).

Cochliobolus sativus (Ito and Kuribayashi) Drechs. ex Dastur (anamorph: *Bipolaris sorokiniana* (Sacc.) Shoem.) is one of the fungal diseases that affect barley production and quality. This pathogen, which causes *Cochliobolus* leaf spot and root rot diseases in the plant (Mathre 1997; Kumar et al.2002), is an important disease agent that leads to a decrease in quality and yield in barley. The disease was more common in barley than in wheat in the central Anatolian Region, and it was determined that one-third of the cultivation areas were contaminated with the pathogen (Aktaş 1982). *Cochliobolus* leaf spot disease is usually seen in humid conditions (Fetch and Steffenson 1999). On the leaves of the plant infected with this disease, the first symptoms are dark chocolate-colored spots and over time they form irregular necrotic patches on the leaf. As the infection progresses more severely, the infected leaf dries up completely (Mathre 1997).

Cochliobolus sativus passes to the next year with seeds and diseased plant residues in the soil and can cause disease in all development stages of the plant. Root and root collar disease symptoms caused by the fungus are dark and pale brown spots. Grain deaths occur due to reasons such as spots on leaves, seedling blight, and root rot; the husk and grain blight seen on the spike causes the embryo to darken (Yıldırım et al. 2016).

This disease causes 16% to 33% product loss with the effect of environmental conditions (Wilcoxson et al. 1990). Overall, the degree of resistance in modern cultivars is still insufficient (Hetzler et al. 1991; Chang et al. 1998; Mujeeb-Kazi 1998; Van Ginkel and Rajaram 1998; Kumar et al.2002).

Although fungicide applications are applied in the fight against this disease, the development and use of lines and varieties resistant to *C. sativus* stand out as an environmentally friendly control method (Kiesling1985). The reactions of the newly developed barley cultivars should be determined. The resistance status of advanced barley lines and wild barley (*Hordeum spontaneum*) genotypes which are important resistance sources should be assessed. *Hordeum spontaneum* genotypes are useful disease-resistance sources (Çelik and Karakaya 2017).

There are studies of resistance to diseases related to *Cochliobolus* leaf spot in the world and in Türkiye (Aktaş and Tunalı 1994; Clear et al. 1997; Legzdina and Buerstmayr 2004; Gerlegiz et al. 2015; Çelik Oğuz et al. 2016; Celik-Oguz and Karakaya 2017; Balcı et al. 2018). On a worldwide scale, yield losses in wheat and barley caused by *C. sativus* reveal the need to search for alternative strategies to combat the disease (Yıldırım 2016).

Several studies have identified quantitative trait loci (QTL) for resistance to *Cochliobolus* leaf spot disease on all seven barley chromosomes. To date, three resistance genes (Rcs 5, Rcs 6, Rbs 7) have been mapped in detail (Zhou and Steffenson 2013; Afanesenko et al. 2015; Novakaziet al. 2020; Visionsi et al. 2020). In addition, common QTLs were detected in all barley chromosomes at seedling and adult plant stages (Visionsi et al. 2020). Wild barley is an important source of genetic variation for disease resistance (Fetch et al. 2003; Yun et al. 2005). Although there are some studies on genetic resistance to *Cochliobolus* leaf spot disease, there are limited genetic studies from the wild barley host. Wild barley accession PI 466423, resistant to Fusarium head blight and *C. sativus*, was crossed with the Rasmusson cultivar, and four resistance QTLs were identified on chromosomes 1H, 2H, 4H, and 5H. These results confirm the value of using wild relatives as a source of new resistance alleles (Haas et al. 2016).

In this study, seedling stage reactions of old and new barley cultivars, advanced barley breeding materials, and wild barley (*Hordeum spontaneum*) genotypes against *C. sativus* leaf spot disease were determined.

2. Materials and Methods

In this study, seedling resistance of 36 old and newly bred barley cultivars, 35 advanced barleylines and 21 wild barley (*Hordeum spontaneum*) genotypes were evaluated under greenhouse conditions against a virulent isolate of *Cochliobolus sativus*. A highly virulent isolate obtained from Yozgat in 2015, which was stored in the culture collection of Ankara University, Faculty of Agriculture, Department of Plant Protection, Mycology laboratory, was used. Before the study, the virulence level of the isolate was tested on the susceptible variety Bülbül 89 (Celik-Oguz and Karakaya 2017; Çelik Oğuz et al. 2019), and the virulence level was again found to be high. Wild barley genotypes were obtained from Elazığ province of Türkiye (16 genotypes) and Güzelyurt district of the Turkish Republic of Northern Cyprus (TRNC) (5 genotypes). For this purpose, the methods outlined by Celik-Oguz and Karakaya (2017) were used. Reproduction of pure wild barley seeds under field conditions was carried out in the experimental field of the Central Research Institute for Field Crops in Yenimahalle, Ankara, Türkiye. Fifteen seeds of each barley and wild barley genotype were planted in pots containing soil, sand, and organic matter (60: 20: 20, v:v:v). Conidia suspension was prepared from 10-day-old cultures grown on Potato Dextrose Agar. To prepare the inoculum, the conidia of the fungus grown in Petri dishes for 14 days were scraped with the help of a brush, filtered through cheesecloth and the density was determined using a Thoma slide as 2×10^4 conidia/ml. 1 drop of Tween 20 was added to each 100 ml (Çelik Oğuz et al. 2016). Cultures were incubated at 20-23°C in 12 hours dark/12 hours light conditions. The plants in each pot were sprayed homogeneously with the inoculum. Inoculation was carried out at Zadoks 12-13 growth stage which corresponds to the 2-2.5 leaf stage (Zadoks et al. 1974). The studies were carried out under greenhouse conditions. Following inoculation, the plants were placed in boxes with transparent lids and closed with a polyethylene bag. Experiments were carried out as 3 replications. After 7 days, evaluations were made according to the 1-9 scale developed by Fetch and Steffenson (1999). This scale is divided into 3 categories. Scale values 1-3, 4-5, and 6-9 represented low, intermediate, and high infection responses, respectively.

3. Results

Seedling stage reactions of 36 barley cultivars, 35 barley lines, and 21 wild barley (*Hordeum spontaneum*) genotypes against *C. sativus* were determined (Tables 1, 2, 3 and Figures 1, 2).

Among barley cultivars and lines, six genotypes showed a low reaction, 29 genotypes showed intermediatereactions and 36 genotypes showed a high reaction. Of the wild barley genotypes, two, 8, and 11 genotypes showed low, intermediate, and high reactions, respectively. Barley cultivars Harman and Pınar showed low reaction responses; Akar, Bolayır, Bozlak, Burgaz, Çumra 2001, Hasat, Misket, Orza 96, Sabribey, Sinanbey, Yaprak, and Yesevi 93 exhibited intermediate reaction responses and cultivars Anka-06, Asil, Avcı 2002, Aydanhanım, Ayrancı, Başgül, Burakbey, Bülbül 89, Cacabey, Cirit, Çetin 2000, Hazar, İnce 04, Keykubat, Larende, Özdemir 05, Sayım 40, Tarm 92, Tosunpaşa, Yalın, Yüksel, and Zeynelağa showed high reaction responses.

Barley line IKABVD Ç-23 (IR 7.33) and wild barley genotype *H. spontaneum* 24 (IR 6.67) and barley cultivar Ayrancı (IR 7.33) showed the most susceptible reactions against *C. sativus*. The most resistant reaction against the disease was exhibited by the *H. spontaneum* 30 (IR 2) genotype (Tables 1, 2, and 3).

Out of 21 genotypes of wild barley (*H. spontaneum*), 9.52%, 38.1% and 52.38% showed low, intermediate, and high infection responses, respectively. Among the barley cultivars, 5.56%, 33.33%, and 61.11% showed low, medium, and high infection responses, respectively. 11.43% of barley lines showed low infection response, 48.57% were placed in the intermediate group and 40% exhibited high infection values. Of the 36 barley cultivars, 35 barley lines and 21 wild barley (*H. spontaneum*) genotypes, 8.70%, 40.22%, and 51.09% were placed in the low (resistant), intermediate, and high (susceptible) infection classes, respectively.

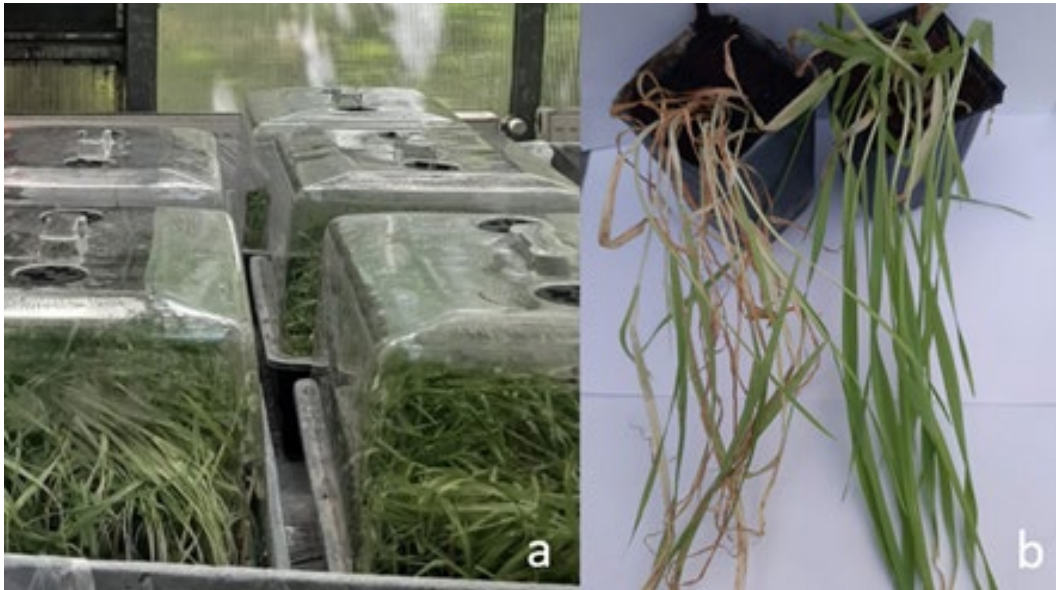


Figure 1. a) Barley genotypes after inoculation with a virulent strain of *Cochliobolus sativus* under greenhouse conditions b) Ayrancı (left) and Pınar (right) barley cultivars 7 days after inoculation

Table 1. Seedling stage reactions of 35 barley genotypes against *Cochliobolus sativus* leaf spot disease.

Barley Lines	Replications	Mean	Infection Classes
Std. Çeş.-50	3	3.33	A
	3		
	4		
Std. Çeş.-63	6	6	C
	6		
	6		
Std. Çeş.-64	3	3	A
	3		
	3		
Std. Çeş.-65	3	3.67	B
	4		
	4		
Std. Çeş.-67	6	5.67	C
	6		
	5		
Std. Çeş.-125	6	6	C
	6		
	6		
Std. Çeş.-126	5	5.33	B
	6		
	5		
Std. Çeş.-127	5	4.67	B
	5		
	4		
Std. Çeş.-128	5	5	B
	5		
	5		
Std. Çeş.-133	7	6.67	C
	6		
	7		
Std. Çeş.-145	5	4.67	B
	5		
	4		
Std. Çeş.-146	5	5	B
	5		
	5		
Std. Çeş.-147	5	5	B
	5		
	5		
Std. Çeş.-148	4	3.33	A
	3		
	3		

(1-9 scale, Fetch and Steffenson, 1999; scale values; a: 1-3 low, b: 4-5 intermediate, c: 6-9 high)

Table 1 (Continued). Seedling stage reactions of 35 barley genotypes against *Cochliobolus sativus* leaf spot disease (continued).

Barley Lines	Replications	Mean	Infection Classes
Std. Çeş.-149	5	5	B
	5		
	5		
Std. Çeş.-150	3	3.33	A
	3		
	4		
Std. Çeş.-151	5	5.33	B
	5		
	6		
Std. Çeş.-152	6	6	C
	6		
	6		
İKABVD Ç-2	7	6.33	C
	6		
	6		
İKABVD Ç-3	5	4.33	B
	4		
	4		
İKABVD Ç-4	4	4	B
	4		
	4		
İKABVD Ç-6	5	5.33	B
	6		
	5		
İKABVD Ç-7	7	6.67	C
	7		
	6		
İKABVD Ç-8	7	6.67	C
	7		
	6		
İKABVD Ç-9	6	5.67	C
	5		
	6		
İKABVD Ç-11	4	4.67	B
	5		
	5		
İKABVD Ç-12	7	6.67	C
	6		
	7		
İKABVD Ç-13	7	6.33	C
	6		
	6		

(1-9 scale, Fetch and Steffenson, 1999; scale values; a: 1-3 low, b: 4-5 intermediate, c: 6-9 high)

Table 1 (Continued). Seedling stage reactions of 35 barley genotypes against *Cochliobolus sativus* leaf spot disease (continued)

Barley Lines	Replications	Mean	Infection Classes
İKABVD Ç-14	5	5	B
	5		
	5		
İKABVD Ç-17	6	5.67	C
	6		
	5		
İKABVD Ç-18	7	6.33	C
	6		
	6		
İKABVD Ç-19	5	4.67	B
	5		
	4		
İKABVD Ç-21	5	5.33	B
	6		
	5		
İKABVD Ç-22	5	4.33	B
	4		
	4		
İKABVD Ç-23	8	7.33	C
	7		
	7		
General Mean	5.34	5.21	B
	5.2		
	5.09		

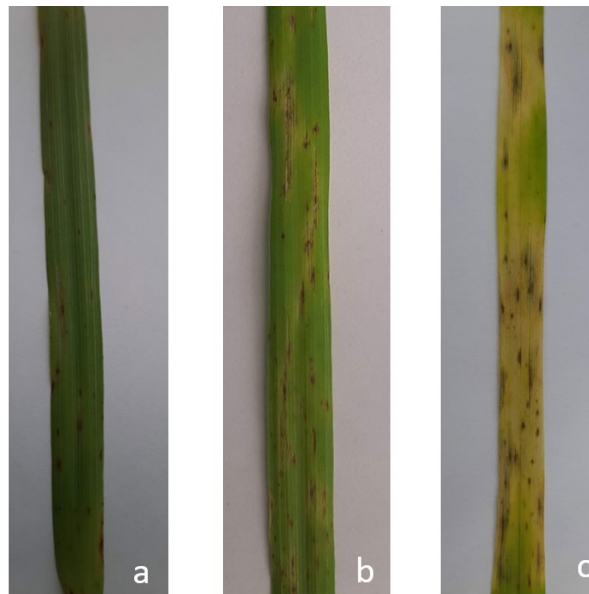
**Figure 2.** Infection classes showing a) low infection response b) intermediate infection response c) high infection response

Table 2. Seedling stage reactions of 36 barley cultivars against *Cochliobolus sativus* leaf spot disease

Barley Cultivars	Replications	Mean	Infection Classes
Akar	5	5	B
	5		
	5		
Anka-06	7	7	C
	7		
	7		
Asil	7	7	C
	7		
	7		
Avcı 2002	7	6.67	C
	6		
	7		
Aydanhanım	6	6.33	C
	6		
	7		
Ayrancı	7	7.33	C
	7		
	8		
Başgöl	7	6.67	C
	6		
	7		
Bolayır	5	5	B
	5		
	5		
Bozlak	6	5.33	B
	6		
	4		
Burakbey	5	5.67	C
	6		
	6		
Burgaz	5	5.33	B
	5		
	6		
Bülbül-89	7	6.67	C
	7		
	6		
Cacabey	7	6.67	C
	7		
	6		
Cirit	6	5.67	C
	6		
	5		

(1-9 scale, Fetch and Steffenson, 1999; scale values; a: 1-3 low, b: 4-5 intermediate, c: 6-9 high)

Table 2 (Continued). Seedling stage reactions of 36 barley cultivars against *Cochliobolus sativus* leaf spot disease (continued)

Barley Cultivars	Replications	Mean	Infection Classes
Çetin 2000	7	6.33	C
	6		
	6		
Çumra 2001	4	4.67	B
	5		
	5		
Harman	4	3.33	A
	3		
	3		
Hasat	4	4.67	B
	5		
	5		
Hazar	6	5.67	C
	5		
	6		
İnce 04	6	6	C
	6		
	6		
Keykubat	6	6	C
	6		
	6		
Larende	6	5.67	C
	5		
	6		
Misket	5	5	B
	5		
	5		
Orza-96	5	4.33	B
	4		
	4		
Özdemir 05	6	5.67	C
	5		
	6		
Pınar	3	2.67	A
	2		
	3		
Sabribey	4	4.67	B
	5		
	5		
Sayım 40	6	6	C
	6		
	6		

(1-9 scale, Fetch and Steffenson, 1999; scale values; a: 1-3 low, b: 4-5 intermediate, c: 6-9 high)

Table 2 (Continued). Seedling stage reactions of 36 barley cultivars against *Cochliobolus sativus* leaf spot disease (continued)

Barley Cultivars	Replications	Mean	Infection Classes
Sinanbey	5	5	B
	5		
	5		
Tarm 92	7	7	C
	7		
	7		
Tosunpaşa	6	6	C
	6		
	6		
Yalın	7	6.33	C
	6		
	6		
Yaprak	5	4.67	B
	5		
	4		
Yesevi 93	5	5.33	B
	5		
	6		
Yüksel	7	6.33	C
	6		
	6		
Zeynelağa	6	5.67	C
	6		
	5		
General Mean	5.75	5.65	C
	5.56		
	5.64		

(1-9 scale, Fetch and Steffenson, 1999; scale values; a: 1-3 low, b: 4-5 intermediate, c: 6-9 high)

Table 3. Seedling stage reactions of 21 wild barley (*Hordeum spontaneum*) genotypes against *Cochliobolus sativus* leaf spot disease

<i>Hordeum spontaneum</i> genotypes	Replications	Mean	Infection Classes
TRNC 1	4	4.67	B
	5		
	5		
TRNC 2	7	7	C
	7		
	7		
TRNC 3	7	7	C
	7		
	7		
TRNC 4	5	5	B
	5		
	5		

(1-9 scale, Fetch and Steffenson, 1999; scale values; a: 1-3 low, b: 4-5 intermediate, c: 6-9 high)

Table 3 (Continued). Seedling stage reactions of 21 wild barley (*Hordeum spontaneum*) genotypes against *Cochliobolus sativus* leaf spot disease (continued)

<i>Hordeum spontaneum</i> genotypes	Replications	Mean	Infection Classes
TRNC 5	5	5	B
	5		
	5		
1	6	6.67	C
	7		
	7		
2	6	5.67	C
	6		
	5		
3	4	4.67	B
	5		
	5		
9	5	5	B
	5		
	5		
21	6	6	C
	6		
	6		
22	6	5.33	B
	5		
	5		
23	3	3.33	A
	3		
	4		
24	7	6.67	C
	7		
	6		
26	3	3.67	B
	4		
	4		
27	7	6.33	C
	6		
	6		
28	7	6.33	C
	6		
	6		
29	7	6.67	C
	7		
	6		
30	2	2	A
	2		
	2		

(1-9 scale, Fetch and Steffenson, 1999; scale values; a: 1-3 low, b: 4-5 intermediate, c: 6-9 high)

Table 3 (Continued). Seedling stage reactions of 21 wild barley (*Hordeum spontaneum*) genotypes against *Cochliobolus sativus* leaf spot disease (continued)

<i>Hordeum spontaneum</i> genotypes	Replications	Mean	Infection Classes
31	6	5.67	C
	6		
	5		
32	5	5	B
	5		
	5		
33	6	6.33	C
	6		
	7		
General Mean	5.43	5.43	B
	5.48		
	5.38		

(1-9 scale, Fetch and Steffenson, 1999; scale values; a: 1-3 low, b: 4-5 intermediate, c: 6-9 high)

4. Discussion

In different studies, the resistance status of barley genotypes and the virulence status of the isolates used were investigated. Aktaş and Tunalı (1994) investigated the leaf spot resistance status of barley genotypes against the S96 strain of *C. sativus*. The barley cultivars and lines used in this study showed very susceptible, susceptible, moderately susceptible, and moderately resistant reactions.

Jana and Bailey (1995) evaluated the responses of wild and cultivated barleys obtained from Türkiye and Jordan against three leaf pathogens, including *C. sativus*. They found that 4.5% of wild barleys and 0.3% of cultured barleys were resistant to *C. sativus*. Fetch et al. (2003) determined the reactions of a total of 116 *H. spontaneum* genotypes obtained from Israel and Jordan against 6 fungal pathogens, including leaf spot disease caused by *C. sativus*. As a result of their study, they found the resistance frequency against *Cochliobolus* leaf spot as 53% and 46% from Israel and Jordan genotypes. In our study, 5.56% of 36 barley cultivars, 11.43% of 35 barley lines, and 9.52% of 21 wild barley genotypes were found to be resistant (showing low infection response). Arabi and Jawhar (2004) investigated the infection responses of 10 barley genotypes against 12 *C. sativus* isolates obtained from different regions of Syria and determined that the reactions of the genotypes ranged from susceptible to moderately resistant. In this study, no genotype was immune to the disease Bonman et al. (2005) evaluated the resistance of barley genotypes obtained from the National Small Grains Collection (USA) against *Cochliobolus* leaf spot disease and found 3 of 48 genotypes to be resistant. Ghazvini and Tekauz (2007) evaluated 160 barley cultivars from Iran in order to determine their responses to head blight, leaf spot, and net blotch diseases. As a result of the study, no resistant barley cultivars were found against leaf spot and head blight. In our study, we found resistant cultivars, lines, and wild barley genotypes using a virulent strain of *C. sativus*.

Çelik Oğuz et al. (2016) determined the seedling reactions of 25 barley lines against 5 single spore isolates of *C. sativus*. Statistically significant differences ($P < 0.01$) were observed among the isolates, and no barley line showed a low infection response. Two barley genotypes exhibited a moderate infection response to all 5 isolates. Six genotypes used in this current study showed low infection response against *C. sativus* isolate. Singh et al. (2017), under natural conditions, determined the responses of 342 barley genotypes to *Cochliobolus* leaf spot disease in their study and found 97 genotypes to be moderately resistant and one

genotype to be resistant. In our study, 8 of 92 barley cultivars, lines, and barley genotypes were resistant and 37 of them gave intermediate reactions.

Celik-Oguz and Karakaya (2017), under greenhouse conditions, determined the seedling stage responses of 39 barley cultivars widely grown in Türkiye against three isolates of *C. sativus*. As a result of the research, differences were observed in the responses of different barley cultivars to pathogen isolates, and Cs1 was the most virulent isolate. Avcı 2002 cultivar showed moderate infection response to Cs3 isolate and high infection response to Cs1 and Cs2 isolates. Akar, Aydanhanım, Bolayır, Burakbey, Bülbül 89, Çetin 2000, İnce 04, Orza 96, Özdemir 05, Tarm 92, Yesevi 93, and Zeynelağa cultivars showed high infection response to all three isolates. In this current study, cultivars Akar, Bolayır, Orza 96, and Yesevi 93 showed moderate infection response against *C. sativus* isolate while Avcı 2002, Aydanhanım, Burakbey, Bülbül 89 Çetin 2000, İnce 04, Özdemir 05, Tarm 92 and Zeynelağa cultivars showed high infection response.

Balcı et al. (2018) evaluated the seedling stage infection responses of one hulless barley cultivar candidate, 2 hulless barley cultivars, and 19 hulless barley genotypes against two isolates of *C. sativus* under greenhouse conditions. Differences in virulence were detected between the isolates. Hulless barley cultivars Yalın and Özen showed moderate infection response to both isolates. A high infection response of cultivar Yalın was observed against *C. sativus* isolate used in this current study.

Çelik Oğuz et al. (2019) determined the seedling stage reactions of 28 six-row barley landraces, as well as Avcı 2002 and Bülbül 89 cultivars, against two *C. sativus* isolates. Avcı 2002 cultivar showed moderate infection response against Kastamonu isolate and low infection response against Hatay isolate; Bülbül 89 cultivar exhibited high and moderate infection responses against Kastamonu and Hatay isolates, respectively. In this current study, Avcı 2002 and Bülbül 89 cultivars showed a high infection response against the *C. sativus* isolate used.

5. Conclusions

Barley, which is one of the main field crops in Türkiye and the World, has an important place in terms of cultivation area and production amount. Breeding studies are important in order to obtain new cultivars that can tolerate diseases and pests well and have high adaptability.

Cochliobolus leaf spot disease in barley is an important disease that reduces yield and quality. In this study, barley lines and varieties and wild barley (*Hordeum spontaneum*) genotypes resistant to *Cochliobolus* leaf spot disease caused by *C. sativus* were determined. These resistant barley lines and varieties and wild barley genotypes are among the gene sources that can be used in breeding work. Further studies should be conducted on the resistance of barley against diseases and breeding studies should be carried out in order to develop disease-resistant varieties.

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References

- Afanasenkov OS, Koziakov AV, Hedlay PE, Lashina NM, Anisimova AV, Manninen O, Jalli M, Potokina EK (2015). Mapping of loci controlling the resistance to *Pyrenophora teres* f. *teres* and *Cochliobolus sativus* in two double haploid barley populations. *Russian Journal of Genetics: Applied Research*, 5: 242-253.
- Aktaş H (1982). Orta Anadolu Bölgesi arpa ve buğday ekim alanlarında görülen kök çürüklüğü hastalık etmeni *Drechslera sorokiniana* (Sacc.) Subram. and Jain'nun yayılışı. In: *III. Türkiye Fitopatoloji Kongresi Bildirileri*, Adana, Türkiye, pp. 10-23.
- Aktaş H, Tunalı B (1994). Türkiye'de ekimi yapılan ve ümitvar olan bazı buğday ile arpa çeşit ve hatlarının önemli hastalıklarına karşı reaksiyonlarının saptanması üzerinde araştırmalar. *Bitki Koruma Bülteni*, 34: 123-133.
- Anonymous A (2020). Toprak Mahsulleri Ofisi Genel Müdürlüğü, 2019 Yılı Hububat Sektör Raporu. Ankara.
- Anonymous B (2020). Ulusal Hububat Konseyi, 2019-2020 Üretim Yılı (1 Ekim 2019-30 Nisan 2020) Buğday-Arpa-Çavdar-Yulaf Üretim Tahmini Raporu. Ankara.
- Anonymous (2021). Türkiye İstatistik Kurumu, Bitkisel Üretim 1. Tahmini, 2021, Website: [https://data.tuik.gov.tr \(/Bulten/Index?p=Bitkisel-Uretim-1.Tahmini-20237247&dil=1\)](https://data.tuik.gov.tr (/Bulten/Index?p=Bitkisel-Uretim-1.Tahmini-20237247&dil=1) (Access date: 21.03.2022).) (Access date: 21.03.2022).
- Arabi MIE, Jawhar M(2004). Identification of *Cochliobolus sativus* (spot blotch) isolates expressing differential virulence on barley genotypes in Syria. *Journal of Phytopathology*, 152: 461-464.
- Balcı S, Karakaya A, Çelik Oğuz A, Ergün N, Sayim İ, Aydoğan S (2018). Bazı kavuzsuz arpa çeşit ve hatlarının *Cochliobolus* yaprak lekesi hastalığına karşı fide dönemi tepkilerinin değerlendirilmesi. *Bitki Koruma Bülteni*, 58: 221-226.
- Bonman MJ, Bockelman HE, Jackson LF, Steffenson B, (2005). Disease and insect resistance in cultivated barley accessions from the USDA National Small Grains Collection. *Crop Science*, 45: 1271-1280.
- Celik-Oguz A, Karakaya A (2017). Seedling response of commonly grown barley cultivars in Turkey to spot blotch disease. *Fresenius Environmental Bulletin*, 26: 6734-6738.
- Chang N, Jia X, Gao Z, Wu W, Liu W, Wu Y (1998). Evaluating spot blotch resistance traits in wheat and related species. In In Duveiller, E., Dubin, H.J., Reeves, J. and McNab A., (Eds), *Helminthosporium Blights of Wheat: Spot Blotch and Tan Spot*. CIMMYT, Mexico, D.F., Mexico, pp. 246-252.
- Clear RM, Patrick SK, Nowicki T, Gaba D, Edney M, Babb JC (1997). The effect of hull removal and pearling on *Fusarium* species and trichothecenes in hullless barley. *Canadian Journal of Plant Science*, 77: 161-166.
- Çelik Oğuz A, Karakaya A, Mert Z, Ergün N, Sayim I, Aydoğan S (2016). Determination of the seedling reactions of advanced barley lines to spot blotch disease caused by *Cochliobolus sativus*. *Works of the Faculty of Agriculture and Food Sciences, University of Sarajevo*, LXI (66/1): 244-246.
- Çelik E, Karakaya A (2017). Yabani arpa (*Hordeum spontaneum*) ve hastalıklara dayanıklılık. *Mustafa Kemal Üniversitesi Ziraat Fakültesi Dergisi*, 22: 65-86.
- Çelik Oğuz A, Akdoğan G, Karakaya A (2019). Determination of the seedling reactions of six-rowed barley landraces to spot blotch disease incited by *Cochliobolus sativus*. *Harran Tarım ve Gıda Bilimleri Dergisi*, 23: 444- 450.

- Duan R, Xiong H, Wang A, Chen G (2015). Molecular mechanisms underlying hull-caryopsis adhesion/separation revealed by comparative transcriptomic analysis of covered/naked barley (*Hordeum vulgare* L.). *Int. J. Molecular Sciences*, 16: 14181-14193.
- Eğilmez S (2021). Tarımsal Ekonomi ve Politika Geliştirme Estitüsü Ürün Raporu Arpa. Ankara. p. 17.
- Eteve G (1985). Breeding for tolerance and winter hardiness in pea. In Hebblethwaite PD, Heath MC, Dawkins TCK (Eds), *The pea Crop: A Basis for Improvement*. Butterworths, London. UK, pp. 131-136.
- Fetch TG, Jr., Steffenson BJ (1999). Rating scales for assessing infection responses of barley infected with *Cochliobolus sativus*. *Plant Disease*, 83: 213-217.
- Fetch TG, Jr., Steffenson BJ, Nevo E (2003). Diversity and sources of multiple disease resistance in *Hordeum spontaneum*. *Plant Disease*, 87: 1439-1448.
- Geçit HH (2016). Tarla Bitkileri. Ankara Üniversitesi Ziraat Fakültesi Yayınları. Yayın no: 1640, Ders Kitabı: 591. 822 pp.
- Gerlegiz TE, Karakaya A, Çelik Oğuz A, Mert Z, Sayim İ, Ergün N, Aydoğan S (2015). Assessment of the seedling reactions of some hullless barley genotypes to *Drechslera teres* f. *maculata*. *Selcuk Journal of Agriculture and Food Sciences*, 28: 63-68.
- Ghazvini H, Tekauz A (2007). Reactions of Iranian barley accessions to three predominant pathogens in Manitoba. *Canadian Journal of Plant Pathology*, 29: 69-78.
- Haas M, Menke J, Chao S, Steffenson BJ (2016). Mapping quantitative trait loci conferring resistance to a widely virulent isolate of *Cochliobolus sativus* in wild barley accession PI 466423. *Theoretical and Applied Genetics*, 129: 1831-1842.
- Hetzler J, Eyal J, Fehrmann H, Mehta YR, Kushnir U, Zekaria-Oren J, Cohen L (1991). Interaction between *Cochliobolus sativus* and wheat cultivars. In Saunders, D.A., (Ed), *Wheat for the Non-Traditional Warmer Areas*. CIMMYT, Mexico, D.F., Mexico, pp. 266-283.
- Jana S, Bailey KL (1995). Responses of wild and cultivated barley from West Asia to net blotch and spot blotch. *Crop Science*, 35: 242-246.
- Kumar J, Hückelhoven R, Beckhove U, Nagarajan S, Kogel K-H (2001). A compromised *Mlo* pathway affects the response of barley to the necrotrophic fungus *Bipolaris sorokiniana* (teleomorph: *Cochliobolus sativus*). *Phytopathology*, 91: 127-133.
- Kumar J, Schäfer P, Hückelhoven R, Langen G, Baltruschat H, Stein E, Nagarajan S, Kogel KH (2002). *Bipolaris sorokiniana*, a cereal pathogen of global concern: cytological and molecular approaches towards better control. *Molecular Plant Pathology*, 3: 185-195.
- Legzdina L, Buerstmayr H (2004). Comparison of infection with *Fusarium* head blight and accumulation of mycotoxins in grain of hullless and covered barley. *Journal of Cereal Science*, 40: 61-67.
- Singh D, Pande SK, Singh SP, (2017). Evaluation of the barley genotypes against spot blotch disease caused by *Bipolaris sorokiniana*. *Plant Archives*, 17: 167-170.
- Mathre DE (1997). Compendium of barley diseases. American Phytopathological Society. APS Press. Minnesota, USA. p. 120.
- Mujeeb-Kazi A (1998). Novel genetic diversity for stress tolerance in the triticale: strategic avenues and applied potentials. In Duveiller, E., Dubin, H.J., Reeves, J. and McNab A., (Eds), *Helminthosporium Blights of Wheat: Spot Blotch and Tan Spot*. CIMMYT, Mexico, D.F., Mexico,, pp. 223-229.

- Novazaki F, Afanasenko O, Lashina N, Platz GJ, Snowdon, Loskutov I (2020). Genome-wide association studies in a barley (*Hordeum vulgare*) diversity set reveal a limited number of loci for resistance to spot blotch (*Bipolaris sorokiniana*). *Plant Breeding*, 139: 521-535.
- Singh D, Pande SK, Singh SP (2017). Evaluation of the barley genotypes against spot blotch disease caused by *Bipolaris sorokiniana*. *Plant Archives*, 17: 167-170.
- Ullrich SE (2011). Significance, adaptation, production, and trade of barley. In: Ullrich, S.E. (Ed.), Blackwell Publishing Ltd., *Barley*. Chichester, UK, pp. 3-13
- USDA (2022). United States Department of Agriculture, Foreign Agricultural Service. Website: <https://apps.fas.usda.gov/psdonline/app/index.html#/app/advQuery> (Access date: 21.03.2022).
- Van Ginkel M, Rajaram S (1998). Breeding for resistance to spot blotch in wheat: global perspective. In Duveiller, E., Dubin, H.J., Reeves, J. and McNab A., (Eds), *Helminthosporium Blights of Wheat: Spot Blotch and Tan Spot*. CIMMYT, Mexico, D.F., Mexico, pp. 162–170.
- Visioni A, Rehman S, Viash SS, Singh SP, Vishwakarma R, Gyawali S, Al-Abdallat AM, Verma RPS (2020). Genome wide association mapping of spot blotch resistance at seedling and adult plant stages in barley. *Frontiers in Plant Science*, 11: 642
- Yıldırım AF, Araz A, Turgay EB, Ünal F, Büyük O (2016). Serin İklim Tahıllarında Kök ve Kökboğazı Hastalıklarının Dünü, Bugünü ve Mücadelesi, T. C. Gıda, Tarım ve Hayvancılık Bakanlığı, Tarımsal Araştırmalar ve Politikalar Genel Müdürlüğü, Ankara Zirai Mücadele Merkez Araştırma Enstitüsü, Ankara. 104 pp.
- Yun SJ, Gyenis L, Hayes PM, Matus I, Smith KP, Steffenson BJ, Muehlbauer GJ (2005). Quantitative trait loci for multiple disease resistance in wild barley. *Crop Science*, 45: 2563–2572.
- Zadoks JC, Chang TT, Konzak CF (1974). A decimal code for the growth stages of cereals. *Weed Research* 14: 415-421.
- Zhou H, Steffenson B (2013). Genome-wide association mapping reveals genetic architecture of durable spot blotch resistance in US barley germplasm. *Molecular Breeding*, 32: 139-154.
- Zohary D, Hopf M (2000). *Domestication of plants in the Old World*. 3rd edn. Oxford: Oxford University Press. p. 666.