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ORIGINAL PAPER

Resistance to stripe rust in Turkish durum wheat varieties and wild emmer genotypes

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Abstract

Stripe or yellow rust caused by *Puccinia striiformis* f. sp. *tritici* (*Pst*) is the most important disease of wheat causing significant yield losses. Growing resistant varieties is the most efficient and sustainable way to control this disease. The aim of this study was to investigate molecularly the presence or absence of the major resistance genes *Yr5*, *Yr10* and *Yr15* to stripe rust in 54 Turkish durum wheat (*Triticum turgidum* var. *durum*) varieties and 11 wild emmer (*Triticum turgidum* var. *dicoccoides*) genotypes. In addition, field trials were conducted during 2019–2020 under natural epidemic conditions in Antalya to determine phenotypic reactions of these genotypes against stripe rust. As a result of molecular analyses, none of the 54 durum wheat varieties had *Yr5* resistance gene; however, the resistance genes *Yr10* and *Yr15* were determined in 12 and 17 varieties, respectively. Moreover, 7 of these varieties had both *Yr10* and *Yr15* genes. None of 11 wild emmer accessions had resistance genes examined. It was also determined that 28 varieties had resistant reaction to *Pst* race(s) under natural infection conditions whereas all wild emmer accessions were highly susceptible. This is the first study to identify major *Yr*-genes in Turkish durum wheat varieties and, therefore, these findings can be beneficial in wheat breeding programs to be conducted for resistance to stripe rust.

Keywords Durum wheat · Yellow rust · *Puccinia striiformis* f. sp. *tritici* · Resistance genes · Molecular detection

Introduction

Wheat (*Triticum* L.) is widely grown among the cereals with 215.9 million hectares and a total production of 766 million tons worldwide (FAO 2020) due to its wide adaptability and main energy source in human nutrition. In addition, wheat provides substantial amounts of a number of components, which are essential for health, especially protein, vitamin B, dietary fibers, and minerals. In Turkey, it is grown on an area of 6.9 million hectares with a total production of 20.5 million tons. Three million tons of this production belongs to durum wheat (*Triticum turgidum* var. *durum*) (TUIK 2020).

Wheat production can be negatively affected by many biotic and abiotic stress factors. Among the biotic stresses, yellow rust caused by *Puccinia striiformis* f.sp. *tritici* (*Pst*) is a destructive disease of wheat in many regions of the world and can cause significant yield losses during severe epidemics, especially in humid, temperate, and cool environments (Schwessinger 2017). Stripe rust epidemics have occurred every 2 of 5 years in over 25% of the wheat growing areas of some countries including Canada, Russia, Kazakhstan, Iran, Iraq, Turkey, etc. (Chen 2020). In 1991, serious yield loss due to yellow rust occurred up to 62.5% in the Seri-82 variety containing *Yr*9 resistance gene which was widely cultivated in coastal regions of Turkey (Braun and Saari 1992; Mamluk et al. 1997). In the following years, Düşünceli et al. (1999) reported that yield loss between 26.5 and 50% due to yellow rust epidemic was recorded in Central Anatolia region of Turkey. Furthermore, severe epidemics have continued to occur in Turkey in recent years (Cat et al. 2021).

Pst is highly aggressive and unstable and new *Pst* races derived from mutation, somatic recombination and sexual production can break the resistance genes (Schwessinger 2017). In order to develop resistance to

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yellow rust disease in wheat, many studies are carried out to identify *Pst* races and resistance genes. More than 80 resistance genes to stripe rust have been characterized in wheat (McIntosh et al. 2020). Many of the *Yr* genes have been identified as race-specific, so these genes provide resistance only against *Pst* isolates carrying the avirulence gene (Goutam et al. 2015). Many resistance genes have also been introgressed from different wild species into bread wheat (Kuraparthy et al. 2007; Chhuneja et al. 2008). Although the majority of these resistance genes are generally identified in a hexaploid background, the major resistance genes *Yr5*, *Yr10* and *Yr15* were characterized on genome B. The *Yr5* gene was first identified in 1966 in *Triticum spelta* var. album and Macer (1966) localized it on chromosome 2B. The *Yr10,* known as race-specific gene, is derived from a Turkish wheat line (PI 178383) and many studies showed that this gene was located on chromosome 1B (Metzger and Silbaugh 1970; Payne et al. 1986). Lastly, the *Yr15* gene was first identified in a wild emmer (*Triticum dicoccoides* Korn) accession G-25 (Gerechter-Amitai et al. 1989) and McIntosh and Silk (1996) showed that it is located on the short arm of chromosome 1B.

The deployment of genetically resistant varieties is the most effective and economically sound approach to control stripe rust. One of the best strategies to improve resistance to stripe rust is to utilize the genetic resources of the wild relatives including wild emmer wheat (*Triticum turgidum* var. *dicoccoides*) (Peng et al. 2011). Wild emmer has a wide range genotypic variation in many important traits like stripe rust resistance (Tene et al. 2022). In addition to *Yr15*, *Yr36* as one of the important resistance genes was first identified in wild emmer (Uauy et al. 2005). At the same time, it is fully compatible with durum wheat and can be easily crossed with bread wheat. Genetic advances in wheat to date have generally relied on breeding activities within a relatively narrow gene pool (Hao et al. 2019). Since this gene pool has also a narrow genetic base for resistance to rust diseases (Olivera et al. 2018), wild emmer genotypes are worth screening for presence of other *Yr* resistance genes.

Molecular markers for resistance genes *Yr5*, *Yr10* and *Yr15* have been widely used in wheat breeding programs worldwide (Zeng et al. 2014; Zheng et al. 2017). In particular, *Yr5* and *Yr15* are still effective against the Turkish *Pst* races (Sharma-Poudyal et al. 2013; Cat et al. 2021). The aim of the present study was to detect the *Yr5*, *Yr10* and *Yr15* resistance genes in 54 Turkish durum wheat varieties and 11 wild emmer genotypes at molecular level. Additionally, field trials were conducted during 2019-2020 under natural epidemic conditions in Antalya to determine phenotypic reactions of these genotypes against stripe rust.

Materials and methods

Genetic material

A total of 54 durum wheat (*Triticum turgidum* var. *durum*) varieties registered in Turkey and 11 wild emmer (*Triticum turgidum* var. *dicoccoides*) genotypes supplied from Turkish Gene Bank were used as genetic material in this study (Table S1). Durum wheat varieties were registered from 1963 to 2012. In addition, three positive control lines, AvsNILYr5, AvsNILYr10 and AvsNILYr15, were used to confirm whether the genotypes carry the *Yr5*, *Yr10* and *Yr15* genes or not.

Field testing under natural infection conditions

Field tests were conducted in the cropping seasons of 2019 and 2020 under natural infection conditions at the experimental station of the Akdeniz University, Antalya. The seeds of each genotype were sown as two rows with 100 cm long and susceptible bread wheat variety "Morocco" was also sown as spreader in two rows for every 10 rows and around the plots to increase disease pressure. The trials were sprinkler-irrigated to guarantee a moist environment for high pathogen development. The top three leaves were visually scored thrice at late booting (Z45), heading (Z55) and dough stages (Z65), respectively (Zadoks et al. 1974) as Morocco plants reached 70% infection at least. Infection type (IT) and disease severity (DS) were evaluated using a Modified-Cobb scale (Peterson et al. 1948). In addition, IT and DS data were combined into a single value called the coefficient of infection (CI) to rank or easily compare the genotypes. CI was calculated by multiplying IT and DS for each genotype as described by Roelfs et al. (1992). The highest IT and DS values observed at dough stages (Z65) were used to calculate CI: where R= 0.2, MR= 0.4, MS= 0.8, and S=1.0.

DNA extraction, PCR amplification and electrophoresis

At least three seeds of each variety were sown in pots (7 × 7 × 10 cm) with mixture of soil and peat in 1:1 ratio and fresh leaves were collected from seedlings of each variety at two-leaf stage. Genomic DNAs were extracted using the CTAB method (Doyle and Doyle 1990). Quality of genomic DNAs was checked by the agarose gel electrophoresis and stored until use at -20 ℃. To detect resistance genes, different molecular markers developed by Chen et al. (2003), Singh et al. (2009) and Murphy et al. (2009) were used. Information about these markers is given in Table 1. Polymerase chain reactions (PCR) were performed in a thermal

Table 1 The information about molecular markers used in this study

Yr gene	Primer	Annealing Temp. (°C)	Primer sequence (5'→3')
Yr5	STS-7	45	GTACAATTCACCTAGAGT
	STS-8		GCAAGTTTTCTCCCTATT
Yr10	*Yr10* F	64	TCAAAGACATCAAGAGCCGC
	Yr10 R		TGGCCTACATGAACTCTGGAT
Yr15	Xbarc8-R	50	GCGGGGGCGAAACATACACATAAAAACA
	Xbarc8-F		GCGGGAATCATGCATAGGAAAACAGAA

cycler (T100, Bio-Rad, USA). The total volume of the reaction mixture was 15 µL containing 1X PCR buffer (50 mmol KCl, 10 mmol Tris-HCI, pH 8.3) (Thermo Fisher Scientific, USA), 2.0-2.5 mM $MgCl_2$ (Thermo Fisher Scientific, USA), 0.2 mM of dNTP (Thermo Fisher Scientific, USA), 0.75 U of Taq DNA polymerase (Thermo Fisher Scientific, USA), 0.4–1.0 µM of each primer and 100 ng of template DNA.

Amplifications were performed under the following conditions for *STS7/8*: initial denaturation at 94 °C for 5 min, followed by 45 cycles (each consisting of 30 s at 94 °C, 30 s at 45 °C, 45 s at 72 °C), final extension for 10 min at 72 °C; for *Yr10F/R*: initial denaturation at 94 °C for 4 min, followed by 35 cycles (each consisting of 30 s at 94 °C, 30 s at 64 °C, 1 min at 72 °C), final extension for 10 min at 72 °C and lastly for *Xbarc8*: initial denaturation at 94 °C for 4 min, followed by 40 cycles (each consisting of 30 s at 94 °C, 30 s at 50 °C, 1 min at 72 °C), final extension for 10 min at 72 °C.

Amplified PCR products with the pairs STS7/8 were digested with the restriction enzyme *DpnII* (New England Biolabs, USA) (Chen et al. 2003). The total volume of reaction mixture for enzymatic digestion was 15 µL containing 8 µL of PCR product, 0.25 µL *DpnII*, 2 µL of 10× NEBuffer and 4.75 µL distilled water. Enzymatic digestion was performed in a thermo-shaker (Biosan, Latvia) under the following conditions: 37 ℃ for 1h, 65 ℃ for 20 min and holding at 10 ℃ for 5 min and the digested products were separated in 2% agarose gel stained with 0.5 µg/mL ethidium bromide with 85 V for 1 h. The fragments were visualized under UV light using a gel imaging system (UVP UVsolo touch, Analytik Jena, Germany).

Results

Evaluation of tetraploid wheat genotypes for stripe rust resistance at adult plant stage

The 54 durum wheat varieties and 11 wild emmer genotypes were evaluated for stripe rust resistance at adult plant stage. Infection types and severity of stripe rust disease were recorded during 2019 and 2020 growing seasons and data are given in Tables 2 and 3. According to the observations in 2019, 45 varieties showed resistance reaction ranging from trace (TR) to moderately resistant (MR) and disease severity was observed with varying intensities from 0 to 10%. Unlike this, 9 varieties were highly susceptible with disease severities ranging from 5 to 40% (Table 2). However, all wild emmer genotypes showed a high level of susceptible reaction and disease severity ranged from 70 to 100% (Table 3). Based on IT and DS for each genotype, coefficient of infection (CI) was calculated. While the highest CI values were determined in the varieties Kunduru 414/44 and Eyyubi, 35 varieties had the lowest CI with zero (Table 2). Akbaşak 073/144, Sarıçanak 98, Altıntoprak 98, Gediz-75, Pınar-2001 and Zenit had also the low CI values. Unlike these, CI values determined in wild emmer genotypes ranged from 70 to 100 (Table 3).

In 2020 growing season, unfavorable weather conditions such as high temperature and low humidity limited the pathogen development, and no disease symptoms were observed on durum wheat varieties. However, wild emmer genotypes showed susceptible reaction ranging from 40 to 70% with moderately susceptible (MS) to susceptible (S) and therefore CI values were determined between 24 and 70 (Table 3).

Identification of the resistance genes Yr5, Yr10 and Yr15 in tetraploid wheat genotypes

The 54 registered durum wheat varieties and 11 wild emmer genotypes were analyzed for the stripe rust resistance genes *Yr5*, *Yr10* and *Yr15* using linked molecular markers shown in Table 1. After enzymatic digestion, genotypes with *Yr5* yielded 308 bp fragment as expected, whereas non-*Yr5* genotypes had 181 bp fragment. The dominant marker *Yr10F/R* produced 543 bp fragment in genotypes with *Yr10*. In addition, the genotypes with *Yr15* had 250 bp fragment and non-*Yr15* genotypes yielded 280 bp. Sample electrophoretograms of different markers linked to *Yr5*, *Yr10* and *Yr15* are given in Figure S1.

According to these data, *Yr5* was not detected in all tested genotypes. While *Yr10* was detected in 12 durum wheat varieties (Berkmen 469, Çakmak 79, Kızıltan 91, Altın 40/98, Yılmaz 98, Çeşit-1252, İmren, Kunduru 1149, Altıntaş 95, Dumlupınar, Selçuklu-97 and Sham-1), none of wild emmer

Table 2 Disease severity (DS), infection type (IT) and coefficient of infection (CI) values on durum wheat varieties in 2019, and identification of resistance gene(s) using molecular markers

No	Varieties	DS	IT*	CI	Resistance gene**			No	Varieties	DS	IT*	CI	Resistance gene**		
					Yr5	*Yr10*	*Yr15*						*Yr5*	*Yr10*	*Yr15*
1	Akbaşak 073/144	5	R	1				28	Fırat-93	20	MS	12			
2	Kunduru 414/44	40	S	40				29	Artuklu	0	TR	0			
3	Berkmen 469	30	S	30		+	+	30	Eyyubi	40	S	40			
4	Çakmak 79	0	R	0		+		31	Şahinbey	0	TR	0			
5	Kızıltan 91	0	R	0		+	+	32	Zühre	10	MR	4			
6	Altın 40/98	0	R	0		+	+	33	Güney Yıldızı	0	TR	0			
7	Yılmaz 98	0	R	0		+	+	34	Gediz-75	5	R	1			
8	Ankara 98	0	R	0				35	Ege 88	0	R	0			
9	Çeşit-1252	0	R	0		+	+	36	Salihli 92	0	TR	0			
10	Mirzabey 2000	0	R	0			+	37	Şölen 2002	10	MR	4			+
11	Eminbey	0	TR	0			+	38	Tüten 2002	0	R	0			
12	İmren	0	TR	0		+	+	39	GAP	0	TR	0			
13	Kunduru 1149	0	TR	0		+	+	40	Turabi	20	MS	12			
14	Altıntaş 95	0	TR	0		+		41	Sham-1	10	MS	6		+	
15	Kümbet 2000	0	R	0				42	Amanos-97	10	R	2			
16	Yelken 2000	5	MS	3				43	Fuatbey 2000	0	TR	0			
17	Dumlupınar	0	R	0		+		44	Sarı Başak	0	TR	0			
18	Fata Sel	0	R	0			+	45	Akçakale-2000	0	TR	0			
19	Selçuklu-97	10	MS	6		+		46	Gündaş	0	R	0			
20	Meram-2002	0	TR	0			+	47	Özberk	0	TR	0			
21	Tunca 79	30	S	30			+	48	Pınar-2001	5	MR	1			+
22	Gökgöl 79	10	MR	4			+	49	Zenit	5	MR	1			
23	Diyarbakır-81	0	TR	0				50	Svevo	0	R	0			+
24	Ceylan 95	0	TR	0				51	Levante	0	R	0			
25	Sarı çanak 98	5	R	1				52	Saragolla	0	R	0			
26	Altın toprak 98	5	R	1				53	Maestrale	0	R	0			+
27	Aydın-93	0	TR	0				54	Bisante	0	TR	0			

*TR: trace, R: resistant, MR: moderately resistant, MS: moderately susceptible, S: susceptible.

**+: presence of resistance gene.

Table 3 Disease severity (DS), infection type (IT), and coefficient of infection (CI) values on 11 wild emmer genotypes, and identification of resistance gene(s) using molecular markers

No	Genotype	2019			2020			Resistance gene		
		DS	IT*	CI	DS	IT*	CI	*Yr5*	*Yr10*	*Yr15*
1	TGB 000777	70	S	70	50	MS	30	–	–	–
2	TGB 000791	70	S	70	40	MS	24	–	–	–
3	TGB 000792	100	S	100	70	S	70	–	–	–
4	TGB 038501	100	S	100	70	S	70	–	–	–
5	TGB 045861	100	S	100	60	S	60	–	–	–
6	TGB 045871	80	S	80	60	S	60	–	–	–
7	TGB 045910	100	S	100	70	S	70	–	–	–
8	TGB 045911	100	S	100	70	MS	42	–	–	–
9	TGB 045912	80	S	80	60	MS	36	–	–	–
10	TGB 045913	100	S	100	50	MS	30	–	–	–
11	TGB 045920	100	S	100	70	S	70	–	–	–

*MS: moderate susceptible, S: susceptible

**: absence of resistance gene

genotypes had *Yr10* gene. Additionally, *Yr15* gene was determined in 17 durum wheat varieties (Berkmen 469, Kızıltan 91, Altın 40/98, Yılmaz 98, Çeşit-1252, Mirzabey 2000, Eminbey, İmren, Kunduru 1149, Fata (Sel), Meram-2002, Tunca 79, Gökgöl 79, Şölen 2002, Pınar 2001, Svevo and Maestrale) (Table 2).

Considering all molecular results, none of wild emmer genotypes had resistance genes examined (Table 3). However, 7 durum wheat varieties (Berkmen 469, Kızıltan 91, Altın 40/98, Yılmaz 98, Çeşit-1252, İmren and Kunduru 1149) carry both *Yr*10 and *Yr*15 resistance genes (Table 2).

Discussion

In this study, we evaluated resistance reactions of Turkish durum wheat varieties and wild emmer genotypes to stripe rust disease under natural infection conditions, and these genotypes were also molecularly screened to investigate presence of major *Yr* genes. With the genotypic studies, we show that seven durum wheat varieties carry both *Yr10* and *Yr15* resistance genes (Table 2). In phenotypic studies, for durum wheat varieties, we recorded more meaningful data only in 2019 growing season (Table 2); however, unfavorable weather conditions such as high temperature and low humidity limited the pathogen development, and no disease symptoms were observed on durum wheat varieties in 2020 growing season.

Growing resistant varieties is the most efficient and sustainable approach to control the wheat stripe rust disease. In general, this disease caused by *Puccinia striiformis* f. sp. *tritici* can be controlled with *Yr5* and *Yr15* resistance genes worldwide (Sharma-Poudyal et al. 2013; Ali et al. 2018). Additionally, although the prevalence of virulent races to the *Yr10* gene was increasing (Afshari 2013; Gharbarnia et al. 2021; Cat et al. 2021), this gene has still provided resistance to many races in the world (Sharma-Poudyal et al. 2013).

It is known that especially the *Yr*5 gene is used in the development of new varieties resistant to stripe rust disease in wheat breeding programs (Sun et al. 2002; Murphy et al. 2009; Zhang et al. 2022). Although *Yr5* and *Yr15* have been still known to be effective to *Pst* races at global level, several races virulent to *Yr5* have been reported in India (Nagarajan 1986), Australia (Wellings and McIntosh 1990) and most recently in China (Zhang et al. 2020), Syria (Kharouf et al. 2021) and Turkey (Tekin et al. 2021). Additionally, it has been known that number of genotypes carrying these major resistance genes in wheat genetic germplasm are quite low. Tabassum et al. (2010) reported that the *Yr*5 resistance gene was not detected in any of the 100 cultivars registered in Pakistan. Huang et al. (2019) also reported that none of 53 Hungarian wheat cultivars had the major resistance genes *Yr5*, *Yr10* and *Yr15*. Zeng et al. (2014) indicated that there were only two genotypes (0.4%) carrying *Yr5* resistance gene among 494 wheat germplasm in China. In another study, Li et al. (2016) determined that 5 (4.3%) of 115 wheat cultivars in China carry *Yr*5 resistance gene (Li et al. 2016). The results obtained from the mentioned studies related to the *Yr5* resistance gene are in agreement with our findings that *Yr5* resistance gene is not found among durum wheat varieties. On the other hand, these frequencies related to presence of *Yr5* are not consistent with the frequency reported by Mukhtar et al. (2015), who stated that 14 (35.9%) among a total of 39 wheat cultivars and breeding lines had resistance gene *Yr*5.

Similar to the *Yr5* gene, there is no study investigating the presence of the *Yr10* and *Yr15* genes in durum wheat varieties in Turkey. However, many studies were conducted to detect these genes in wheat germplasm in many regions of the world. Zheng et al. (2017) reported that 16.67% of breeding lines, 38.82% of landraces and 13.57% of modern varieties in China carry the *Yr10* resistance gene. Contrary to this, Zeng et al. (2014) stated that none of the 494 Chinese wheat entries have *Yr10* and *Yr15*. Gebreslasie et al. (2020) also reported that none of the Ethiopian wheat varieties and breeding lines have *Yr5*, *Yr8*, *Yr10* and *Yr15*. Similarly, Tabassum et al. (2010) showed that none of the 100 Pakistani wheat cultivars have *Yr15* resistance gene. Considering all these studies, it is very promising that the *Yr10* gene was found in 12 and the *Yr15* gene in 17 durum wheat cultivars in Turkey (Table 2). In addition, it was determined that the varieties Berkmen 469, Kızıltan 91, Altın 40/98, Yılmaz 98, Çeşit-1252, İmren and Kunduru 1149 have both *Yr10* and *Yr15* genes. However, none of wild emmer genotypes had resistance genes examined (Table 3).

On the other hand, in field testing, it was found that most of the tested varieties showed resistance reactions to stripe rust, while only 9 varieties were susceptible (Table 2). As we mentioned above, due to unfavorable weather conditions, no disease symptoms were observed on durum wheat varieties in 2020 growing season. However, all wild emmer genotypes had susceptible reactions in both years (Table 3). As mentioned above, frequencies of major *Yr* genes and gene combination (*Yr10*+*Yr15*) examined in this study were quite low among durum wheat varieties. However, most varieties were observed to be phenotypically resistant against *Pst* race(s) under natural infection conditions as given in Table 2. These varieties can have other *Yr* genes not examined in this study, effective to *Pst* race(s), except for the *Yr5*, *Yr10*, and *Yr15*. Moreover, it is considered that the combination of genes conferring partial resistance may provide resistance to *Pst* race(s). Zheng et al. (2017) reported that the number of pyramided *Yr* genes positively correlated with *Pst* resistance ($R^2 > 0.8$, $p < 0.01$) based on field resistance evaluation, and significant additive effects were observed in some

gene combinations such as *Yr9+Yr18* and *Yr30+Yr46*. On the other hand, some varieties with *Yr10* (Selçuklu 97, Sham-1) or the combination *Yr10+Yr15* (Berkmen 469) gave surprisingly susceptible reactions (Table 2). In such studies carried out under natural infection conditions, the virulence formula of the races infecting the genotypes is not known since race analysis was not performed. Cat et al. (2021) first detected *Yr10*-virulent races with moderate frequency (25%) in the coastal regions of Turkey where this study was also conducted. Therefore, susceptible genotypes with *Yr* gene/gene combinations may have been infected by more than one *Pst* races or *Yr10*-virulent races. It is considered that the phenotypical differences between resistant varieties without *Yr5, Yr10, Yr15* genes and susceptible varieties carrying *Yr10* and/or *Yr15*, may have resulted from these factors.

It is known that the *Yr10* was derived from a Turkish wheat line (PI 178383) (Metzger and Silbaugh 1970) and the *Yr15* gene was first identified in a wild emmer accession G-25 (Gerechter-Amitai et al. 1989). Ozkan et al. (2002) stated that wild emmer domesticated from western Fertile Crescent including southeastern Turkey. Therefore, it is considered that there is a wide variation in wild emmer accessions for many important traits like stripe rust resistance. However, it was determined that none of 11 wild emmer genotypes had resistance genes in this study. This finding is supported by He et al. (2020), who reported that only 13.6% of 361 wild emmer accessions was positive for the *Yr15* gene-specific markers, and 21 accessions from Lebanon, Syria, and Turkey populations were *Yr15* negative. In durum wheat production, southeastern region of Turkey ranks first among the regions with approximately 1.6 million tons (TUIK 2020). In this region, many wild relatives of cereals such as *Aegilops* spp. and *Hordeum* spp. distribute naturally (Özkan et al. 2020), and these are known as super spreaders of wheat stripe rust pathogen (Tekin et al. 2020). Therefore, susceptible wild emmer accessions like these wild relatives have also the potential to be super-spreading and threaten durum wheat production in western Fertile Crescent including Turkey, Lebanon, Jordan, Syria, and Israel.

To sum up, this is the first report to identify major *Yr*-genes in Turkish durum wheat varieties and wild emmer genotypes. None of durum wheat varieties had *Yr5* gene but seven durum wheat varieties have both *Yr10* and *Yr15* genes. The pedigrees of these varieties, containing resistance gene(s), (Table S1) show that old durum wheat landraces such as Üveyik, Berkmen 469 and Kunduru 414/44 are one of the common parents of them. It is considered that these parents and varieties containing both *Yr10* and *Yr15* genes can be used in breeding studies to be conducted for resistance to stripe rust. Additionally, much attention should be paid to the role of susceptible wheat genotypes in stabilization of the *Pst* races and the spread of new *Pst* races from susceptible wild relatives.

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Author contributions EI, MT and AC were involved in the formal analysis. EI performed investigation. MT and TA were involved in conceptualization and writing—review and editing. MT and AC were involved in validation and writing—original draft. AC performed methodology. TA was involved in supervision.

Declarations

Conflict of interest The authors declare that they have no conflicts of interest.

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