International Journal of Agriculture, Forestry and Life Sciences 2026; 10 (1): 42-48 Research Article
https://doi.org/10.66598/ijafls.1915038 https://izlik.org/JA42CU53LS

ASSESSMENT OF SEEDLING RESISTANCE TO CROWN ROT CAUSED BY *Fusarium culmorum* IN DIVERSE WHEAT GENOTYPES

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Received: March 30, 2026 | **Accepted:** April 17, 2026 | **Published Online:** May 22, 2026

ABSTRACT

Fusarium culmorum is one of the most destructive species causing root, crown, and basal rot in wheat. Crown rot (CR), primarily caused by *Fusarium culmorum*, remains a significant biotic constraint to wheat productivity globally, which requiring the identification of robust genetic resistance. Despite extensive screening efforts to date, only a limited number of wheat genotypes have been identified as resistant. This study was conducted to identify novel sources of resistance to *Fusarium culmorum* among wheat genotypes at both the seedling stages. In this study, two distinct bread wheat panels totaling 601 genotypes (comprising 300 and 301 accessions, respectively) obtained from the International Center for Agricultural Research in the Dry Areas (ICARDA) were evaluated for seedling resistance to *Fusarium culmorum* under controlled growth room conditions. The analyses revealed that the number of moderately susceptible (MS) genotypes was high, while resistant genotypes and highly susceptible (VS) genotypes were not observed. According to the data obtained, one genotype (#12) from set 1 and six genotypes (83, 182, 185, 201, 208, 222) from set 2 were found to be moderately resistant (MR). The analysis revealed that the moderately resistant genotypes observed could be used in breeding programmes aimed at developing varieties resistant to crown rot.

Keywords: *Fusarium culmorum* | bread wheat | disease resistance | root and crown rot

INTRODUCTION

Wheat (*Triticum aestivum* L.) is one of the most important staple crops, meeting approximately 55% of the daily carbohydrate requirement and 20% of the daily energy intake for about 40% of the world's population (Tanane et al., 2026). Türkiye ranks among the world's largest wheat-producing countries (FAO, 2026). In 2024, wheat was cultivated on 219,518,805 hectares worldwide, with a total production of 798,481,711.07 tonnes (FAO, 2026). In Türkiye, 7,023,807.8 hectares of land were planted with wheat in the same year, and total production amounted to 20,800,000 tonnes (TÜİK, 2026). Wheat consumption is steadily increasing due to population growth, urbanisation, rising income levels, diversity in dietary habits, and the rapid spread of wheat-based foods. (Yasmin and Moniruzzaman., 2026). However, approximately 20% of wheat production is lost due to diseases and pests (Boulahouat et al., 2026). Soil-borne pathogens are one of the primary biotic factors limiting wheat production worldwide. The decay of the root system and stem base, plant wilting, and a reduction in both vegetative and grain weight are among the primary symptoms induced by soil-borne fungi. The most important fungal genera that can cause root rots in wheat are *Fusarium* spp. and *Bipolaris* spp. (Lupaşcu et al., 2025).

Crown rot is the generally accepted name when *Fusarium* spp. are dominant members of the complex and common root rot describes the complex when *B. sorokiniana* is dominant. Other names used includes dryland foot rot, dryland root rot, foot rot, *Fusarium* crown rot, and *Fusarium* root rot (Smiley, 2005). In addition, many pathogens *Fusarium* spp. actively produce the mycotoxin, leading to grain contamination and increased toxicity. All these symptoms weaken plants and cause significant yield losses, posing a serious food safety and health risk to domestic animals and natural ecosystems. Furthermore, grain germination is negatively affected, and the technological quality of flour products decreases (Lupaşcu et al., 2025) and (Boulahouat et al., 2026). *Fusarium culmorum* is a predominant pathogen responsible for seedling blight, root and crown rot, *Fusarium* Head Blight (FHB), and the subsequent accumulation of mycotoxins in wheat. The main mycotoxins produced by *F. culmorum* are deoxynivalenol, nivalenol and zearalenone; these toxins pose a potential health risk to both humans and animals (Lupaşcu et al., 2025).

Citation: Türkmen, A., Ayter Arpacıoğlu, N.G., Dababat, A.A., Tadesse, W., Erginbaş Orakçı, G. (2026). Assessment of Seedling Resistance to Crown Rot Caused by Fusarium Culmorum in Diverse Wheat Genotypes. International Journal of Agriculture, Environment and Food Sciences, 10 (1): 42–48. https://doi.org/10.66598/ijafls.1915038
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Infections at the root collar and stem base during the seedling stage cause discolouration ranging from brown to reddish at the root collar and stem base; this is often accompanied by the strengthening of cell walls through lignification as a defence response by the host plant. However, this defence response cannot completely halt the progression of the disease (Tanane et al., 2026). Root infections, on the other hand, are characterised by brown or reddish-brown lesions extending along the root axis, caused by the same pathogens affecting the root collar and stem base. Root infection results in symptoms such as root necrosis, honey-coloured browning at the tillering node, white head formation, reduced tillering, and premature ageing (Smiley et al., 2005, Tanane et al., 2026,). *Fusarium* crown rot (FCR) is a devastating soil-borne disease prevalent in major semi-arid wheat-producing regions, with significant yield losses documented across Australia, North America (USA and Canada), and the West Asia and North Africa (WANA) region, including Egypt, Tunisia, Morocco, Algeria, and Türkiye (Smiley et al., 2005; Tunali et al., 2008; Chakraborty et al., 2010). Documented yield losses fluctuate depending on environmental conditions and host susceptibility, ranging from 3% to 35% in the Pacific Northwest of the USA (Smiley et al., 2005) to as high as 89% in Australia (Daniel & Simpfendorfer, 2014), while across the West Asia and North Africa (WANA) region and Türkiye, reductions between 10% and 43% are frequently reported (Tunali et al., 2008; Erginbas-Orakci et al., 2016). Developing high-yielding cultivars with robust host resistance is the primary objective for managing soil-borne diseases in dryland production systems. Current control strategies for *Fusarium*, such as chemical fungicides, crop rotation practices, the use of resistant varieties, and biological control agents, have various limitations in terms of efficacy, cost, and environmental impact. Furthermore, to date, no wheat variety with complete resistance to this disease has been developed, and the efficacy of fungicide applications is around 70%. Therefore, innovative and sustainable methods incorporating integrated control approaches are needed to manage *Fusarium* and reduce mycotoxin contamination (Buivydaitė et al., 2026) and (Lupaşcu et al., 2025). The im of this study was to characterize novel sources of resistance to *Fusarium culmorum* within a diverse set of bread wheat genotypes, providing elite germplasm that can be directly integrated into national and international breeding programs worldwide.

MATERIALS AND METHODS

The research was conducted at the CIMMYT-Türkiye facilities within the Transitional Zone Agricultural Research Institute (TZARI) in Eskişehir, Türkiye.

Plant Material

In the present study, two distinct bread wheat germplasm sets, the 23rd Heat and Drought Tolerant Spring Bread Wheat Observation Nursery (23rd-HTDTSBWON) and the 24th Heat and Drought Tolerant Spring Bread Wheat Observation Nursery (24th-HTDTSBWON)) comprising 301 and 300 genotypes, respectively—were sourced from the International Center for Agricultural Research in the Dry Areas (ICARDA) and evaluated for their seedling-stage resistance to *Fusarium culmorum* under controlled growth room conditions. Additionally, nine standard breeding lines/varieties with known resistant reactions to *F. culmorum*-induced dryland crown rot were included as reference controls (Table 1). Control genotypes 2-49, Ahmetağa, Altay 2000, Sunco were classified as moderately resistant (MR), while Bezostaja 1, Eminbey, Dumlupınar, Kızıltan 91, Kutluk 94 were classified as susceptible (S) (Erginbaş-Orakcı et al., 2016; Erginbaş-Orakcı et al., 2022; Yazıcı Kuzu et al., 2022).

Table 1. Characteristics of the standard check varieties/lines utilized for seedling-stage resistance to *F. culmorum* at the soil borne disease program at CIMMYT-Türkiye.

Wheat Genotype	Resistance Rating	Type	Source
2-49	MR	SW/BW	Australia
Ahmetağa	MR	WW/BW	Türkiye
Altay 2000	MR	WW/ BW	Türkiye
Sunco	MR	SW/ BW	Australia
Bezostaja 1	S	WW/ BW	Russia
Eminbey	S	WW/DW	Türkiye
Dumlupınar	S	WW/BW	Türkiye
Kızıltan 91	S	FAC/DW	Türkiye
Kutluk 94	S	WW/BW	Türkiye

Abbreviations stand for: MR= Moderately Resistant, MS= Moderately Susceptible, S= Susceptible, MS= Moderately Susceptible, HS= Highly Susceptible, WW= Winter Wheat, SW= Spring Wheat, FAC= Facultative, BW= Bread Wheat, DW= Durum Wheat.

Potting Mixture

Genotypes were evaluated in a standard potting mixture of field soil, sand, and organic matter (50:40:10, v/v/v). To ensure a clean environment, the soil and sand were sterilized at 110 °C for 2 h, and the organic fertilizer at 70 °C for 5 h.

Fungal Inoculum Preparation

A monosporic isolate of *F. culmorum*, originally obtained from infected wheat in field in Kırşehir, Türkiye (39°39′709″ N, 34°25′515″ E) and provided by the CIMMYT soil-borne pathogens program, was used for inoculation. To induce sporulation, the isolate was subcultured on synthetic nutrient agar (SNA) and incubated at 23 ± 1 °C under a 12 h photoperiod for 10 days.

The monosporic isolate was grown on Saccharose Nutrient Agar (SNA) medium (KH_2PO_4 1 g, KNO_3 1 g, $MgSO_4 \cdot 7H_2O$ 0.5 g, KCl 0.5 g, glucose 0.2 g, sucrose 0.2 g, agar 20 g, 1000 mL distilled water) at 23°C for 10 days. For inoculum production, 200 g of wheat bran and 30 ml of water were added to oven bags (25 cm x 38 cm). The bags were tied with wire to prevent contact with air and autoclaved at 121°C for 20 minutes, at two consecutive days. Bags of autoclaved wheat bran were left to cool. The cooled sterile wheat bran bags were inoculated with *F. culmorum* culture grown on SNA medium. The bags were sealed with autoclaved cotton and incubated at 23°C for two weeks. During incubation, the bags were shaken every other day to ensure homogeneous distribution of bran and spores. After two weeks, fungus-colonized wheat bran was left to dry at room temperature. The spore suspension was obtained by filtering the colonized wheat bran substrate through a double layer of cheesecloth after suspension in sterile distilled water. The spore suspension was adjusted to $1x10^6$ spores/ml and made ready for use by adding methyl cellulose (0.1%, v/v) prior to inoculation. (Erginbas-Orakci et al., 2016).

Seedling Stage Screening (Growth Room)

Screening for resistance to *F. culmorum* was done in two consecutive trials (CR1 and CR2) under growth room (GR) conditions. A total of 10 seeds per line were placed on moist filter paper in sterile petri dishes and germinated at 22 °C for 3 days. Germinated seeds that reached a similar phenological development level were planted in plastic tubes (Stuewe and Sons, Corvallis, OR) (2,5 cm diameter × 16 cm length) filled with a potting mixture (see above). One week after sowing, the stem base of each seedling (0.5–1 cm above the soil level, including the coleoptile) was inoculated with *F. culmorum* at a concentration of 1×10^6 spores mL^{-1} of the spore suspension. After inoculation, the tubes were covered with plastic tent and incubated at 23 ± 1°C for 48 hours under 80–90% humidity conditions. After incubation, the seedlings were then left in GR conditions until the early tillering stage (Zadoks stage 14, approximately 42 days) under a 16/8 hour light/dark photoperiod, at 23 ± 1°C temperature and 60–80% (±5%) relative humidity. Following the initial incubation period, the seedlings were maintained in a GR until the early tillering stage (Zadoks stage 14, approximately 42 days). The environmental conditions were set to a 16/8 h (light/dark) photoperiod at 23 ± 1 °C with a relative humidity of 60–80% (±5%) (Mitter et al., 2006). Each treatment was replicated 5 times and tubes were placed in a completely randomised block design. Trials were repeated once for data validation, in two independent experiments.

Disease Assessment and Statistical Analysis

Plants were evaluated based on the rate of browning and decay occurring at the root and crown (1 cm above the soil surface). Disease severity was scored according to a modified form of the 1–5 scale defined by Wildermuth and McNamara (1994), Nicol et al. (2001) and Erginbaş-Orakcı et al. (2016). Accordingly, 1 = 1–9% (Resistant, R), 2 = 10–29% (Moderately resistant, MR), 3 = 30–69% (Moderately susceptible, MS), 4 = 70–89% (Susceptible, S) and 5 = 90–100% (Very susceptible, VS). The data obtained were subjected to one-way analysis of variance according to the randomised block design, and differences between means were compared at the 5% significance level (Least Significant Difference, LSD test) (Steel and Torrie, 1960).

RESULTS AND DISCUSSION

In the present study, two distinct wheat diversity panels (comprising 300 and 301 genotypes, respectively) were screened under controlled GR conditions to characterize their phenotypic responses to *Fusarium culmorum*. The findings revealed significant genetic variation ($P < 0.05$) among the tested genotypes.

In the set consisting of 300 genotypes, 209 genotypes (68%) were classified as moderately susceptible (MS), 70 genotypes (23%) as susceptible (S), and 30 genotypes (10%) as moderately resistant (MR). Similarly, in a set comprising 301 genotypes, 189 genotypes (61%) were classified as moderately susceptible (MS), 73 genotypes (24%) as susceptible (S), and 47 genotypes (15%) as moderately resistant (MR). The fact that the majority of genotypes in both sets were grouped as MS indicates that high levels of resistance to *F. culmorum* are limited.



Figure 1. Seedling-stage disease severity progressed along a 1–5 scale, where a score of 1 represented a resistant reaction and 5 indicated maximum susceptibility to F. culmorum. (Right)

Figure 2. Representative phenotypes corresponding to the extreme values (1 and 5) of the disease severity scale used to evaluate Fusarium culmorum–induced symptoms at the seedling stage. (Left)

The reactions of the control genotypes showed some variation between sets. In set 300, Ahmetağa, Altay 2000 and Sunco were classified as moderately resistant (MR); 2-49 as moderately susceptible (MS); and Bezostaja1, Dumlupınar, Eminbey, Kızıltan

91 and Kutluk 94 as susceptible (S). In set 301, 2-49, Ahmetağa, Altay 2000 and Sunco were found to be moderately resistant (MR); Bezostaja 1 and Kutluk 94 were found to be moderately susceptible (MS); Dumlupınar, Eminbey and Kızıltan 91 were found to be susceptible (S).

Table 2. Resistance levels (1–5 scale) of 300 bread wheat genotypes and 9 control genotypes against *Fusarium culmorum* at the seedling stage, evaluated under growth room conditions. Disease severity was determined according to the evaluation system developed by Wildermuth and McNamara (1994) and modified by Erginbas-Orakci et al. (2018).

Genotype ID	Disease Score (1–5)	Reaction Class
12	1.7^{s*}	MR
155	1.8^{rs}	MR
102, 220	2^{qrs}	MR
64	2.1^{pqrs}	MR
11, 61, 71, 74, 96, 119, 151, 190, 302, 309	2.2^{opqr}	MR
41, 56, 112, 182, 219, 240, 303	$2,3^{nopq}$	MR
37, 161, 168, 171, 185, 221, 282, 289	$2,4^{monpq}$	MR
28, 29, 40, 63, 94, 170, 177, 183, 187, 194, 200, 226, 238, 259, 273, 301	2.5^{lmnop}	MS
15, 17, 62, 93, 150, 179, 181, 206, 213, 279, 286	$2,6^{klmno}$	MS
2, 36, 98, 101, 152, 195, 202, 229, 234, 236, 243, 268, 269, 293, 222	2.7^{jklmn}	MS
38, 42, 46, 47, 60, 73, 77, 81, 88, 90, 95, 97, 99, 115, 131, 138, 143, 149, 156, 158, 166, 172, 174, 178, 188, 191, 192, 228, 231, 239, 241, 248, 270, 278, 298	$2,8^{ijklm}$	MS
14, 55, 75, 82, 121, 122, 135, 139, 154, 173, 242, 246, 288, 300	$2.9^{hıjkl}$	MS
16, 19, 22, 45, 50, 54, 57, 58, 67, 78, 118, 130, 132, 137, 144, 157, 162,193,216,223,232,235,262,266,275,283,284	3^{ghijk}	MS
8, 18, 20, 25, 43, 48, 51, 68, 76, 83, 85, 86, 136, 142, 145, 146, 165, 176, 180, 196, 198, 207, 218, 237, 244, 252, 253, 254, 256, 263, 276, 277, 280, 281, 285, 291	$3,1^{fghıj}$	MS
1, 9, 23, 26, 30, 31, 34, 44, 59, 65, 66, 79, 84, 87, 103, 117, 133 ,247,249,250,257,260,265,294,295,299	$3.2^{efghı}$	MS
7, 27, 49, 72, 80, 89, 105, 123, 163, 167, 175, 186, 199, 233, 251, 271, 272, 292	3.3^{defgh}	MS
32, 69, 124, 148, 164, 189, 230, 261, 264, 274, 287	$3,4^{cdefg}$	MS
3,4,5,10,13,35,53,70,92,100,104,106,109,114,116,120 ,126,127,128,129,140,159,160,197,204,205,208,210 ,217,224,225,227,258,290,297,305	$3,5^{bcdef}$	S
21, 39, 52, 91, 108, 125, 134, 141, 147, 153, 169, 184, 209, 245, 255, 267	3.6^{abcde}	S
24, 203, 212, 214, 215, 296, 304, 306, 307	3.7^{abcd}	S
107, 113, 201, 308,	3.8^{abc}	S
33,110,111,211	3.9^{ab}	S
6	4^{a}	S

** Means followed by different letters are statistically significant (P≤0.05)*

1 Numbers are the mean of 5 replications

2 R= Resistant, MR= Moderately resistant, MS= Moderately susceptible, H= Susceptible, VS= Very susceptible 3 Resistant= 1-1.4, Moderately resistant = 1.5-2.4, Moderately susceptible = 2.5-3.4, Susceptible = 3.5-4.4, Very susceptible = 4.5-5

Check lines/Varieties: 301= 2-49, 302=Ahmetağa, 303= Altay 2000, 304=Bezostaja 1, 305=Dumlupınar, 306=Eminbey , 307=Kızıltan 91, 308=Kutluk 94, 309=Sunco

The findings obtained generally correspond with the results reported in the literatures, but also contain some differences. Erginbaş Orakcı et al. (2022), in their study examining the reactions of Turkish durum wheat genotypes to *F. culmorum*, reported that the Dumlupınar variety was the most susceptible genotype during the adult plant stage, while the Kızıltan 91 variety showed high sensitivity during the seedling stage. In this study, the Dumlupınar and Kızıltan 91 varieties also showed susceptible reactions during the seedling stage, yielding results consistent with the literature.

In a study by Erginbaş Orakcı et al. (2018) evaluating tolerance to dryland root rot, Kızıltan 91 showed a high level of sensitivity, while 2-49 was moderately resistant; Altay 2000 and Sunco were reported as moderately susceptible. In the present study, Kızıltan 91's susceptible reaction is consistent with previous findings. However, the determination of Altay 2000 and Sunco as moderately resistant differs somewhat from the moderately susceptible reaction reported in the literature. These differences are thought to stem from variations in the isolates used, inoculum density.

Karakaya et al. (2022) evaluated the reactions of 200 bread wheat genotypes of CIMMYT origin to *Fusarium pseudograminearum* and reported that the majority of genotypes were moderately susceptible (56%). Control genotypes 2-49, Altay 2000, and Sunco were classified as moderately resistant. The current study shows similarity in that the majority of genotypes belong to the moderately susceptible group. However, the classification of 2-49 as moderately susceptible (2.5) in the 300 set partially slightly differs from previous findings.

Erginbas Orakcı et al. (2016) reported that the Sunco, Altay 2000, and 2-49 genotypes are moderately resistant to F. pseudograminearum. In this study, the determination of these genotypes as moderately resistant, particularly in set 301, is consistent with the literature.

Table 3. Resistance levels of 301 bread wheat genotypes and 9 control genotypes against *Fusarium culmorum* during the seedling stage (scale 1–5) evaluated under growth room conditions. Disease severity was determined according to the evaluation system developed by Wildermuth and McNamara (1994) and modified by Erginbas-Orakci et al. (2018).

Genotype ID	Disease Score (1–5)	Reaction Class
83, 182, 185, 201, 208, 222	1.5^{s}	MR
105, 127, 172, 184, 200, 299,	2^{r}	MR
119,125,226,230,251	$2{,}1^{qr}$	MR
4,173,216,219,223,231,250,266,287	2.2^{pqr}	MR
11, 20, 36, 61, 75, 98, 178, 186, 233, 303, 304	2.3^{opqr}	MR
10, 17, 35, 47, 112, 159, 180, 240, 302, 310	$2{,}4^{nopq}$	MR
45, 96, 134, 138, 179, 193, 205, 220, 293	2.5^{mnop}	MS
69.87, 136, 157, 197, 217, 285, 289	2.6^{lmno}	MS
14, 40, 43, 103, 149, 154, 160, 176, 191, 218, 243, 268, 281, 286	2.7^{klmn}	MS
12, 31, 59, 62, 63, 80, 84, 100, 117, 135, 162, 273, 279, 288, 296	2.8^{jklm}	MS
121, 123, 128, 188, 224, 253, 298	$2{,}9^{ijkl}$	MS
2, 3, 8, 13, 15, 22, 25, 28, 29, 38, 41, 46, 48, 52, 55, 60, 65, 67, 68, 70, 71, 78, 81, 82, 85, 88, 89, 91, 94, 97, 102, 106, 111, 113, 120, 132, 133, 145, 146, 151, 153, 187, 190, 195, 202, 209, 211, 212, 213, 221, 227, 228, 236, 246, 247, 254, 258, 267, 270, 271, 277, 280, 283, 284, 291, 297	$3^{hıjk}$	MS
1, 5, 6, 30, 34, 74, 76, 99, 109, 118, 126, 142, 155, 165, 181, 183, 207 235,252,259,276,282,294	$3.1^{ghıj}$	MS
21, 23, 27, 37, 53, 64, 66, 93, 108, 129, 137, 170, 196, 198, 210, 215 ,234,238,256,260,290,295,309	$3{,}2^{fghı}$	MS
9, 26, 32, 57, 72, 86, 104, 122, 124, 139, 175, 192, 272, 300, 305,	3.3^{efgh}	MS
33, 42, 73, 77, 164, 262, 274, 292	$3{,}4^{defg}$	MS
16, 18, 24, 49, 51, 79, 95, 107, 116, 130, 156, 166, 171, 174, 189, 194, 225, 242, 248, 249, 263, 264, 269, 278,	3.5^{cdef}	S
44, 54, 90, 92, 110, 144, 147, 152, 199, 204, 229, 261	3.6^{bcde}	S
7, 19, 39, 50, 101, 150, 167, 206, 237, 239, 241, 244	3.7^{abcd}	S
56, 58, 115, 140, 141, 143, 148, 161, 168, 177, 203, 214, 232, 245 ,265,275,307,	3.8^{abc}	S
114, 131, 163, 169, 306	$3{,}9^{ab}$	S
158,255,308	4^{a}	S

** Means followed by different letters are statistically significant (P ≤ 0.05)1 Numbers are the mean of 5 replications*
2 R = Resistant, MR = Moderately resistant, MS = Moderately susceptible, H = Susceptible, VS = Very susceptible 3 Resistant = 1–1.4, Moderately resistant = 1.5–2.4, Moderately susceptible = 2.5–3.4, Susceptible = 3.5–4.4, Very susceptible = 4.5–5
Check lines/Varieties: 301= 2-49, 302=Ahmetağa, 303= Altay 2000, 304=Bezostaja1, 305=Dumlupınar, 306=Eminbey, 307=Kızıltan91, 308=Kutluk 94, 309=Sunco

In the study conducted by Yılmaz et al. (2023), most of the CIMMYT durum wheat genotypes were reported as moderately susceptible; Kızıltan 91 and Bezostaja 1 were found to be susceptible, while 2-49 and Sunco were moderately resistant. In the present study, while Kızıltan 91 showed a susceptible reaction, which is consistent with the literature, Bezostaja 1 was classified as moderately susceptible in some sets, showing a partial difference.

In an evaluation of *F. culmorum* by Laasli et al. (2022), Kutluk 94 and Bezostaja 1 were reported as susceptible; Sunco and Altay 2000 as moderately susceptible; and 2-49 as moderately resistant.

Overall, the absence of resistant genotypes in both sets and the fact that the majority of genotypes fall into the moderately susceptible category indicate that high levels of resistance to *F. culmorum* are limited. This situation supports the view, emphasised by Karakaya et al. (2022), that breeding efforts should target combined resistance to multiple root rot pathogens rather than just a single pathogen.

CONCLUSIONS

The present study revealed that there is a certain level of variation among wheat genotypes against *F. culmorum*, but that the source of high resistance is limited. The findings indicate that moderately resistant genotypes should be considered as potential parental material in resistance breeding programmes. Furthermore, further studies involving different isolates and multiple environmental conditions are important for determining the stability of resistance.

Acknowledgements

This study is part of the M.Sc. thesis conducted by the first author, Arzu TÜRKMEN, from the Department of Field Crops at the Graduate School of Natural and Applied Sciences, Eskişehir Osmangazi University, Türkiye.

The authors would like to thank the Turkish Ministry of Agriculture and Livestock (TMFAL) especially Transitional Zone Agriculture Research Institute of Eskisehir, Türkiye for providing the support and The International Center for Agricultural Research in the Dry Areas (ICARDA) for providing wheat materials. And I would like to thank Dr. Oğuz Önder for his help with the statistical analysis.

Author Contributions

All authors contributed to the emergence of the manuscript and approved the final version

Conflict of Interest

The authors declare that they have no conflict of interest.

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