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Identification of *Hordeum spontaneum* Genotypes Resistant to Net Blotch Disease

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ABSTRACT

Wild barley (*Hordeum spontaneum*) is a progenitor of cultivated barley and naturally grows in Turkey. *H. spontaneum* genotypes possess superior characteristics for biotic and abiotic stress tolerance factors. In this study, 3 virulent *Pyrenophora teres* f. *maculata* and 3 virulent *P. teres* f. *teres* isolates were tested under greenhouse conditions in order to find net blotch resistant *H. spontaneum* genotypes. A total of 104 *H. spontaneum* genotypes were used. Twenty-six *H. spontaneum* genotypes which corresponded to 25% of the genotypes (genotypes numbered 8, 13, 14, 16, 22, 24, 27, 31, 37, 44, 47, 54, 58, 62, 65, 66, 69, 74, 78, 81, 89, 94, 99, 102, 104 and 107) exhibited reactions classified in the resistant group to 3 virulent *P. teres* f. *maculata* isolates. Eight *H. spontaneum* genotypes which corresponded to 7.6% of the genotypes (genotypes numbered 24, 27, 29, 33, 44, 54, 89 and 94) exhibited reactions classified in the resistant group to 3 virulent *P. teres* f. *teres* isolates. Six *H. spontaneum* genotypes which corresponded to 5.7% of the genotypes (genotypes numbered 24, 27, 44, 54, 89 and 94) exhibited reactions in the resistant group to both 6 virulent *P. teres* f. *teres* and *P. teres* f. *maculata* isolates. In addition, a considerable number of genotypes exhibited resistant group reactions to one or two isolates of both forms of the pathogen. These genotypes could be used for developing net blotch resistant barley cultivars.

Keywords: Barley; Disease resistance; *Hordeum spontaneum*; Net blotch; *Pyrenophora teres*

1. Introduction

Wild barley (*Hordeum spontaneum,* syn: *Hordeum vulgare* subsp. *spontaneum*) is a progenitor of cultivated barley and naturally grows in Turkey (Kün 1996; Karakaya et al 2016). *Hordeum spontaneum* could hybridize with cultivated barley (*Hordeum vulgare*) and is an important plant for developing disease resistant barley cultivars. Wild barleys and barley landraces possess superior characteristics for abiotic and biotic stress tolerance factors (Ceccarelli & Grando 2000; Karakaya et al 2016; Çelik & Karakaya 2017). Because of these characteristics, it is advised to preserve *H. spontaneum* genotypes *in situ* and *ex situ* conditions for future research (Nevo 2012).

China, India, Central Asia, Near East, Mediterranean region, Ethiopia, Southern Mexico and Central and South America are eight main

regions in the world considered as plant gene centers. Turkey has a rich genetical diversity due to its location. Turkey is located at the intersection of the Mediterranean and the Near East gene centers, and it is on the historical migration and transportation routes of China, India, Central Asia and Ethiopia gene centers. In addition, Fertile Crescent region which includes Turkey's Southeastern Anatolia region is known as the region where barley, wheat, lentil, hard-seeded fruit and olive are cultivated for the first time (Vavilov 1951). In addition, Jakob et al (2014) reported that Levant, Turkey and east of Turkey are three main regions of wild barley (*H. spontaneum*) populations. Wild barleys including *H. spontaneum* are commonly grown under natural conditions in Turkey (Karakaya et al 2016).

Net blotch is caused by the fungus *Pyrenophora teres* that belongs to ascomycota. Anamorphic stage of the fungus is named as *Drechslera teres*. Two biotypes of the fungus are recognized. *Pyrenophora teres* f. *maculata* incites the spot form and *Pyrenophora teres* f. *teres* incites the net form of the disease (Karakaya & Akyol 2006; Liu et al 2011). The disease is commonly reported from different parts of the world and reduces the yield and quality of barley considerably (Mathre 1982; Liu et al 2011; Karakaya et al 2014).

In this study, 3 virulent *P. teres* f. *maculata* (*Ptm*) and 3 virulent *P. teres* f. *teres* (*Ptt*) isolates were tested under greenhouse conditions in order to find net blotch resistant *H. spontaneum* genotypes. A total of 104 *H. spontaneum* genotypes were used. An abstract of this study has been published previously (Çelik Oğuz et al 2017).

2. Materials and Methods

2.1. Experimental materials

In this study, 107 wild barley (*H. spontaneum*) genotypes that collected from various parts of Turkey and conserved by Field Crops Central Research Institute (Ankara, Turkey) were used. The seeds of these *H. spontaneum* genotypes were multiplied from single heads. Out of 107 genotypes, 104 provided the sufficient amount of seeds and were included in this study. No sufficient seeds were obtained from genotypes No: 4, No: 15 and No: 41. Three *Ptm* isolates and 3 *Ptt* isolates that were found to be the most virulent ones in the study by Çelik Oğuz (2015) were used in determination of seedling stage resistance of 104 *H. spontaneum* genotypes under greenhouse conditions.

2.2. Treatments

Sterile mixtures of soil, sand and organic substances (60, 20, 20; v/v/v, respectively) were placed in plastic pots with diameters of 7 centimeters and depending on the quantity of seeds of genotypes, 5-10 seeds were placed to the pots. The pots were maintained under greenhouse conditions. Inoculation was performed at growth stages 12-13 (Zadoks et al 1974). The inoculum was prepared from cultures grown on Potato Dextrose Agar maintained at 16-23±2 °C night/day with a 10 h/14 h dark/light period. In order to prepare inoculum, mycelia were harvested from Petri dishes using a no.12 brush and concentration of inoculum was adjusted to $15\text{-}20\times10^4$ mycelial parts/ml (Douiyssi et al 1998; Taşkoparan & Karakaya 2009; Usta et al 2014; Yazıcı et al 2015). One drop of Tween 20 was added to each 100 mL of inoculum (Aktaş 1995). Inoculum was sprayed onto barley seedlings using a hand sprayer and all leaves were covered with inoculum. The greenhouse temperature ranged between 18-23±1 °C night/day with a 10 h/14 h dark/light period. Plants were kept covered with nylon in transparent boxes with moist lids for 76 h following inoculation. Then, plants were maintained for another 48 h with the nylon uncovered and the ventilation of the boxes activated. There were three replications.

2.3. Evaluation of the disease

Plant evaluations were carried out seven days later following inoculation. For evaluation, scales developed for both forms of net blotch by Tekauz (1985) were used. Plant evaluations were based on lesion size, morphology, necrosis and chlorosis. Scale values of 1, 2 and 3 were considered as resistant group in this study. In the scale for the spot

form of net blotch, seven numerical classes were defined (1= R: resistant, 2= R: resistant to MR: moderately resistant, 3= MR: moderately resistant, 5= MR: moderately resistant to MS: moderately susceptible, 7= MS: moderately susceptible, 8= MS: moderately susceptible to S: susceptible, and 9= S: susceptible). In net form of net blotch scale ten numerical classes were defined (1= R: resistant, 2= R: resistant to MR: moderately resistant, 3= MR: moderately resistant, 4= MR: moderately resistant to MS: moderately susceptible, 5= MR: moderately resistant to MS: moderately susceptible, 6= MR: moderately resistant to MS: moderately susceptible, 7= MS: moderately susceptible, 8= MS: moderately susceptible to S: susceptible, 9= S: susceptible, and 10= VS: very susceptible). Resistant or moderately resistant genotypes have small net blotch lesions. Moderately susceptible or susceptible genotypes have chlorotic zones surrounding the necrotic areas and coalescence of these areas and death of leaves can occur.

2.4. Data analysis

Experiment was carried out using randomized block design with three replications. Data were square root transformed before statistical analysis. Separate two way analysis of variance was performed for each isolate and means of responses of *H. spontaneum* genotypes were separated by Least Significant Difference (LSD) test. Statistical tests were accomplished using JMP software (version 11; SAS Institute).

3. Results and Discussion

Seedling resistance reactions of 104 wild barley genotypes to 3 virulent *Ptm* isolates and 3 virulent *Ptt* isolates were determined. Analysis of variance revealed significant differences among the *H. spontaneum* genotypes ($P<0.01$). Response of the genotypes ranged between resistant (scale value 1) and susceptible (scale value 9) (Table 1). Thirty-nine, 9 and 2 genotypes exhibited moderately resistant, resistant-moderately resistant and resistant reactions to *Ptm* isolate GPS 263 PTM, respectively. Thirty-six and 3 genotypes showed moderately resistant and resistant-moderately resistant reactions to *Ptm* isolate 13-179 PTM, respectively. Fifty-three, 9 and 3 genotypes exhibited moderately resistant, resistant-moderately resistant and resistant reactions to *Ptm* isolate 13-167 PTM, respectively.

Twenty-six *H. spontaneum* genotypes which corresponded to 25% of the genotypes (genotypes numbered 8, 13, 14, 16, 22, 24, 27, 31, 37, 44, 47, 54, 58, 62, 65, 66, 69, 74, 78, 81, 89, 94, 99, 102, 104 and 107) exhibited reactions classified in the resistant group to 3 virulent *Ptm* isolates.

Nine and 1 genotypes showed moderately resistant and resistant reactions to *Ptt* isolate GPS 18 PTT, respectively. Thirteen, 6 and 2 genotypes exhibited moderately resistant, resistant-moderately resistant and resistant reactions to *Ptt* isolate UHK 77 PTT, respectively. Twenty-one and 8 genotypes exhibited moderately resistant and resistant-moderately resistant reactions to *Ptt* isolate 13-130 PTT, respectively.

Eight *H. spontaneum* genotypes which corresponded to 7.6% of the genotypes (genotypes numbered 24, 27, 29, 33, 44, 54, 89 and 94) exhibited reactions classified in the resistant group to 3 virulent *Ptt* isolates.

Six *H. spontaneum* genotypes which corresponded to 5.7% of the genotypes (genotypes numbered 24, 27, 44, 54, 89 and 94) exhibited reactions in the resistant to moderately resistant group range (Tekauz (1985) scale 1 to 3) to both 6 virulent *Ptt* and *Ptm* isolates. In addition, a considerable number of genotypes exhibited resistant to moderately resistant reactions to one or two isolates of both forms of the pathogen (Table 1).

Wild barleys are important resistance sources for controlling biotic and abiotic stress factors. Finding disease resistant wild barley genotypes facilitate disease resistance studies. In this current study, we determined *H. spontaneum* genotypes resistant to both forms of *P. teres*.

There are limited studies related to reactions of *H. spontaneum* genotypes to net blotch disease. In a study conducted by Kopahnke (1998), 770

Table 1- Seedling reactions of 104 *Hordeum spontaneum* genotypes to 3 virulent *Pyrenophora teres* f. *maculata* isolates and 3 virulent *Pyrenophora teres* f. *teres* isolates. Means not connected by same letter are significantly different (P<0.01)

Isolate	*GPS 263*		*13-179*		*13-167*		*GPS 18*		*UHK 77*		*13-130*	
Genotype	*PTM**		*PTM**		*PTM**		*PTT***		*PTT***		*PTT***	
1	5 cde	MR-MS	5 bcd	MR-MS	3 cde	MR	4 fghı	MR-MS	4 ıjk	MR-MS	6 bcde	MR-MS
2	3 efg	MR	5 bcd	MR-MS	5 abc	MR-MS	5 efgh	MR-MS	5 ghı	MR-MS	6 cdef	MR-MS
3	3 def	MR	5 bcd	MR-MS	5 bcd	MR-MS	6 abcd	MR-MS	5 fgh	MR-MS	6 abcd	MR-MS
4	Not enough seeds											
5	7 abc	MS	5 bc	MR-MS	5 abc	MR-MS	4 ghıj	MR-MS	4 ıjk	MR-MS	5 efgh	MR-MS
6	3 def	MR	5 bcd	MR-MS	3 cde	MR	4 hıjk	MR-MS	4 ıjk	MR-MS	4 hıjk	MR-MS
7	5 bcd	MR-MS	5 bcd	MR-MS	3 cde	MR	6 bcde	MR-MS	7 bc	MS	6 bcde	MR-MS
8	3 efg	MR	3 de	MR	2 gh	R-MR	4 ghıj	MR-MS	6 efg	MR-MS	5 defg	MR-MS
9	5 cde	MR-MS	5 bcd	MR-MS	3 efg	MR	6 bcde	MR-MS	8 ab	MS-S	5 defg	MR-MS
10	7 abc	MS	3 cde	MR	5 bcd	MR-MS	4 ghıj	MR-MS	4 ıjk	MR-MS	4 ıjk	MR-MS
11	5 cde	MR-MS	3 cde	MR	3 def	MR	6 abc	MR-MS	7 bc	MS	8 a	MS-S
12	3 efg	MR	3 de	MR	5 bcd	MR-MS	6 bcde	MR-MS	4 ıjk	MR-MS	5 efgh	MR-MS
13	3 efg	MR	3 de	MR	3 def	MR	3 defg	MR	4 jkl	MR-MS	3 lmn	MR
14	2 fgh	R-MR	3 de	MR	3 def	MR	4 fghı	MR-MS	3 lmn	MR	4 ghıj	MR-MS
15	Not enough seeds											
16	3 efg	MR	3 de	MR	2 fgh	R-MR	6 bcde	MR-MS	6 defg	MR-MS	4 ghıj	MR-MS
17	7 abc	MS	7 ab	MS	5 bcd	MR-MS	5 defg	MR-MS	6 cdef	MR-MS	5 fghı	MR-MS
18	7 abc	MS	5 abc	MR-MS	3 cde	MR	4 fghı	MR-MS	5 efg	MR-MS	5 fghı	MR-MS
19	5 abc	MR-MS	5 bc	MR-MS	5 abc	MR-MS	5 cdef	MR-MS	7 cd	MS	7 ab	MS
20	5 cde	MR-MS	5 bcd	MR-MS	3 def	MR	6 abc	MR-MS	5 efg	MR-MS	4 ghıj	MR-MS
21	7 abc	MS	3 cde	MR	3 def	MR	6 bcde	MR-MS	5 fgh	MR-MS	4 ıjk	MR-MS
22	3 fgh	MR	3 de	MR	3 def	MR	5 cdef	MR-MS	6 cdef	MR-MS	5 defg	MR-MS
23	5 cde	MR-MS	3 cde	MR	2 gh	R-MR	5 defg	MR-MS	2 no	R-MR	6 abcd	MR-MS
24	3 def	MR	2 e	R-MR	2 efgh	R-MR	2 m	R-MR	2 o	R-MR	3 klm	MR
25	5 bcd	MR-MS	5 bcd	MR-MS	5 bcd	MR-MS	5 efgh	MR-MS	6 defg	MR-MS	5 efgh	MR-MS
26	7 abc	MS	5 bc	MR-MS	3 cde	MR	4 fghı	MR-MS	4 ıjk	MR-MS	3 klm	MR
27	3 efg	MR	3 de	MR	2 efgh	R-MR	3 l	MR	3 lmn	MR	3 jkl	MR
28	5 bcd	MR-MS	5 bcd	MR-MS	3 cde	MR	5 defg	MR-MS	5 fgh	MR-MS	7 abc	MS
29	3 efg	MR	3 de	MR	5 bcd	MR-MS	3 l	MR	1 p	R	3 klm	MR
30	7 abc	MS	5 abc	MR-MS	3 efg	MR	4 ghıjk	MR-MS	6 defg	MR-MS	5 efgh	MR-MS
31	3 def	MR	3 de	MR	3 efg	MR	6 bcde	MR-MS	6 defg	MR-MS	6 bcde	MR-MS
32	3 efg	MR	5 bcd	MR-MS	3 cde	MR	5 efgh	MR-MS	6 cde	MR-MS	7 abc	MS
33	2 fgh	R-MR	3 de	MR	5 bcd	MR-MS	3 ıjkl	MR	3 klm	MR	3 lmn	MR
34	5 cde	MR-MS	5 bcd	MR-MS	5 ab	MR-MS	6 abcd	MR-MS	4 ıjk	MR-MS	4 ghıj	MR-MS
35	7 abc	MS	5 abc	MR-MS	5 abc	MR-MS	7 ab	MS	5 ghı	MR-MS	6 bcde	MR-MS
36	5 bcd	MR-MS	5 bc	MR-MS	5 abc	MR-MS	6 bcde	MR-MS	6 cdef	MR-MS	6 cdef	MR-MS
37	3 efg	MR	3 de	MR	3 def	MR	4 hıjk	MR-MS	3 mn	MR	3 lmn	MR
38	5 cde	MR-MS	3 cde	MR	3 cde	MR	6 abcd	MR-MS	6 cdef	MR-MS	6 abcd	MR-MS
39	5 bcd	MR-MS	5 bcd	MR-MS	3 def	MR	6 bcde	MR-MS	6 cdef	MR-MS	5 efgh	MR-MS
40	7 abc	MS	5 abc	MR-MS	5 abc	MR-MS	6 bcde	MR-MS	3 mn	MR	5 fghı	MR-MS
41	Not enough seeds											
42	3 efg	MR	5 bcd	MR-MS	3 def	MR	6 bcde	MR-MS	3 klm	MR	3 lmn	MR
43	7 abc	MS	5 bc	MR-MS	3 def	MR	6 bcde	MR-MS	3 lmn	MR	2 no	R-MR
44	3 efg	MR	3 de	MR	3 def	MR	3 ıjkl	MR	2 no	R-MR	3 lmn	MR
45	5 cde	MR-MS	5 bcd	MR-MS	3 def	MR	4 fghı	MR-MS	6 defg	MR-MS	3 lmn	MR
46	5 abc	MR-MS	5 bc	MR-MS	5 bcd	MR-MS	5 defg	MR-MS	7 cd	MR-MS	3 lmn	MR
47	3 efg	MR	3 de	MR	3 efg	MR	6 bcde	MR-MS	2 no	R-MR	2 mno	R-MR
48	7 abc	MS	5 abc	MR-MS	5 bcd	MR-MS	6 bcde	MR-MS	4 ıjk	MR-MS	3 lmn	MR
49	7 abc	MS	5 bc	MR-MS	3 def	MR	4 hıjk	MR-MS	5 fgh	MR-MS	4 ıjk	MR-MS
50	7 abc	MS	5 bc	MR-MS	3 def	MR	4 hıjkl	MR-MS	5 ghı	MR-MS	4 ıjk	MR-MS
51	5 cde	MR-MS	5 bcd	MR-MS	5 bcd	MR-MS	6 abcd	MR-MS	6 cdef	MR-MS	6 cdef	MR-MS
52	3 efg	MR	5 bcd	MR-MS	5 bcd	MR-MS	6 bcde	MR-MS	6 cde	MR-MS	6 bcde	MR-MS
53	3 efg	MR	5 bcd	MR-MS	5 bcd	MR-MS	6 bcde	MR-MS	5 fgh	MR-MS	4 ıjk	MR-MS
54	2 fgh	R-MR	3 de	MR	1 h	R	3 kl	MR	2 no	R-MR	2 mno	R-MR
55	3 efg	MR	5 bcd	MR-MS	5 bcd	MR-MS	6 bcde	MR-MS	5 efg	MR-MS	3 lmn	MR
56	5 cde	MR-MS	3 de	MR	3 def	MR	6 bcde	MR-MS	4 ıjk	MR-MS	3 jkl	MR
57	3 def	MR	5 abc	MR-MS	5 ab	MR-MS	6 bcde	MR-MS	4 jkl	MR-MS	6 bcde	MR-MS
58	3 efg	MR	3 de	MR	3 def	MR	4 fghı	MR-MS	6 cde	MR-MS	4 ıjk	MR-MS
59	2 fgh	R-MR	5 bcd	MR-MS	3 def	MR	4 hıjk	MR-MS	6 cdef	MR-MS	2 mno	R-MR
60	5 bcd	MR-MS	5 bcd	MR-MS	3 def	MR	6 abcd	MR-MS	9 a	S	6 abcd	MR-MS
61	2 fgh	R-MR	5 bcd	MR-MS	3 cde	MR	5 defg	MR-MS	5 fgh	MR-MS	6 cdef	MR-MS
62	1 h	R	3 de	MR	2 fgh	R-MR	6 bcde	MR-MS	7 Cd	MS	5 efgh	MR-MS
63	3 def	MR	5 bcd	MR-MS	3 cde	MR	6 bcde	MR-MS	4 ıjk	MR-MS	4 hıjk	MR-MS
64	3 efg	MR	5 bcd	MR-MS	5 bcd	MR-MS	4 fghı	MR-MS	4 jkl	MR-MS	3 klm	MR

Table 1- (continued)- Seedling reactions of 104 *Hordeum spontaneum* genotypes to 3 virulent *Pyrenophora teres* f. *maculata* isolates and 3 virulent *Pyrenophora teres* f. *teres* isolates. Means not connected by same letter are significantly different (P<0.01)

Isolate	*GPS 263*		*13-179*		*13-167*		*GPS 18*		*UHK 77*		*13-130*	
Genotype	*PTM**		*PTM**		*PTM**		*PTT***		*PTT***		*PTT***	
65	1h	R	3 de	MR	3 def	MR	4 fghı	MR-MS	3 klm	MR	3 klm	MR
66	2 fgh	R-MR	3 de	MR	3 efg	MR	6 bcde	MR-MS	4 jkl	MR-MS	6 cdef	MR-MS
67	5 cde	MR-MS	3 cde	MR	5 abc	MR-MS	6 bcde	MR-MS	6 defg	MR-MS	4 hıjk	MR-MS
68	8 a	MS-S	7 a	MS	7 a	MS	7 a	MR-MS	6 defg	MR-MS	7 abc	MS
69	3 def	MR	3 de	MR	3 efg	MR	5 efgh	MR-MS	7 bc	MS	4 ıjk	MR-MS
70	3 efg	MR	5 bcd	MR-MS	3 def	MR	4 ghıjk	MR-MS	6 cdef	MR-MS	4 hıjk	MR-MS
71	7 abc	MS	5 bcd	MR-MS	3 def	MR	4 ghıj	MR-MS	4 jkl	MR-MS	3 klm	MR
72	5 bcd	MR-MS	5 bc	MR-MS	5 abc	MR-MS	6 bcde	MR-MS	7 cd	MS	7 abc	MS
73	3 def	MR	5 bcd	MR-MS	5 bcd	MR-MS	6 bcde	MR-MS	6 cde	MR-MS	5 efgh	MR-MS
74	2 fgh	R-MR	3 cde	MR	3 cde	MR	6 bcde	MR-MS	7 bc	MS	5 defg	MR-MS
75	7 abc	MS	5 bc	MR-MS	3 efg	MR	4 fghı	MR-MS	5 fgh	MR-MS	4 ıjk	MR-MS
76	5 cde	MR-MS	3 cde	MR	3 def	MR	6 bcde	MR-MS	6 cde	MR-MS	6 cdef	MR-MS
77	7 abc	MS	5 abc	MR-MS	5 bcd	MR-MS	6 bcde	MR-MS	4 hıj	MR-MS	4 hıjk	MR-MS
78	3 efg	MR	3 cde	MR	3 cde	MR	6 bcde	MR-MS	6 defg	MR-MS	5 defg	MR-MS
79	3 def	MR	5 bcd	MR-MS	5 bcd	MR-MS	6 abcd	MR-MS	7 bc	MS	6 defg	MR-MS
80	5 bcd	MR-MS	5 bcd	MR-MS	2 fgh	R-MR	7 ab	MS	8 ab	MS-S	5 efgh	MR-MS
81	3 def	MR	2 e	R-MR	1 h	R	6 bcde	MR-MS	6 defg	MR-MS	5 defg	MR-MS
82	3 efg	MR	5 bcd	MR-MS	5 bcd	MR-MS	6 abcd	MR-MS	7 cd	MS	5 defg	MR-MS
83	3 def	MR	5 bcd	MR-MS	3 cde	MR	4 fghı	MR-MS	6 defg	MR-MS	4 ıjk	MR-MS
84	2 fgh	R-MR	5 bcd	MR-MS	3 cde	MR	4 ghıj	MR-MS	4 hıj	MR-MS	2 mno	R-MR
85	5 cde	MR-MS	3 de	MR	3 def	MR	5 defg	MR-MS	7 cd	MS	6 bcde	MR-MS
86	7 abc	MS	7 ab	MS	5 abc	MR-MS	6 bcde	MR-MS	5 efg	MR-MS	7 ab	MS
87	5 bcd	MR-MS	5 bcd	MR-MS	5 bcd	MR-MS	4 ghıj	MR-MS	6 defg	MR-MS	7 abc	MS
88	5 abc	MR-MS	5 bc	MR-MS	5 abc	MR-MS	6 abc	MR-MS	7 bc	MS	6 bcde	MR-MS
89	3 def	MR	3 de	MR	3 def	MR	3 jkl	MR	3 klm	MR	3 klm	MR
90	7 abc	MS	5 abc	MR-MS	5 bcd	MR-MS	6 bcde	MR-MS	2 no	R-MR	5 fghı	MR-MS
91	7 abc	MS	5 bcd	MR-MS	5 bcd	MR-MS	4 ghıj	MR-MS	5 fgh	MR-MS	4 ıjk	MR-MS
92	7 ab	MS	5 abc	MR-MS	5 bcd	MR-MS	4 fghı	MR-MS	6 defg	MR-MS	5 efgh	MR-MS
93	7 abc	MS	3 de	MR	3 efg	MR	3 ıjkl	MR	4 jkl	MR-MS	3 klm	MR
94	3 efg	MR	3 de	MR	3 def	MR	3 jkl	MR	3 klm	MR	2 o	R-MR
95	5 bcd	MR-MS	5 bcd	MR-MS	5 bcd	MR-MS	6 abcd	MR-MS	4 jkl	MR-MS	5 efgh	MR-MS
96	7 abc	MS	5 bc	MR-MS	5 bcd	MR-MS	6 bcde	MR-MS	4 ıjk	MR-MS	3 jkl	MR
97	7 abc	MS	5 abc	MR-MS	3 cde	MR	6 bcde	MR-MS	6 defg	MR-MS	5 defg	MR-MS
98	5 cde	MR-MS	5 bcd	MR-MS	3 def	MR	6 abc	MR-MS	5 fgh	MR-MS	5 fghı	MR-MS
99	3 efg	MR	3 de	MR	1 h	R	4 ghıj	MR-MS	1 p	R	4 ıjk	MR-MS
100	3 def	MR	5 bcd	MR-MS	3 def	MR	6 abcd	MR-MS	5 fgh	MR-MS	4 ghıj	MR-MS
101	3 def	MR	5 cde	MR-MS	3 efg	MR	6 bcde	MR-MS	3 klm	MR	3 jkl	MR
102	2 fgh	R-MR	2	R-MR	2 efgh	R-MR	5 defg	MR-MS	3 lmn	MR	4 ghıj	MR-MS
103	5 cde	MR-MS	5 bcd	MR-MS	3 cde	MR	6 abcd	MR-MS	4 jkl	MR-MS	4 ıjk	MR-MS
104	3 efg	MR	3 de	MR	2 fgh	R-MR	5 defg	MR-MS	3 klm	MR	2 o	R-MR
105	5 cde	MR-MS	7 ab	MS	5 bcd	MR-MS	7 a	MS	6 efg	MR-MS	4 ıjk	MR-MS
106	5 bcd	MR-MS	5 bc	MR-MS	5 abc	MR-MS	7 a	MS	5 fgh	MR-MS	2 mno	R-MR
107	3 def	MR	3 cde	MR	3 cde	MR	7 ab	MS	6 cdef	MR-MS	4 ıjk	MR-MS
CV%	9.41%		9.98%		9.58%		5.16%		4.46%		5.53%	

**P. teres* f. *maculata* scale values: 1= R: resistant, 2= R: resistant to MR: moderately resistant, 3= MR: moderately resistant, 5= MR: moderately resistant to MS: moderately susceptible, 7= MS: moderately susceptible, 8= MS: moderately susceptible to S: susceptible, 9= S: susceptible. ***P. teres* f. *teres* scale values: 1= R: resistant, 2= R: resistant to MR: moderately resistant, 3= MR: moderately resistant, 4= MR: moderately resistant to MS: moderately susceptible, 5= MR: moderately resistant to MS: moderately susceptible, 6= MR: moderately resistant to MS: moderately susceptible, 7= MS: moderately susceptible, 8= MS: moderately susceptible to S: susceptible, 9= S: susceptible, 10= VS: very susceptible

H. spontaneum and 300 *H. vulgare* accessions were evaluated for their resistance status to *P. teres* under greenhouse and field conditions. *H. spontaneum* genotypes exhibited different resistance reactions and 143 genotypes showed resistant reaction to all isolates. Fetch et al (2003) determined the diversity of 116 *H. spontaneum* genotypes for their reaction to six barley fungal pathogens. The genotypes were obtained from Israel and Jordan. At seedling stage, a high level of diversity was found. Resistance frequency of genotypes from Israel and Jordan was high for net blotch (68% and 72%, respectively). Two genotypes were found resistant to 6 pathogens. Similarly, in our current study variation was found among the *H. spontaneum* genotypes. In our study, six *H. spontaneum* genotypes showed resistant to moderately resistant reactions to all *Ptt* and *Ptm* isolates. Jana & Bailey (1995) determined the resistance status of *H. vulgare* subsp. *spontaneum* and *H. vulgare* subsp. *vulgare* genotypes from Jordan and Turkey to *P. teres* f. *maculata, P. teres* f. *teres* and *Cochliobolus sativus.* More *H. vulgare* subsp. *spontaneum* genotypes were resistant to *P. teres* f. *teres* (21.8% vs. 0.5%) than *H. vulgare* subsp. *vulgare*. An equal number of *H. vulgare* subsp. *spontaneum* and *H. vulgare* subsp. *vulgare* genotypes were resistant to *P. teres* f. *maculata*. A larger percentage of *H. vulgare* subsp. *spontaneum* genotypes (10.5%) had at least moderate resistance to *P. teres* f. *teres*, *P. teres* f. *maculata* and *C. sativus* compared to only 1.3% in *H. vulgare* subsp. *vulgare*. However, in our current study, 25% of the genotypes and 7.6% of the genotypes exhibited resistant group reactions to *P. teres* f. *maculata* and *P. teres* f. *teres*, respectively. This finding is hopeful, because *P. teres* f. *maculata* is more prevalent in Turkey than *P. teres* f. *teres* (Karakaya et al 2014). *H. spontaneum* accessions showed different resistance reactions, depending upon their origin. Sato & Takeda (1997) evaluated net blotch resistance in 175 *H. vulgare* subsp. *spontaneum* (*H. spontaneum*) accessions and 149 wild *Hordeum* accessions of thirteen species or subspecies. Most *H. spontaneum* accessions showed resistance to each of the four *P. teres* f. *teres* isolates (Japanese isolates K105 and Pt860514 and Canadian isolates WRS102 and WRS1581) tested. Some accessions from Russia and Afghanistan showed a high level of resistance and Morocco accessions were susceptible. *H. spontaneum* accessions susceptible to the Canadian isolate WRS102 but resistant to the other three isolates were found in Iraq. This suggested the geographical differentiation of resistance genes in *H. spontaneum*. All accessions of the other wild *Hordeum* species, especially some accessions of *H. marinum* subsp. *gussoneanum*, showed high levels of resistance. Sato & Takeda (1997) concluded that resistance genes may be useful candidates for incorporation into cultivated barley.

H. spontaneum is a rich source of genes for disease resistance. Many resistant barley genotypes were found in barley evolution centers (Afanasenko et al 2000). Suitable habitat conditions for *H. vulgare* subsp. *spontaneum* exist especially in the Levant and Turkey and genetic diversity was observed in these populations (Jakob et al 2014). Turkey is an important gene center of barley and wild barleys (Kün 1996). Karakaya et al (2016) examined a total of 40 naturally growing *H. spontaneum* field populations in Şanlıurfa, Mardin, Şırnak, Siirt, Diyarbakır, Gaziantep, Kilis and Hatay provinces of Turkey for the presence of diseases and their severities in 2015. Nine *H. spontaneum* populations were disease free. The following diseases were found: Scald incited by *Rhynchosporium commune*, powdery mildew incited by *Blumeria graminis* f. sp. *hordei*, both forms of net blotch incited by *Drechslera teres* f. *teres* and *D. teres* f. *maculata*, semi loose smut incited by *Ustilago nigra*, loose smut incited by *Ustilago nuda*, brown rust (leaf rust) incited by *Puccinia hordei* and barley stripe caused by *Drechslera graminea*. Scald was the most commonly encountered disease followed by powdery mildew and net blotch. The incidence and severity values of diseases varied. The authors reported a wide range of variation in terms of disease resistance status of naturally growing *H. spontaneum* populations.

4. Conclusions

The use of disease resistant cultivars is the desirable control method of diseases. For sustainable crop production, monitoring virulence changes in pathogen is necessary. New pathotypes could be more virulent than previous pathotypes. For this reason, a broad base of genetical source is necessary. Wild barleys and especially *H. spontaneum* are valuable sources for disease resistance. Useful traits including disease resistance could be transferred to barley cultivars. Nevo (1992) pointed out the importance of *H. spontaneum* for disease resistant barley breeding programs and for developing a gene pool for desired traits. Also, Nevo et al (1986) examined the *H. spontaneum* populations of Israel, Turkey and Iran in the Fertile Crescent and reported their genetic diversity as well as their adaptability. Turkey is an important gene center of *Hordeum* species (Kün 1996). *Hordeum spontaneum* populations are naturally growing in Turkey and heterogenous nature of disease resistance among the populations has been reported (Karakaya et al 2016).

With this study, novel wild barley (*H. spontaneum*) genotypes resistant to both forms of *Pyrenophora teres* have been identified. These genotypes could be used in obtaining disease resistant and high yielding barley cultivars.

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