

Kadir AKAN^{1*} , **Onur HOCAOĞLU²** , **Ahmet ÇAT³** , **Alaettin KEÇELİ⁴** , **Kamil KARA⁵** , **Taşkın EROL⁶** , **Mehmet TEKİN⁷** ,
Kander KOÇ⁸ 

¹Kırşehir Ahi Evran University, Faculty of Agriculture, Department of Plant Protection, Kırşehir, Türkiye.

²Çanakkale Onsekiz Mart University, Faculty of Agriculture, Department of Field Crops, Çanakkale, Türkiye.

³Siirt University, Faculty of Agriculture, Department of Plant Protection, Siirt, Türkiye.

⁴Pamukkale University, Faculty of Applied Sciences, Department of Organic Farming Management, Çivril/Denizli, Türkiye.

⁵Kırıkkale University, Delice Vocational School, Department of Plant and Animal Production, Plant Protection Program, Kırıkkale, Türkiye.

⁶Kırıkkale Vocational School, Department of Plant and Animal Production, Organic Agriculture Program, Delice/Kırıkkale, Türkiye.

⁷Akdeniz University, Faculty of Agriculture, Department of Field Crops, Antalya, Türkiye.

⁸Yenice, Tarsus/Mersin, Türkiye.

* e-mail: kadir.akan@ahievran.edu.tr

EVALUATION OF COMMON BUNT RESISTANCE IN BREAD WHEAT GENOTYPES FROM PRIMARY YIELD TRIALS

This study was conducted to determine the reactions of 50 bread wheat (*Triticum aestivum* L.) genotypes at the preliminary yield trial stage against common bunt (*Tilletia foetida*) across seven different locations in Türkiye, including Antalya, Çanakkale, Denizli, Kırıkkale, Kırşehir, Mersin, and Siirt under artificial epidemic conditions during the 2024-2025 growing season. The pathogen population was virulent on *Bt*-0, *Bt*-2, *Bt*-3, *Bt*-4, *Bt*-6 and *Bt*-7 resistance genes, but avirulent on *Bt*-1, *Bt*-5, *Bt*-8, *Bt*-9, *Bt*-10, *Bt*-8,9,10, *Bt*-11, *Bt*-12, *Bt*-13, *Bt*-14 and *Bt*-15. The high disease severity (85-100%) in the susceptible controls, Little Club and Yakar-99, confirmed successful infection across all locations. Among the tested genotypes, 94% (46 genotypes) were in the susceptible reaction group, while only 6% (3 genotypes) showed moderately resistant reactions. The crosses of Esperia/Sönmez 2001 (line 10), Bezostaja-1/Sönmez 2001 (line 17), and Tosunbey/Sönmez 2001 (line 31) showed the highest resistance, with maximum disease severity values of 12%, 13%, and 14%, respectively. Disease severity varied across locations, with Kırşehir showing the highest infection rate (95%), while infection remained relatively low in Antalya, likely due to climatic conditions. The findings show that genetic diversity for resistance to common bunt is limited in the tested wheat gene pool and reveal that Sönmez 2001 can be used as a donor in resistance breeding programs.

Keywords: *Tilletia laevis*, *Bt* resistance genes, Artificial epidemic, Breeding material, Genetic resistance

Кадир АКАН^{1*}, **Онур ХОДЖАОĞЛУ²**, **Ахмет ЧАТ³**, **Алаеттин КЕЧЕЛІ⁴**, **Камил КАРА⁵**, **Ташкын ЕРОЛ⁶**, **Мехмет ТЕКИН⁷**, **Кандер КОЧ⁸**

¹ Kırşehir Ahi Evran University, Ауыл шаруашылығы факультеті, Өсімдіктерді қорғау кафедрасы, Кыршехир, Түркия.

- ² Çanakkale Onsekiz Mart University, Ауыл шаруашылығы факультеті, Далалық дақылдар кафедрасы, Чанаккале, Түркия.
- ³ Siirt University, Ауыл шаруашылығы факультеті, Өсімдіктерді қорғау кафедрасы, Сиирт, Түркия.
- ⁴ Pamukkale University, Қолданбалы ғылымдар факультеті, Органикалық егіншілік менеджменті кафедрасы, Чиврил/Денизли, Түркия.
- ⁵ Kırıkkale University, Делидже кәсіптік мектебі, Өсімдік және мал шаруашылығы бөлімі, Өсімдіктерді қорғау бағдарламасы, Кырыккале, Түркия.
- ⁶ Kırıkkale Vocational School, Өсімдік және мал шаруашылығы бөлімі, Органикалық ауыл шаруашылығы бағдарламасы, Делидже/Кырыккале, Түркия.
- ⁷ Akdeniz University, Ауыл шаруашылығы факультеті, Далалық дақылдар кафедрасы, Анталия, Түркия.
- ⁸ Йенидже, Тарсус/Мерсин, Түркия.
- *e-mail: kadir.akan@ahievran.edu.tr

Бастапқы өнімділік сынақтарындағы жұмсақ бидай генотиптерінің қатты қаракүйеге төзімділігін бағалау

Бұл зерттеу 2024–2025 жылғы вегетациялық маусымда жасанды індет жағдайында Түркияның жеті түрлі аймағында — Анталия, Чанаккале, Денизли, Кырыккале, Кыршехир, Мерсин және Сииртте — бастапқы өнімділік сынағы кезеңіндегі 50 жұмсақ бидай (*Triticum aestivum* L.) генотипінің қатты қаракүйеге (*Tilletia foetida*) реакциясын анықтау мақсатында жүргізілді.

Патоген популяциясы Bt-0, Bt-2, Bt-3, Bt-4, Bt-6 және Bt-7 төзімділік гендеріне вирулентті, ал Bt-1, Bt-5, Bt-8, Bt-9, Bt-10, Bt-8,9,10, Bt-11, Bt-12, Bt-13, Bt-14 және Bt-15 гендеріне авирулентты болды.

Сезімтал бақылау сорттары — Little Club және Yakar-99 — бойынша аурудың жоғары даму деңгейі (85–100%) барлық аймақтарда жұқтырудың сәтті өткенін растады.

Зерттелген генотиптердің ішінде 94%-ы (46 генотип) сезімтал реакция тобына жатқызылды, ал тек 6%-ы (3 генотип) орташа төзімді реакция көрсетті. Esperia/Sönmez 2001 (10-линия), Bezostaja-1/Sönmez 2001 (17-линия) және Tosunbey/Sönmez 2001 (31-линия) будандары ең жоғары төзімділікті көрсетті; олардың аурудың ең жоғарғы даму деңгейі тиісінше 12%, 13% және 14% болды.

Аурудың даму деңгейі аймақтарға байланысты өзгеріп отырды: ең жоғары залалдану деңгейі Кыршехирде (95%) байқалса, Анталияда климаттық жағдайларға байланысты аурудың таралуы салыстырмалы түрде төмен болды.

Алынған нәтижелер зерттелген бидай генофондында қатты қаракүйеге төзімділік бойынша генетикалық әртүрліліктің шектеулі екенін көрсетті және Sönmez 2001 сортының төзімділік селекциясы бағдарламаларында донор ретінде пайдаланылуы мүмкін екенін анықтады.

Түйін сөздер: *Tilletia laevis*, Bt төзімділік гендері, жасанды індет, селекциялық материал, генетикалық төзімділік.

Кадир АКАН^{1*}, Онур ХОДЖАОГЛУ², Ахмет ЧАТ³, Алаэттин КЕЧЕЛИ⁴, Камиль КАРА⁵, Ташкын ЭРОЛ⁶, Мехмет ТЕКИН⁷, Кандер КОЧ⁸

¹ Kırşehir Ahi Evran University, сельскохозяйственный факультет, кафедра защиты растений, Кыршехир, Турция.

² Çanakkale Onsekiz Mart University, сельскохозяйственный факультет, кафедра полевых культур, Чанаккале, Турция.

³ Siirt University, сельскохозяйственный факультет, кафедра защиты растений,

Сиирт, Турция.

⁴ Pamukkale University, факультет прикладных наук, кафедра управления органическим земледелием, Чивриль/Денизли, Турция.

⁵ Kırıkkale University, профессиональная школа Делидже, отделение растениеводства и животноводства, программа защиты растений, Кырыккале, Турция.

⁶ Kırıkkale Vocational School, отделение растениеводства и животноводства, программа органического сельского хозяйства, Делидже/Кырыккале, Турция.

⁷ Akdeniz University, сельскохозяйственный факультет, кафедра полевых культур, Анталя, Турция.

⁸ Йенидже, Тарсус/Мерсин, Турция.

*e-mail: kadir.akan@ahievran.edu.tr

Оценка устойчивости генотипов мягкой пшеницы к твёрдой головне в предварительных сортоиспытаниях

Данное исследование было проведено с целью определения реакции 50 генотипов мягкой пшеницы (*Triticum aestivum* L.) на твёрдую головню (*Tilletia foetida*) на этапе предварительного сортоиспытания в условиях искусственного инфекционного фона в течение вегетационного сезона 2024–2025 гг. в семи различных регионах Турции: Анталя, Чанаккале, Денизли, Кырыккале, Кыршехир, Мерсин и Сиирт.

Популяция патогена была вирулентна к генам устойчивости Bt-0, Bt-2, Bt-3, Bt-4, Bt-6 и Bt-7, но авирула к генам Bt-1, Bt-5, Bt-8, Bt-9, Bt-10, Bt-8,9,10, Bt-11, Bt-12, Bt-13, Bt-14 и Bt-15.

Высокая степень развития болезни (85–100%) у восприимчивых контрольных сортов Little Club и Yakar-99 подтвердила успешное заражение во всех пунктах испытаний.

Среди исследованных генотипов 94% (46 генотипов) были отнесены к группе восприимчивых, тогда как только 6% (3 генотипа) проявили умеренно устойчивую реакцию. Наибольшую устойчивость показали гибридные комбинации Esperia/Sönmez 2001 (линия 10), Bezostaja-1/Sönmez 2001 (линия 17) и Tosunbey/Sönmez 2001 (линия 31), максимальная степень поражения у которых составила соответственно 12%, 13% и 14%.

Степень развития болезни варьировала в зависимости от региона: наибольший уровень заражения был отмечен в Кыршехире (95%), тогда как в Анталье распространение болезни оставалось сравнительно низким, вероятно, из-за климатических условий.

Полученные результаты показывают, что генетическое разнообразие по устойчивости к твёрдой головне в исследованном генофонде пшеницы ограничено, а также свидетельствуют о возможности использования сорта Sönmez 2001 в качестве донора устойчивости в селекционных программах.

Ключевые слова: *Tilletia laevis*, гены устойчивости Bt, искусственный инфекционный фон, селекционный материал, генетическая устойчивость.

Introduction

Bread wheat (*Triticum aestivum* L.) is a strategic crop used for both human and animal nutrition and one of the most widely produced cereals worldwide. Breeding studies have contributed significantly to increasing yield per unit area worldwide (Tekin et al., 2022). In recent years, particularly following developments related to global climate change and geopolitical instability in major wheat-producing countries, further exacerbated by the COVID-19 pandemic, the strategic importance of wheat has increased. Wheat is also one of the most important agricultural products in international trade, and the demand for sustainable food security continues to rise, as cereals, especially wheat, can be stored for long periods under suitable conditions.

However, abiotic and biotic stress factors causing yield and quality losses in global wheat production pose a significant threat to food security, potentially leading to unpredictable price fluctuations. It is clear that challenges arising from food insecurity may have serious consequences for both social stability and public health.

It has been reported that six species associated with common bunt have been described, among which the fungal pathogens *Tilletia laevis* (syn. *Tilletia foetida*) and *Tilletia caries* (syn. *Tilletia tritici*) are the primary causal agents. Common bunt is a seed-borne disease that causes varying levels of yield and quality losses in bread wheat (*Triticum aestivum* L.) (Goates, 2012). In addition to yield losses, the disease is among the critical diseases that cause a trimethylamine odor in the grain and a dark color in the flour in the milling sector (Aydoğdu and Kaya, 2020).

It is important to reduce, and if possible, completely eliminate, economic losses caused by common bunt at all levels. Seed treatment is the adopted method for controlling the disease on a near-global scale. It has been reported that, in the absence of seed treatment, yield losses in susceptible cultivars average 15-20%, and disease incidence can reach up to 96% (Dodov and Todorova, 1974; Aktaş, 2001). Given the effectiveness of seed treatments in disease control, selection for genetic resistance has not been a primary selection criterion in global and Türkiye wheat breeding programs (Barroga-Matanguihan et al., 2011; Akçura and Akan, 2018; Akan et al., 2026).

As in other breeding studies, the classification of common bunt reactions is critically important. In cases where the susceptible control cultivar shows 100% susceptibility, the resistant and moderately resistant reactions of the tested genotype are more critical. However, previous studies have examined different evaluation scales, assigning varying percentage ranges to reaction groups such as resistant, moderately resistant, moderately susceptible, and susceptible when classifying host reactions in breeding materials. For example, Hoffman and Metzger (1976), Dumalasová and Bartoš (2007), Dumalasová and Bartoš (2010), and Dumalasová et al. (2014) classified pathogen virulence as 0-10% disease incidence (avirulent) and 11-100% (virulent). Similarly, Dodoff and Todorova (1974) defined reaction classes as 1-10% (Resistant), 11-30% (Moderately Resistant), 30-50% (Susceptible), and 51-100% (Highly Susceptible). Szunics and Szunics (1990) and Veisz et al. (2000) proposed a more detailed scale: 0.0% (Highly resistant), 0.1-5.0% (Resistant), 5.1-10.0% (Moderately resistant), 10.1-30.0% (Moderately susceptible), 30.1-50.0% (Susceptible), and 50.1-100.0% (Highly susceptible). More recently, Akçura and Akan (2018) and Akan et al. (2026) classified reactions as 0% (Immune), 0.1-10.0% (Resistant), 10.1-25.0% (Moderately resistant), 25.1-40.0% (Moderately susceptible), 40.1-70.0% (Susceptible), and $\geq 70.1\%$ (Very susceptible).

The main objectives of this study are (i) to determine the disease reactions of bread wheat genotypes at the preliminary yield trial stage against common bunt (*Tilletia foetida*) across multiple locations Türkiye, including Antalya, Çanakkale, Denizli, Kırıkkale, Kırşehir, Mersin and Siirt; (ii) to evaluate these reactions according to the most recent classification scale proposed by Akçura and Akan (2018) and Akan et al. (2026), to classify genotypes.

Material and Method

Plant Material

The plant material used in this study consisted of 50 bread wheat genotypes at the preliminary yield trial stage, provided by Tasaco Tarım (Antalya, Türkiye) (Table 1). In addition, a differential set of 17 genotypes was used to confirm the pathogen's race and to determine its virulence/avirulence pattern against specific resistance genes. The differential set includes the

genotypes: Heines VI (*Bt-0*), SEL 2092 (*Bt-1*), SEL 1102 (*Bt-2*), Ridit (*Bt-3*), Turkey 1558 (*Bt-4*), Hohenheimer (*Bt-5*), Rio (*Bt-6*), Sel 50077 (*Bt-7*), M78-9496 (*Bt-8*), M82-2098 (*Bt-9*), M82-2102 (*Bt-10*), P.I. 178383 (*Bt-8,9,10*), M82-2123 (*Bt-11*), P.I. 119333 (*Bt-12*), P.I. 181463 (*Bt-13*), Doubbi (*Bt-14*) and Carleton (*Bt-15*).

Table 1. Breeding and origin of tested materials and maximum bunt reaction

No	Pedigree	Average of maximum scores for all environments (%)	Maximum disease score (%)	Reaction group	Ranking*
1	Esperia / Alcione // Esperia	55	77	Susceptible	21
2	Esperia / Bezostaja-1	54	73	Susceptible	6
3	Esperia / Flamura 85	57	86	Susceptible	38
4	Esperia / İkizce 96	55	86	Susceptible	39
5	Esperia / Kate A-1	58	89	Susceptible	46
6	Esperia / Konya-2002	58	74	Susceptible	9
7	Esperia / Pehlivan	58	74	Susceptible	10
8	Esperia / TSCK-9	57	88	Susceptible	43
9	Esperia / TSCK-10	55	75	Susceptible	12
10	Esperia / Sönmez 2001	9	12	Moderately Resistant	1 (Most Resistant)
11	Esperia / Tosunbey	54	74	Susceptible	11
12	Genesi/ Kate A-1	58	77	Susceptible	22
13	Genesi/ Pehlivan	60	87	Susceptible	40
14	Kate A-1 / Aldane	60	77	Susceptible	23
15	Kate A-1 / Tosunbey	61	88	Susceptible	44
16	Bezostaja-1 / Kate A-1	53	75	Susceptible	13
17	Bezostaja-1 / Sönmez 2001	9	13	Moderately Resistant	2
18	Bezostaja-1 / Flamura 85	57	78	Susceptible	26
19	Bezostaja-1 / Konya-2002	58	75	Susceptible	14
20	Bezostaja-1 / İkizce 96 // Bezostaja-1	57	88	Susceptible	45
21	Bezostaja-1 / Esperia // Esperia	57	90	Susceptible	48
22	Tosunbey / TSCK-9	61	79	Susceptible	27
23	Tosunbey / Bezostaja-1	59	77	Susceptible	24
24	Tosunbey / Konya-2002	59	77	Susceptible	25
25	Tosunbey / Flamura 85 // Esperia	58	76	Susceptible	15
26	Tosunbey / Esperia // Esperia	60	76	Susceptible	16
27	Tosunbey / Ahmetağa	57	76	Susceptible	17
28	Tosunbey / Sagittario	60	76	Susceptible	18
29	Tosunbey / Genesi// Genesi	60	90	Susceptible	49
30	Tosunbey / Cömert	60	84	Susceptible	37
31	Tosunbey / Sönmez 2001	9	14	Moderately Resistant	3
32	Tosunbey / TSCK-10	61	87	Susceptible	41
33	Tosunbey / Bora	60	87	Susceptible	42
34	Bora/ Rumeli	58	69	Susceptible	4
35	Bora/ Adana-99	61	90	Susceptible	50 (Most Susceptible)

36	Bora/ Ahmetağa	60	83	Susceptible	35
37	Bora/ Axum	60	76	Susceptible	19
38	Ahmetağa / Bora	57	73	Susceptible	7
39	Ahmetağa / Bezostaja-1 // Ahmetağa	60	89	Susceptible	47
40	Ahmetağa / Genesi	60	81	Susceptible	32
41	Ahmetağa / Cömert	61	82	Susceptible	34
42	Ahmetağa / Bayraktar 2000	60	79	Susceptible	28
43	Ahmetağa / Altındane	61	83	Susceptible	36
44	Ahmetağa / Rebelde	59	79	Susceptible	29
45	Ahmetağa / Sagittario	60	79	Susceptible	30
46	Bayraktar 2000 / Tosunbey	59	81	Susceptible	33
47	Bayraktar 2000 / Adana-99	59	80	Susceptible	31
48	Bayraktar 2000 / Sagittario	58	76	Susceptible	20
49	Bayraktar 2000 / Axum	58	72	Susceptible	5
50	Bayraktar 2000 / Ahmetağa	58	73	Susceptible	8

*The ranking of tested materials from the most resistant (1) to the most susceptible (50) considering the “Maximum disease score (%)”

Disease Inoculation

The inoculum source for the common bunt pathogen consisted of a fresh spore population of *Tilletia laevis* (syn. *Tilletia foetida*), which was collected annually and used in a previous study by Akçura and Akan (2018). The spores used in this study were collected on July 30, 2024, from infected spikes obtained from the experimental fields of Kırşehir Ahi Evran University, where disease reaction tests were conducted under artificial epidemic conditions. The collected material was stored at +4°C until inoculation.

Prior to inoculation, random samples were taken from infected wheat spikes, and the pathogen was re-identified as *T. laevis* based on teliospore morphology, as described by Goates (1996). Diseased grains were crushed in a sterile mortar, and teliospores were separated from plant debris using a sterile sieve. Approximately 4 g of teliospores for each test genotype were placed in new paper envelopes. Inoculation was carried out prior to sowing at all locations by mixing teliospores with healthy seeds at approximately 0.5% (w/w), following the method described by Akan et al. (2026).

The experiments were conducted in multiple locations in Türkiye, including Antalya, Çanakkale, Denizli, Kırıkkale, Kırşehir, Mersin, and Siirt during the 2024-2025 growing season. All genotypes were sown manually between October and December 2024, in a randomized design with three replications. Sowing was carried out at a depth of 5-7 cm, in 1 m rows with 33 cm row spacing. The cultivar Little Club (LC) was used as a susceptible control and was sown after every 10 test genotypes. Along with LC, the susceptible control cultivar Yakar-99 was also sown in four border rows around the experiments. No chemical or organic fertilizers were applied, and all experiments were conducted under rainfed conditions without irrigation.

Disease Evaluation

The spikes of each tested genotype were evaluated between May and July 2025 at Zadoks growth stage 91 or later, according to the Zadoks development scale (Zadoks et al., 1974). In this context, the number of healthy and infected spikes was recorded separately for all test materials and genotypes in the differential set. Based on these data, the disease infection rate (%) was

calculated using Equation 1 (Akan et al., 2006; Dumalasová and Bartoš, 2007, 2010; Dumalasová et al., 2014; Akçura and Akan, 2018; Aydoğdu and Kaya, 2020)

$$\text{Infection rate (\%)} = (\text{Number of diseased spikes} / \text{Total number of spikes}) \times 100$$

To evaluate the results, genotypes were grouped based on the maximum disease rate (%) observed at each location. Disease reactions were categorized according to the classification scale proposed by Akçura and Akan (2018) and Akan et al. (2026): 0% (Immune), 0.1-10.0% (Resistant), 10.1-25.0% (Moderately resistant), 25.1-40.0% (Moderately susceptible), 40.1-70.0% (Susceptible), and over 70.1% (Very susceptible).

In evaluating the differential set, the highest disease reaction observed for each genotype was considered. According to the method of Hoffman and Metzger (1976), a disease rate of 0-10% was considered resistant (pathogen avirulent), whereas 10.1-100% was considered susceptible (pathogen virulent).

The pedigree information of tested materials, along with the mean of maximum disease scores across all environments (%), the maximum disease score (%), reaction group, and the ranking of genotypes from the most resistant (1) to the most susceptible (50) for common bunt, are presented in Table 1.

Results

Common bunt developed under artificial epidemic conditions in all locations. Disease reactions of the susceptible control genotypes LC and Yakar-99 ranged from 85% to -100% across all locations. These high reaction rates in the susceptible controls confirmed the effectiveness of the inoculation and the reliability of the disease evaluation.

It was determined that the pathogen population was virulent on the *Bt-0*, *Bt-2*, *Bt-3*, *Bt-4*, *Bt-6*, and *Bt-7* resistance genes, while it was avirulent on *Bt-1*, *Bt-5*, *Bt-8*, *Bt-9*, *Bt-10*, *Bt-8,9,10*, *Bt-11*, *Bt-12*, *Bt-13*, *Bt-14*, and *Bt-15*.

The grouping of the test materials based on their reactions to common bunt is presented in Tables 1 and 2.

Table 2. Grouping of the reactions of test materials to common bunt

Test Location	Material											
	First group		Second group		Third group		Fourth group		Fifth group		Sixth group	
	Immune		Resistant		Moderately resistant		Moderately susceptible		Susceptible		Very susceptible	
	%0		%0.1-10.0		%10.1-25.0		%25.1-45		%45.1-70.0		>%70.1	
	Number	%	Number	%	Number	%	Number	%	Number	%	Number	%
Antalya	0	0	1	2	2	4	0	0	4	8	43	86
Çanakkale	0	0	3	6	0	0	5	10	42	84	0	0
Denizli	0	0	0	0	4	8	9	18	36	72	1	2
Kırıkkale	0	0	3	6	0	0	0	0	38	76	9	18
Kırşehir	0	0	0	0	3	6	0	0	1	2	46	92
Mersin	0	0	3	6	0	0	0	0	47	94	0	0
Siirt	0	0	3	6	0	0	0	0	47	94	0	0
Total	0	0	0	0	3	6	0	0	1	2	46	92

Common Bunt Reaction Evaluations of Test Materials

Evaluation of the 50 genotypes at the tested preliminary yield trial stage revealed that the majority of the population was highly susceptible. According to Table 1, 46 genotypes (92%) were classified as susceptible, whereas only 3 genotypes (6%) showed moderately resistant reaction.

Among the test materials, the most resistant reactions were observed in genotypes derived from crosses involving the Sönmez 2001 cultivar. The genotype Esperia/Sönmez 2001 (line number 10) stood out as the most resistant line, with a mean disease rate of 9% and a maximum of 12%. This line was followed by Bezostaja-1/Sönmez 2001 (line number 17) and Tosunbey / Sönmez 2001 (line number 31), with maximum disease rates of 13% and 14%, respectively. These three genotypes were classified as moderately resistant (Table 1).

The most susceptible reactions were observed in genotypes involving Bora and Adana-99. The genotype Bora/Adana-99 (line number 35) was found to be the most susceptible, ranking 50th with a maximum disease rate of 90%. Similarly, Bezostaja-1/Esperia//Esperia (line number 21) and Tosunbey/Genesi//Genesi (line number 29) were also among the most susceptible genotypes, with a disease rate of 90%.

The results showed that genotypes derived from widely used parents such as Esperia and Tosunbey generally showed high disease rates, with reactions typically exceeding 70% (Table 2).

Evaluation of Common Bunt Reactions of Test Materials on a Location Basis

Studies conducted across different locations revealed that common bunt reaction levels varied significantly depending on ecological conditions. According to Table 2, the highest disease rate was observed in Kırşehir and Antalya. In Kırşehir, 92% of tested genotypes were classified as highly susceptible, compared with 86% in Antalya (Table 2).

At the Mersin and Siirt locations, 94% of the genotypes were classified as susceptible (Table 2). A clear contrast was observed between locations: while 46 genotypes showed a very susceptible reaction in Kırşehir, only 1 genotype was in the very susceptible reaction group in Denizli, highlighting substantial variation among environments. Overall, 46 of the 50 genotypes were in the very susceptible reaction group.

When the highest disease scores were evaluated across all locations, no genotype was classified as immune or resistant at any location. Genotypes derived from Sönmez 2001 had relatively lower disease scores than other genotypes and were identified in the moderately resistant group (Table 2).

The susceptible controls LC and Yakar-99 showed reactions ranging from 85% to -100% across all locations, confirming the effectiveness of inoculation and disease evaluation. The maximum disease reaction observed in the test materials was 58% in Antalya and 69% in Çanakkale. In Denizli, Kırıkkale, Mersin, and Siirt, the highest disease rate reached to 70%, whereas Kırşehir had the highest disease severity, with a rate of 95%.

Since no chemical or organic fertilizers were applied during the experimental period, it was concluded that plant nutrients had no possible effect on disease reactions. Climate data indicated that temperatures were generally above, and precipitation below, long-term averages during the winter and spring seasons across all locations.

Discussion

The findings of this study, which analyzed the common bunt (*Tilletia foetida*) reactions and genotype × environment interactions of the bread wheat breeding materials, are comprehensively discussed in light of the current literature. Within the scope of the study conducted in Antalya, Çanakkale, Denizli, Kırıkkale, Kırşehir, Mersin, and Siirt provinces during the 2024-2025 growing season, common bunt reactions were successfully determined under artificial epidemic conditions. The methodological validity of the study was confirmed by the susceptible control genotypes LC

and Yakar-99, which showed disease reactions ranging from 85% to 100% across all locations. This result indicates that inoculation and disease reaction tests were successfully conducted in accordance with scientific standards (Akçura and Akan, 2018; Tekin, 2023; Akan et al., 2026).

When the effectiveness of the pathogen population on the differential set was evaluated, it was determined to be virulent on *Bt-0*, *Bt-2*, *Bt-3*, *Bt-4*, *Bt-6*, and *Bt-7* resistance genes, whereas it was avirulent on *Bt-1*, *Bt-5*, *Bt-8*, *Bt-9*, *Bt-10*, *Bt-8,9,10*, *Bt-11*, *Bt-12*, *Bt-13*, *Bt-14*, and *Bt-15*. The results are consistent with those of Akçura and Akan (2018), Tekin (2023), and Akan et al. (2026), indicating that the pathogen population has not changed significantly. Similarly, Mourad et al. (2023) reported that *Bt-10*, *Bt-11*, *Bt-12*, and *Btp* resistance genes are effective against common bunt races in the USA and Türkiye. Furthermore, it has been reported that the *Bt-10* gene is widely used in breeding programs worldwide due to its effectiveness against many races of *T. laevis* and *T. caries* (Menzies et al., 2006). The use of differential sets to identify pathogen races and evaluate the effectiveness of resistance genes, as proposed by Goates (2012), was found to be methodologically consistent with this study's findings.

In a similar study conducted by Akan et al. (2026), genotype, environment, and genotype $\times$ environment interaction were highly significant ($p < 0.01$) for common bunt reactions, as indicated by variance analysis. In another study, Tekin (2023) reported a broad-sense heritability of 0.92 for reaction groups among 102 Turkish bread wheat cultivars, indicating substantial genetic variation. In the present study, only 3 out of 50 genotypes (6%) were in the moderately resistant reaction group, indicating that the tested breeding materials have limited resistance potential against common bunt. Aydoğdu and Kaya (2020) reported that 77.41% of Turkish spring wheat cultivars showed a very susceptible reaction. These findings confirm that resistance sources are limited in modern breeding materials and suggest that genotypes such as Sönmez 2001 can be considered as strategic gene sources in breeding programs for resistance to common bunt (Tekin, 2023).

Variation in disease reactions among locations reflects the pathogen's environmental adaptation and infection success. The high infection level observed in Kırşehir (up to 95%) indicates that this environment is highly conducive to the common bunt epidemic (Akan et al., 2026). In contrast, relatively lower disease reactions in Antalya, a region more suitable for spring production, were directly associated with climatic factors.

During the growing season, winter and spring temperatures were above long-term averages, accelerating plant phenology and causing genotypes to reach the Zadoks 91+ stage earlier than expected. This rapid development process temporally limited the systemic progression of the pathogen toward the spike (Zadoks et al., 1974; Akan et al., 2026). Environmental factors in these locations, especially soil temperature and moisture content during the sowing period, are thought to increase the pathogen's ability to penetrate. Previous studies have shown that climatic factors influence common bunt infection; for example, Johnsson (1992) reported that climatic factors influence common bunt infection in winter wheat, while Liatukas and Ruzgas (2009) found a positive correlation between low temperatures and disease incidence. However, in this study, it was found that the phenological escape mechanism had a more dominant limiting effect on pathogen penetration.

It is thought that these climatic conditions could accelerate plant phenology, leading to test materials maturing earlier. It is estimated that this rapid development process, depending on climate conditions, temporarily negatively affected the pathogen's systemic development and limited disease progression. This situation is thought to have prevented the disease's severity from becoming more severe, especially in the Antalya area.

As previous studies have indicated, the availability of resistance sources to common bunt within the modern wheat gene pool remains limited (Tekin et al., 2022). Nevertheless, Türkiye is

recognized as one of the gene centers of wheat, and it has been stated that it hosts genetic resources that can provide resistance against many diseases, including different cultivars, landraces, and wild relatives, and a significant portion of these resources has been characterized (İpek et al., 2023; Tekin et al., 2022).

Conclusion

In conclusion, line 10 was identified as resistant among the 50 lines evaluated and represents a promising donor for breeding programs to develop new resistant varieties to common bunt. In the absence of chemical or organic fertilization, the observed reactions largely reflect the genetic resistance of the tested materials. Keeping resistant lines derived from genitor parents, such as Sönmez 2001, in the gene pool and enhancing their resistance through marker-assisted pyramiding strategies targeting avirulent pathogen genotypes is of great importance for sustainable management of common bunt.

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Ethics Committee Approval

There is no requirement for ethics committee permission for this study.

Conflict of Interest Statement

As the authors of the article, we declare that there is no conflict of interest.

Author Contribution Statement

Planning and Coordination K. Akan. Material and Method K. Akan and O. Hocaoglu. Data Collection and Processing K. Akan, A. Çat, A. Keçeli, K. Kara, T. Erol, O. Hocaoglu, M. Tekin, and K. Koç. Statistical Analysis O. Hocaoglu. Manuscript Writing, Review, and Editing K. Akan, O. Hocaoglu, A. Çat, and M. Tekin.

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Information about authors:

Kadir AKAN - Kırşehir Ahi Evran University, Faculty of Agriculture, Department of Plant Protection, Kırşehir, Türkiye. ORCID 0000-0001-5133-0032

Onur HOCAOĞLU - Çanakkale Onsekiz Mart University, Faculty of Agriculture, Department of Field Crops, Çanakkale, Türkiye. ORCID 0000-0001-9439-8969

Ahmet ÇAT - Siirt University, Faculty of Agriculture, Department of Plant Protection, Siirt, Türkiye. ORCID 0000-0002-5638-0319

Alaettin KEÇELİ - Pamukkale University, Faculty of Applied Sciences, Department of Organic Farming Management, Çivril/Denizli, Türkiye. ORCID 0000-0003-1263-8952

Kamil KARA - Kırıkkale University, Delice Vocational School, Department of Plant and Animal Production, Plant Protection Program, Kırıkkale, Türkiye. ORCID 0000-0002-7729-4532

Taşkın EROL - Kırıkkale Vocational School, Department of Plant and Animal Production, Organic Agriculture Program, Delice/Kırıkkale, Türkiye. ORCID 0000-0002-4263-3776

Mehmet TEKİN - Akdeniz University, Faculty of Agriculture, Department of Field Crops, Antalya, Türkiye. ORCID 0000-0002-3447-1586

Kander KOÇ - Yenice, Tarsus/Mersin, Türkiye. ORCID 0000-0002-6784-8423

Сведения об авторах:

Кадир АКАН — Kırşehir Ahi Evran University, сельскохозяйственный факультет, кафедра защиты растений, Кыршехир, Турция. ORCID: 0000-0001-5133-0032

Онур ХОДЖАОГЛУ — Çanakkale Onsekiz Mart University, сельскохозяйственный факультет, кафедра полевых культур, Чанаккале, Турция. ORCID: 0000-0001-9439-8969

Ахмет ЧАТ — Siirt University, сельскохозяйственный факультет, кафедра защиты растений, Сиурт, Турция. ORCID: 0000-0002-5638-0319

Алаэттин КЕЧЕЛИ — Pamukkale University, факультет прикладных наук, кафедра управления органическим земледелием, Чивриль/Денизли, Турция. ORCID: 0000-0003-1263-8952

Камиль КАРА — Kırıkkale University, профессиональная школа Делидже, отделение растениеводства и животноводства, программа защиты растений, Кырыккале, Турция. ORCID: 0000-0002-7729-4532

Ташкын ЭРОЛ — Kırıkkale Vocational School, отделение растениеводства и животноводства, программа органического сельского хозяйства, Делидже/Кырыккале, Турция. ORCID: 0000-0002-4263-3776

Мехмет ТЕКИН — Akdeniz University, сельскохозяйственный факультет, кафедра полевых культур, Анталия, Турция. ORCID: 0000-0002-3447-1586

Кандер КОЧ — Йенидже, Тарсус/Мерсин, Турция. ORCID: 0000-0002-6784-8423

Авторлар туралы мәлімет:

Кадир АКАН — Kırşehir Ahi Evran University, Ауыл шаруашылығы факультеті, Өсімдіктерді қорғау кафедрасы, Кыршехир, Түркия. ORCID: 0000-0001-5133-0032

Онур ХОДЖАОГЛУ — Çanakkale Onsekiz Mart University, Ауыл шаруашылығы факультеті, Далалық дақылдар кафедрасы, Чанаккале, Түркия. ORCID: 0000-0001-9439-8969

Ахмет ЧАТ — Siirt University, Ауыл шаруашылығы факультеті, Өсімдіктерді қорғау кафедрасы, Сиурт, Түркия. ORCID: 0000-0002-5638-0319

Алаеттин КЕЧЕЛИ — Pamukkale University, Қолданбалы ғылымдар факультеті, Органикалық егіншілік менеджменті кафедрасы, Чиврил/Денизли, Түркия. ORCID: 0000-0003-1263-8952

Камил КАРА — Kırıkkale University, Делидже кәсіптік мектебі, Өсімдік және мал шаруашылығы бөлімі, Өсімдіктерді қорғау бағдарламасы, Кырыккале, Түркия. ORCID: 0000-0002-7729-4532

Ташкын ЕРОЛ — Kırıkkale Vocational School, Өсімдік және мал шаруашылығы бөлімі, Органикалық ауыл шаруашылығы бағдарламасы, Делидже/Кырыккале, Түркия. ORCID: 0000-0002-4263-3776

Мехмет ТЕКИН — Akdeniz University, Ауыл шаруашылығы факультеті, Далалық дақылдар кафедрасы, Анталия, Түркия. ORCID: 0000-0002-3447-1586

Кандер КОЧ — Йенидже, Тарсус/Мерсин, Түркия. ORCID: 0000-0002-6784-8423