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Research Paper

Resistance of wild barley (*Hordeum spontaneum*) and barley landraces to leaf stripe (*Drechslera graminea*)

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Summary. Wild barley (*Hordeum spontaneum*) and barley landraces are important sources of genetic variation for disease resistance. Thirty wild barley (*H. spontaneum*) genotypes and 30 barley landraces were evaluated for susceptibility to two *Drechslera graminea* isolates. Virulence differences were observed between the isolates, while the responses of the host genotypes to the isolates also varied. Of the *H. spontaneum* genotypes, 23% and 63%, respectively, were resistant to the Yozgat *D. graminea* isolate, and Eskişehir *D. graminea* isolates. On the other hand, 43% and 90% of the barley landraces were resistant to Yozgat and Eskişehir *D. graminea* isolates, respectively. *Hordeum spontaneum* genotypes 13, 24, 27, 29, 54, 86, and 91 exhibited resistance to both *D. graminea* isolates, while genotypes 14 and 32 showed intermediate reactions to the Yozgat isolate and resistant reactions to the Eskişehir isolate. Barley landraces 21, 37, 38, 39, 40, 73, 98, 128, 139, 153, 159,167, and 171 showed resistant reactions, and barley landrace 8 showed an intermediate reaction to both isolates. Barley landraces 3, 20, 24, 71, 101, 103, 104 and 160 exhibited intermediate responses to the Yozgat isolate and a resistant response to the Eskişehir isolate. Using resistant barley genotypes would reduce the need for pesticides for control of leaf stripe, and be an environmentally preferred strategy for disease control. The disease resistance present in wild barley and barley landraces are important for expanding the genetic basis of cultivated barley (*H. vulgare*). The resistant and intermediate genotypes identified in this study could be used as resistance sources in barley breeding, or landraces could be used directly for commercial barley production.

Keywords. Disease resistance, *Pyrenophora graminea, Hordeum vulgare.*

INTRODUCTION

Barley (*Hordeum vulgare* L.) is the second most cultivated cereal crop, after wheat, in Turkey, constituting 22% of the cereal production area. In this country, 7.1 million tons of barley are produced per year, with an average yield of 293 kg ha^{-1} (Tuik, 2017). It is believed that approx. 10,000 years ago, the first area where barley was cultivated was in the Fertile Crescent Region, located between the Mediterranean and Arab peninsulas, and bordered by

the Tigris and Euphrates valleys (Harlan and Zohary, 1966; Nesbitt, 1995; Willcox, 1995; Ladizinski, 1998). Throughout history, this region has been considered as one of the richest centres of plant diversity (Zohary and Hopf, 2000). Turkey is uniquely situated in terms of plant genetic diversity, as it has an abundance of plant species and endemism due to a combination of geomorphologic, topographic, and seasonal diversity (Fao, 2015). Turkey is located at the intersection point between Mediterranean and Near East gene centres, and this area is one of the most significant genetic centres for barley (Kün, 1996).

Barley landraces (*H. vulgare* L. subsp. *vulgare*) are heterogeneous plant species grown by farmers and are populations exposed to natural and artificial selection (Brown, 2000), and barley landraces are genetically closer to modern varieties compared to wild barley (Thomas *et al*., 1998). Local barley varieties are the main sources of seed used in regions of low annual rainfall and where 'traditional' agriculture is practiced (Ceccarelli and Grando, 2000). Wild barley (*H. spontaneum* C. Koch) is accepted as the progenitor of cultivated barley (*H. vulgare*), and its habitat is in the Fertile Crescent Region. This plant is indigenous to the area between the south and southeast of Turkey and the area between North Africa and southwest Asia (Harlan and Zohary, 1966; Nevo, 1992; Von Bothmer *et al*., 1995). *Hordeum spontaneum* is often found in secondary habitats such as Mediterranean scrub lands or roadsides (Zohary and Hopf, 2000).

Wild barley genotypes and barley landraces are important resources for genetic variation, as they are highly adapted to abiotic and biotic stresses and can therefore be cultivated under unfavorable conditions (Allard and Bradshaw, 1964; Yitbarek *et al*., 1998; Ellis *et al*., 2000; Ceccarelli and Grando, 2000; Karakaya *et al*., 2016a). This genetic variation provides a potential source of disease resistance alleles for breeding programmes (Allard and Bradshaw, 1964; Ceccarelli, 1996). Turkey is one of the most important genetic centres for barley, as landraces are widely planted and wild barley genotypes grow under natural conditions (Helbaek, 1969; Kün, 1996; Pourkheirandish and Komatsuda, 2007; Karakaya *et al*., 2016a; Ergün *et al*., 2017).

The causal agent of barley leaf stripe is the fungus *Drechslera graminea* (Rabenh. ex Schlecht.) Shoemaker (=*Helminthosporium gramineum* Rabh.) (teleomorph: *Pyrenophora graminea* (S. Ito & Kurib.). This fungus is a single-cycle, seed borne pathogen that causes reductions in barley yields and quality throughout world cereal production areas. The pathogen survives as mycelium within host pericarps and grows into developing seedlings via the coleorhizae when the barley seeds germinate (Platenkamp, 1976). Subsequently, the pathogen grows systemically in developing host plants (Çetinsoy, 1995; Mathre, 1997; Aktaş 2001). The first symptoms of disease occur as yellow stripes on seedling leaves, and these progress to chlorotic and necrotic stripes areas along the leaves. As results of the disease, sterile spikes and stunting also occur in affected plants (Tekauz and Chiko, 1980; Zad *et al*., 2002). Severe infections result in drying out and premature death of plants (Mathre, 1997). Yield losses due to leaf stripe have been reported from various countries (Porta-Puglia *et al*., 1986; Arabi *et al*., 2004). The disease is present in Turkish barley fields, causing yield losses between 3% and 15% (Mamluk *et al*., 1997). In 2012 and 2013, it was found that 40% of the surveyed barley fields in Central Anatolia were affected by leaf stripe (Karakaya *et al*., 2016b). Kavak (2004) emphasized that in addition to yield losses, quarantine issues can be important, because the pathogen is readily seed transmitted. While barley leaf stripe can be controlled through the use of seed treatment fungicides, growing of resistant varieties would minimize the need for pesticides and be an economic and environmentally friendly method for controlling the disease.

Research has shown a diversity of morphological characters and virulence levels for populations of *D. graminea* (Gatti *et al*., 1992; Jawhar and Arabi, 2006; Karakaya *et al*., 2017). McDonald and Linde (2002) emphasized that pathogen populations that vary genetically can quickly evolve and overcome plant resistance. Significant virulence diversity and the possible results of a shrinking genetic basis of cultivated barley have been studied by plant pathologists and plant breeders (Jensen, 1988; Ulus and Karakaya, 2007; Çelik *et al*., 2016). Plant breeders need sustainable sources of disease resistance for effective long-term disease control.

In this study, 30 barley landraces and 30 wild barley (*H. spontaneum*) genotypes were selected from a collection maintained by the Gene Bank of the Central Research Institute for Field Crops located in Ankara, Turkey. These host germplasm lines were assessed for their resistance to leaf stripe using two isolates of *D. graminea*.

MATERIALS AND METHODS

*Barley landraces, wild barley (*H. spontaneum*) genotypes and* Drechslera graminea *isolates*

Thirty *H. spontaneum* genotypes and 30 barley landraces were obtained from the Gene Bank of the Field Crops Central Research Institute, in Ankara, Turkey.

These plant lines had been collected from different regions of Turkey, and seeds of these genotypes had been multiplied from single spikes and maintained in the Gene Bank.

The virulent Yozgat isolate of *D. graminea* and the moderately virulent Eskişehir isolate were compared. The virulence of these isolates was previously determined by Çelik *et al*. (2016) and Karakaya *et al*. (2017). The isolates were maintained at the Mycology Laboratory of Ankara University, Faculty of Agriculture, Department of Plant Protection, Turkey. Barley cultivars 'Çumra 2001' and 'Larende' were used, respectively, as resistant and susceptible controls (Çelik *et al*., 2016). The disease responses of these 30 landraces and 30 wild barley genotypes used in the present study against *Pyrenophora teres* f. *teres*, *P. teres* f. *maculata* and *Rhynchosporium commune* had been determined in previous studies (Çelik Oğuz *et al*., 2017b; Çelik Oğuz *et al*., 2019; Azamparsa *et al*., 2019).

Treatments and disease evaluations

The sandwich method described by Mohammad and Mahmood (1974) was used to inoculate the barley landraces and wild barley genotypes. Seeds were surface sterilized with a 1% NaOCI solution for 3 min and then rinsed with sterile water. Cultures of *D. graminea* were grown on potato dextrose agar medium in Petri dishes at 22 ± 2°C for 10 d. Fifteen seeds of each host landrace or wild genotype were placed on the surface of half of a *D. graminea* culture followed by folding the other half of the culture over the seeds under sterile conditions. Cultures folded as 'sandwiches' were kept at 22°C for 4 d. After germination, seeds were incubated at 4°C for an additional 5 d. Three replications were used for each host line and isolate combination. Following treatment, the incubated seeds were taken from the sandwich cultures using sterile forceps and planted in pots containing growth medium (soil, sand, and animal manure at 3:1:1 w:w:w). The resulting plants were grown under greenhouse conditions of 15 ± 2°C at night, 22 ± 2°C during the day, using a 15/9 h light/dark regime. Pots were arranged on a greenhouse bench in a completely randomized fashion. Disease ratings were taken at 45 and 60 d after planting of inoculated seeds and were recorded separately. The responses of the plants to the two *D. graminea* isolates were evaluated using the scale developed by Tekauz (1983). Scale values were: 1 = infection < 5% (Resistant, R); 2 = infection 5–17% (Intermediate, I); and 3 = infection > 17% (Susceptible, S).

Data analyses

The percentage of leaf barley stripe was calculated using the following equation (Dumalasova *et al*., 2014).

% Disease incidence = No. of infected plants ÷ Total no. of plants ×100.

Separate analyses of variances were performed for disease assessed at 45 and 60 d after planting for isolate, genotype and isolate*genotype interaction effects (Tables 1-4).

Biplot analysis was performed for the isolates and disease percentage values to assess the disease responses of each genotype tested to the two *D. graminea* isolates used (MSTAT, Michigan State University).

RESULTS

At 45 d after planting of inoculated seeds, there were 20 wild barley (*H. spontaneum*) genotypes showing susceptible reactions to the virulent Yozgat isolate of *D. graminea*, three genotypes with intermediate reactions and seven genotypes with resistant reactions to this isolate. At 60 days after planting, 21 genotypes were susceptible, two were intermediate and seven were resistant to the Yozgat isolate. Five genotypes were susceptible to

Table 1. Analysis of variance for the resistance of 30 *Hordeum spontaneum* genotypes 45 d after planting following seed inoculation with two isolates of *Drechslera graminea.*

Source	DF	SS	MS	F	P
H. spontaneum genotypes	29	66151.3	2281.1	1105.86	<0.001
Isolates	1	46217.7	46217.7	22406.17	<0.001
*H. spontaneum**isolates	29	33414.9	1152.2	558.60	<0.001
Error	120	247.5	2.1		
Total	179	146031.4			

Table 2. Analysis of variance for the resistance of 30 *Hordeum spontaneum* genotypes 60 d after planting following seed inoculation with two isolates of *Drechslera graminea.*

Source	DF	SS	MS	F	P
H. spontaneum genotypes	29	72401.8	2496.6	1842.90	<0.001
Isolates	1	52473.2	52473.2	38733.54	<0.001
*H. spontaneum**Isolates	29	36521.1	1259.3	929.60	<0.001
Error	120	162.6	1.4		
Total	179	161558.6			

Table 3. Analysis of variance for the resistance of 30 barley landraces 45 d after planting following seed inoculation with two isolates of *Drechslera graminea*.

Source	DF	SS	MS	F	P
Barley landraces	29	13938.64	480.64	706.65	<0.001
Isolates	1	5261.77	5261.77	7736.00	<0.001
Barley landraces*Isolates	29	7961.87	274.55	403.65	<0.001
Error	120	81.62	0.68		
Total	179	27243.90			

Table 4. Analysis of variance for the resistance of 30 barley landraces 60 d after planting following seed inoculation with two isolates of *Drechslera graminea*.

Source	DF	SS	MS	F	P
Barley landraces	29	13551.12	467.28	687.01	<0.001
Isolates	1	6646.66	6646.66	9772.10	<0.001
Barley landraces*Isolates	29	7878.26	271.66	399.41	<0.001
Error	120	81.62	0.68		
Total	179	28157.66			

the moderately virulent Eskişehir isolate, six genotypes had intermediate reactions, and 19 were resistant to this isolate. The numbers of genotypes showing susceptible, intermediate, and resistant reactions to the Eskişehir isolate remained unchanged at 60 d after planting (Table 5).

At 45 d after planting, seven barley landraces exhibited susceptible reactions to the Yozgat isolate of *D. graminea*, eight landraces showed intermediate reactions, and 15 ladraces were resistant to the isolate. At 60 d after planting, eight barley landraces were susceptible to the Yozgat isolate, nine landraces were intermediate, and 13 landraces showed resistant reactions to this isolate. At 45 d after planting, three landraces showed intermediate reactions and 27 landraces showed resistant reactions to the Eskişehir isolate. At the 60 day assessment, the reactions of the genotypes to the Eskişehir isolate were the same as those assessed at 45 d (Table 6).

The susceptible control barley cultivar 'Larende' exhibited susceptible reactions to both *D. graminea* isolates, and the resistant control cultivar 'Çumra 2001' was resistant to the two isolates.

Separate analyses of variance revealed statistically significant ($P < 0.01$) differences among the *H. sponatenum* genotypes and barley landraces and between the two *D. graminea* isolates, both at 45 and 60 d after planting of inoculated seeds. Significant ($P < 0.01$) isolate*genotype interactions were also detected (Tables 1-4).

Disease resistance evaluations require clear understanding of host/pathogen interactions. Visual analyses of these interactions are possible with biplot analyses. Low Component 1 negative values, and Component 2 values close to zero in biplots clearly illustrate the resistance of genotypes to disease (Yan and Falk 2002). In the biplot analyses, *H. spontaneum* genotypes 13, 24, 27, 29, 54, 86, 91, and the resistant control cultivar 'Çumra 2001' were grouped together, and representing the most resistant genotypes of those studied (Figure 1). The wild barley genotypes 32 and 14 showed intermediate responses to the Yozgat isolate, but they were resistant to the Eskişehir isolate. These two genotypes were closest to the point where the resistant genotypes were placed. Genotypes 1, 52, 62, 107, and the susceptible control cultivar 'Larende' which showed a susceptible reaction to both isolates, were between the two isolates in the biplot. The wild barley genotype 4, which was susceptible to both *D. graminea* isolates, was closer to the Eskişehir isolate biplot line because it was more susceptible to the Eskişehir isolate than to the Yozgat isolate (Table 1, Figure 1).

Barley landraces 39, 21, 38, 139, 98, 40, 159, 73, 167, 171, 37, 128, 153 and the resistant control cultivar 'Çumra 2001' were the genotypes that were most resistant to *D. graminea*. These landraces exhibited resistant reactions to both *D. graminea* isolates, and they were all at the same point on the biplot graph (Figure 2). Landraces 160, 24, 103, 20, 101, 104, 71, and 3 exhibited intermediate reactions to the Yozgat isolate and resistant reactions to the Eskişehir isolate. No genotypes were susceptible to both pathogen isolates, except for the susceptible control cultivar 'Larende'. Barley landraces 148 and 74 were susceptible to the Yozgat isolate and exhibited intermediate responses to the Eskişehir isolate (Figure 2).

DISCUSSION

The present study is the first evaluation of resistance to leaf stripe for these 30 barley landraces and 30 wild barley genotypes. Differences in host reactions to inoculation with *D. graminea* were detected. Virulence differences between two isolates of the pathogen were also evident. Overall, the barley landraces were more resistant to *D. graminea* than the *H. spontaneum* genotypes examined in this study. Other reports from Turkey and elsewhere have also shown variable levels of resistance in barley to *D. graminea*. Mueller *et al.* (2003) carried out a study using 612 barley accessions, and determined that they exhibited different reactions to natural infections by *D. graminea* under organic agriculture conditions.

Table 5. Reactions of 30 wild barley (*Hordeum spontaneum*) genotypes following inoculation with two isolates of *Drechslera graminea*. For disease values, the scale of Tekauz (1983) was used.

D. graminea, Yozgat isolate					*D. graminea*, Eskişehir isolate				
Hordeum spontaneum genotype	45 d after planting		60 d after planting		*Hordeum spontaneum* genotype	45 d after planting		60 d after planting	
	Mean disease percent	Scale value	Mean disease percent	Scale value		Mean disease percent	Scale value	Mean disease percent	Scale value
1	100	3 (S)	100	3 (S)	1	22.2	3 (S)	22.2	3 (S)
4	25	3 (S)	25	3 (S)	4	33.3	3 (S)	33.3	3 (S)
5	16.6	2 (I)	33.3	3 (S)	5	0	1 (R)	0	1 (R)
6	25	3 (S)	25	3 (S)	6	0	1 (R)	0	1 (R)
8	40	3 (S)	40	3 (S)	8	0	1 (R)	0	1 (R)
9	66.6	3 (S)	83.3	3 (S)	9	12.5	2 (I)	12.5	2 (I)
13	0	1 (R)	0	1 (R)	13	0	1 (R)	0	1 (R)
14	14.2	2 (I)	14.2	2 (I)	14	0	1 (R)	0	1 (R)
16	55.5	3 (S)	55.5	3 (S)	16	0	1 (R)	0	1 (R)
24	0	1 (R)	0	1 (R)	24	0	1 (R)	0	1 (R)
27	0	1 (R)	0	1 (R)	27	0	1 (R)	0	1 (R)
29	0	1 (R)	0	1 (R)	29	0	1 (R)	0	1 (R)
32	12.5	2 (I)	12.5	2 (I)	32	0	1 (R)	0	1 (R)
33	28.5	3 (S)	28.5	3 (S)	33	0	1 (R)	0	1 (R)
38	66.6	3 (S)	66.6	3 (S)	38	0	1 (R)	0	1 (R)
44	33.3	3 (S)	33.3	3 (S)	44	16.6	2 (I)	16.6	2 (I)
45	71.4	3 (S)	71.4	3 (S)	45	11.1	2 (I)	11.1	2 (I)
49	42.8	3 (S)	42.8	3 (S)	49	14.2	2 (I)	14.2	2 (I)
52	71.4	3 (S)	100	3 (S)	52	28.5	3 (S)	28.5	3 (S)
54	0	1 (R)	0	1 (R)	54	0	1 (R)	0	1 (R)
62	75	3 (S)	75	3 (S)	62	50	3 (S)	50	3 (S)
66	50	3 (S)	50	3 (S)	66	0	1 (R)	0	1 (R)
70	40	3 (S)	40	3 (S)	70	0	1 (R)	0	1 (R)
76	71.4	3 (S)	71.4	3 (S)	76	0	1 (R)	0	1 (R)
80	87.5	3 (S)	87.5	3 (S)	80	11.1	2 (I)	11.1	2 (I)
86	0	1 (R)	0	1 (R)	86	0	1 (R)	0	1 (R)
91	0	1 (R)	0	1 (R)	91	0	1 (R)	0	1 (R)
93	75	3 (S)	75	3 (S)	93	10	2 (I)	10	2 (I)
99	75	3 (S)	75	3 (S)	99	0	1 (R)	0	1 (R)
107	57.1	3 (S)	57.1	3 (S)	107	28.5	3 (S)	28.5	3 (S)
Larende	80	3 (S)	80	3 (S)	Larende	60	3 (S)	60	3 (S)
Çumra 2001	0	1 (R)	0	1 (R)	Çumra 2001	0	1 (R)	0	1 (R)
	40.01*		41.09*			7.93*		9.31*	

*Significant at $P < 0.01$ (Tables 1 and 2).

More than 30% of the accessions were resistant to *D. graminea*. In the same study, a small group of accessions was selected and tested using the sandwich inoculation method for reactions to two aggressive *P. graminea* isolates. They found that the accessions BGRC 5592, HOR 333, HOR 11475, and OU J362 showed resistant reactions. Similarly, the sandwich method was applied in the present study, and we determined that 23% of the wild barley genotypes and 43% of the barley landraces were resistant to both isolates of *D. graminea*.

Arabi *et al.* (2004) tested ten widely cultivated barley varieties against a virulent *D. graminea* isolate (Sy3) in southern Syria. Differential reactions were observed among the varieties, and as the level of disease increased, there were decreases in crop yield, kernel weight, and plant biomass. It has also been reported

Table 6. Reactions of 30 barley landraces following inoculation with two isolates of *Drechslera graminea*. For disease valuaes, the scale of Tekauz (1983) was used.

D. graminea, Yozgat isolate					*D. graminea,* Eskişehir isolate				
Barley landrace	45 d after planting		60 d after planting		Barley landrace	45 d after planting		60 d after planting	
	Mean disease percent	Scale value	Mean disease percent	Scale value		Mean disease percent	Scale value	Mean disease percent	Scale value
3	12.5	2 (I)	12.5	2 (I)	3	0	1 (R)	0	1 (R)
8	16	2 (I)	16	2 (I)	8	12.5	2 (I)	12.5	2 (I)
12	20	3 (S)	20	3 (S)	12	0	1 (R)	0	1 (R)
18	22.2	3 (S)	22.2	3 (S)	18	0	1 (R)	0	1 (R)
20	0	1 (R)	16.6	2 (I)	20	0	1 (R)	0	1 (R)
21	0	1 (R)	0	1 (R)	21	0	1 (R)	0	1 (R)
22	12.5	2 (I)	25	3 (S)	22	0	1 (R)	0	1 (R)
24	14.2	2 (I)	14.2	2 (I)	24	0	1 (R)	0	1 (R)
37	0	1 (R)	0	1 (R)	37	0	1 (R)	0	1 (R)
38	0	1 (R)	0	1 (R)	38	0	1 (R)	0	1 (R)
39	0	1 (R)	0	1 (R)	39	0	1 (R)	0	1 (R)
40	0	1 (R)	0	1 (R)	40	0	1 (R)	0	1 (R)
71	16.6	2 (I)	16.6	2 (I)	71	0	1 (R)	0	1 (R)
73	0	1 (R)	0	1 (R)	73	0	1 (R)	0	1 (R)
74	50	3 (S)	50	3 (S)	74	14.2	2 (I)	14.2	2 (I)
83	37.5	3 (S)	37.5	3 (S)	83	0	1 (R)	0	1 (R)
90	37.5	3 (S)	37.5	3 (S)	90	0	1 (R)	0	1 (R)
98	0	1 (R)	0	1 (R)	98	0	1 (R)	0	1 (R)
101	16.6	2 (I)	16.6	2 (I)	101	0	1 (R)	0	1 (R)
103	12.5	2 (I)	12.5	2 (I)	103	0	1 (R)	0	1 (R)
104	16.6	2 (I)	16.6	2 (I)	104	0	1 (R)	0	1 (R)
128	0	1 (R)	0	1 (R)	128	0	1 (R)	0	1 (R)
139	0	1 (R)	0	1 (R)	139	0	1 (R)	0	1 (R)
148	50	3 (S)	50	3 (S)	148	11.1	2 (I)	11.1	2 (I)
153	0	1 (R)	0	1 (R)	153	0	1 (R)	0	1 (R)
159	0	1 (R)	0	1 (R)	159	0	1 (R)	0	1 (R)
160	0	1 (R)	11.1	2 (I)	160	0	1 (R)	0	1 (R)
162	28.5	3 (S)	28.5	3 (S)	162	0	1 (R)	0	1 (R)
167	0	1 (R)	0	1 (R)	167	0	1 (R)	0	1 (R)
171	0	1 (R)	0	1 (R)	171	0	1 (R)	0	1 (R)
Larende	66.6	3 (S)	66.6	3 (S)	Larende	33.3	3 (S)	33.3	3 (S)
Çumra 2001	0	1 (R)	0	1 (R)	Çumra 2001	0	1 (R)	0	1 (R)
	12.10*		14.68*			1.26*		2.22*	

*Significant at $P < 0.01$ (Tables 3 and 4).

that a decrease in plant biomass affects vital activities of plants such as photosynthesis and respiration (Mathre, 1997). In Turkey, the reactions of 1,216 barley lines to barley leaf stripe were assessed and it was found that 25 lines were resistant and eight were intermediate to resistant to the disease (Albustan *et al*., 1999). Ulus and Karakaya (2007) assessed the resistance of 15 widely used barley varieties to five *D. graminea* isolates, and determined that the barley cultivars 'Çumra 2001' and 'Yerçil 147' were resistant to all five isolates, and that the isolate Dg3 was the most virulent. Bayraktar and Akan (2012) reported that barley cultivars 'Durusu', 'Balkan 96 (Igri)', 'Çumra 2001' and 'Anadolu 98' were resistant to the 13 *D. graminea* isolates they tested, and that isolate 1003 was the most virulent.

Çelik *et al*. (2016) evaluated the reactions of three barley cultivars and 20 barley landraces to ten *D. graminea* isolates, and found that one barley landrace

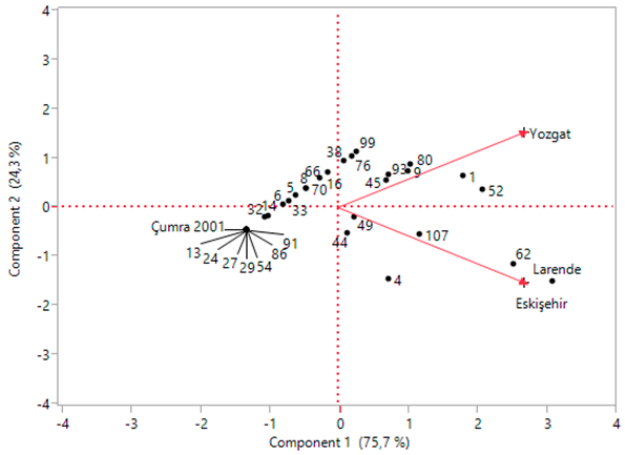

Figure 1. Biplot based on PCA analysis of the mean disease incidences of wild barley (*H. spontaneum*) genotypes inoculated with two isolates of *Drechslera graminea*.

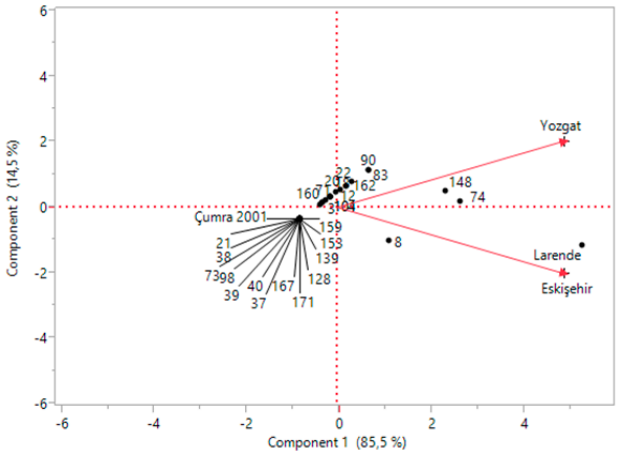

Figure 2. Biplot based on PCA analysis of the mean disease incidences of barley landraces inoculated with two isolates of *Drechslera graminea*.

was resistant to eight *D. graminea* isolates and had intermediate reactions to the other two isolates. The barley variety 'Çumra 2001' was resistant to all ten isolates. These authors also reported virulence differences among the isolates. In their study, average disease incidence for the Yozgat isolate was 40.2%, and for the Eskişehir isolates was 15.4%. Çelik Oğuz *et al.* (2017a), also found virulence differences among *D. graminea* isolates, and that only one of the 23 hulless barley lines they tested was resistant to three isolates of the pathogen. Karakaya *et al.* (2017) tested the same three isolates on 25 Iranian barley landraces and found similar virulence differences among the isolates. In their study, no Iranian barley landraces were resistant to all three isolates.

Turkey is a major genetic centre for cultivated and wild barleys, and there are barley genotypes in this country that are resistant to different abiotic and biotic stresses (Vavilov, 1951; Kün, 1996; Afanasenko *et al.*, 2000; Jakob *et al.*, 2014; Çelik *et al.,* 2016; Karakaya *et al.*, 2016a). Barley landraces and wild barley genotypes show great variation in agronomic traits as well as reaction to biotic stress factors. Resistance to different diseases has been reported in barley landraces and wild barley (*H. spontaneum*) genotypes (Azamparsa *et al.*, 2019; Karakaya *et al.*, 2017; Çelik and Karakaya, 2017; Çelik Oğuz *et al.*, 2017b; Çelik Oğuz *et al.*, 2019). Resistance among barley genotypes originating from the Middle East has been reported, with Anatolian landraces being superior compared to those from other origins, in terms of yield, drought, and disease tolerance (Chakrabarti, 1968; Khan and Boyd, 1969; Gökgöl, 1969).

In the present study, *H. spontaneum* genotypes 13, 24, 27, 29, 54, 86, and 91 were resistant to two *D. graminea* isolates. Genotypes 24, 27, and 54 were also resistant to virulent isolates of both forms of *Pyrenophora teres* (Çelik Oğuz *et al.*, 2019). *Hordeum spontaneum* genotype 13 was found to be resistant to virulent isolates of *P. teres* f. *maculata* (which causes the spot form of net blotch), while *H. spontaneum* genotype 29 was resistant to virulent isolates of *P. teres* f. *teres* (which causes the net form of net blotch) (Çelik Oğuz *et al.*, 2019). In addition, all seven of these wild barley genotypes showed resistance to up to four of six *Rhynchosporium commune* isolates (Azamparsa *et al.*, 2019).

Barley landraces 21, 37, 38, 39, 40, 73, 98, 128, 139, 153, 159, 167, and 171 were resistant to both *D. graminea* isolates examined in the present study. Among these landraces, landrace 40 was also resistant to virulent isolates of both forms of *P. teres* (Çelik Oğuz *et al.*, 2017b). Barley landraces 98, 167, and 171 were found to be resistant to virulent isolates of *P. teres* f. *maculata* (causing the spot form of net blotch), while barley landraces 21 and 153 were resistant to virulent isolates of *P. teres* f. *teres* (causing the net form of net blotch) (Çelik Oğuz *et al.*, 2017b). In addition, barley landraces 21, 38, 40, 218, 139, 153 and 167 showed resistance to up to three of six *R. commune* isolates (Azamparsa *et al.*, 2019).

The disease resistance of different *H. spontaneum* and barley landraces to other diseases has also been determined in other studies. For example, Kopahnke (1998) evaluated the reactions of wild barley and barley landraces to *P. teres* and found that 143 genotypes exhibited resistant reactions to all isolates tested. Jana and Bailey (1995) found resistance among the *H. spontaneum* genotypes and cultivated barley landraces obtained from Turkey and Jordan to the fungal pathogens *P. teres*

f. *maculata*, *P. teres* f. *teres*, and *Cochliobolus sativus*. The percentage of *H. spontaneum* accessions resistant to these pathogens (10.5%) was greater compared to that of the cultivated accessions (1.3%). Fetch *et al*. (2003) determined the reactions of 116 *H. spontaneum* genotypes originating from Jordan and Israel to six fungal pathogens. They showed that 98% of the genotypes from Jordan and 77% of the genotypes from Israel were resistant to Septoria leaf blotch, 70% and 90%, respectively from the two countries, were resistant to leaf rust, 72% and 78%, respectively, were resistant to net blotch, 58% and 70%, respectively, were resistant to powdery mildew, 53% and 46%, respectively, were resistant to spot blotch, and 2% and 26%, respectively from the two countries, were resistant to stem rust.

Wild barley (*H. spontaneum*) has greater genetic variation than cultivated barley (Saghai-Maroof *et al*., 1994; Provan *et al*., 1999; Nevo, 2004), and it is possible to crossbreed *H. spontaneum* with cultured barley (*H. vulgare*). Useful traits including disease resistance can be transferred to cultivated barley from *H. spontaneum* (Çelik and Karakaya, 2017), so wild barley is a significant potential genetic source for barley genetic improvement. Wild barley populations in the Middle East also possess considerable genetic variation (Nevo, 1992). It has been suggested that *H. spontaneum* genotypes should be preserved under *in situ* and *ex situ* conditions for barley improvement programmes, including those selecting for enhanced disease resistance (Nevo, 1992; Ceccarelli and Grando, 2000; Nevo, 2012). *Hordeum spontaneum* genotypes may show different resistance reactions based on their origins, and resistance genes can vary depending on geographic conditions (Sato and Takeda, 1997). *Hordeum spontaneum* populations from the Fertile Crescent Region, including parts of the Levant (eastern Mediterranean, including Turkey and Israel) and Iran are genetically variable for adaptation capability and population sustainability (Nevo, 2004; Jakob *et al*., 2014). In the present study, *H. spontaneum* genotypes resistant to *D. graminea* isolates were observed. Seven and two of the *H. spontaneum* genotypes showed resistant reactions to the Yozgat isolate and two genotypes were of intermediate resistance. On the other hand, 19 of *H. spontaneum* genotypes were resistant to the Eskişehir isolate while six genotypes were of intermediate resistance to this isolate. The heterogenous nature of wild barley (*H. spontaneum*) resistance to diseases has been reported previously (Çelik and Karakaya, 2017; Karakaya *et al*., 2016a). In a survey carried out in 2015, a total of 40 *H. spontaneum* populations in their natural habitat were examined, and it was determined that nine of these were disease-free. In these fields, the fungal pathogens *R. commune*, *Blumeria graminis* f. sp. *hordei*, *D. teres* f. *teres*, *D. teres* f. *maculata*, *Ustilago nigra*, *U. nuda*, *Puccinia hordei*, and *D. graminea* were identified (Karakaya *et al*., 2016a).

The region between the south of the Fertile Crescent and the Himalayan mountains was the first area in which barley was domesticated (Azhaguvel and Komatsuda, 2007; Morrell and Clegg, 2007; Saisho and Purugganan, 2007). In recent years, barley varieties and yields in the area of Fertile Crescent have been under serious threat because of climate change and environmental pollution originating from human activities. Barley landraces provide gene resources that can be used to decrease the negative impacts of climate change (Mzid *et al*., 2016). It is known that wild barleys and barley landraces have wide variation in terms of resistance to diseases (Simmonds, 1987; Çelik and Karakaya, 2017; Çelik Oğuz *et al*., 2017b; Azamparsa *et al*., 2019). In conventional agriculture systems, barley leaf stripe is controlled through treating seed with fungicides. However, European Union regulations state that under certified organic production practices, barley leaf stripe can only be controlled using hot water treatments. But, these may not always be fully effective. Barley stripe, which is very important under organic agriculture conditions, is prevalent in Northern Germany due to the cool and humid climatic conditions found there (Mueller *et al*., 2003). Genetic resistance can be transferred from wild relatives to cultivated crops to decrease the use of chemicals (Laurei *et al*., 1992).

In summary, barley leaf stripe is an important disease that can cause significant yield losses when no disease management practices are utilized. In the present study, new sources of resistance to *D. graminea* have been identified. The wild barley genotypes and barley landraces identified here could be used in plant breeding programmes to develop leaf stripe resistant genotypes, which would be ecosystem-friendly and also enhance farmer profitability.

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