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Resistance Sources for Fusarium Head Blight Disease of Bread Wheat in Ethiopia

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Abstract

Fusarium head blight (FHB); caused by several Fusarium species, is an important disease that causes significant losses in bread wheat yield and quality. This investigation aimed to identify the resistance source(s) against FHB of bread wheat in Ethiopia. Fifty-two genotypes (including two checks) had evaluated against the mixture of dominant FHB pathogens (Fusarium graminearum and Fusarium culmorum). Percent Fusarium damaged kernel (% FDK) varied from 6.9% to 100%. Out of 52 genotypes screened, genotype 31 was showed highly resistant for diseased spikelets per spike (1.0), resistance for %FDK (6.9%), resistance for disease scores (1.0), and lower AUDPC (20.2), followed by genotype 29, which showed similar response except for the %FDK which was moderately resistant (9.3). This investigation concluded that genotypes 31 and 29 can be used as a source of donors to improve the resistance of Ethiopian bread wheat varieties against FHB disease.

Keywords: Triticum aestivum; Fusarium culmorum; Fusarium graminearum; FHB; Type-II resistance; %FDK

Introduction

Globally wheat ranks first among cereal crops in area harvested, second in amount of production, and fifth in productivity. The contribution of Africa to world's wheat production was 4.55% in area harvested and 3.32% in tonnes. From African countries, Ethiopia ranked third in area allocated for wheat, second in tonnes of wheat production, and seventh in wheat productivity in 2020 [1]. Nowadays, the government of Ethiopia encourages wheat production in all regions for food security. But, wheat production in the country is challenged by Fusarium head blight (FHB) both under rain-fed [2-6]. And irrigated fields [7]. FHB infected wheat fields with 97.5% in Arsi and West-Arsi [41], 93.56% in Southern Nations and Nationalities People (SNNP) and Oromia [5], 93.90% in southwestern Ethiopia [40], and 88.75% in West Shewa [2]. This disease is known for damaging the quality [8, 9]. And quantity of wheat production [10]. FHB is a concern due to the associated secondary metabolites, such as deoxynivalenol and trichothecene mycotoxin [11], which are unsafe for both humans and livestock.

Previous studies in Ethiopia reported that Fusarium graminearum Schwabe and Fusarium culmorum (W.G. Smith) Saccardo were the dominant species responsible for FHB disease of bread wheat in the country [2, 3]. Both of them are capable of causing DON contamination in wheat grains [12-14]. The previous studies in Ethiopia focused on surveys [2, 3, 5], evaluation of released varieties and fungicide trial [4, 6]. But, there is lack of genotype screening efforts in Ethiopia. Therefore, this study was aimed to identify sources of resistance against the dangerous FHB disease of bread wheat in Ethiopia through screening bread wheat genotypes.

Materials and Methods

Description of the study area

This experiment had done in 2020 under Lath-house condition of Assosa Agricultural Research Center (AsARC), Assosa, Benishangul Gumuz region, Ethiopia. Geographically it is situated at 10° 03 N and 34° 59 E (Figure 1). The area has an altitude of 1580 m above sea level. It receives a mean annual rainfall of 1299.2 mm and minimum and maximum temperatures of 13.3-157.7 °C and 24.1-32.8 °C, respectively. The relative humidity ranged from 26-80% during experimentation (Figure 1).

Planting materials

Fifty-two bread wheat genotypes (including susceptible and resistant checks) were screened to determine resistance sources against FHB of bread wheat in Ethiopia. 50 genotypes had obtained from International Maize and Wheat Improvement Center (CIMMYT), Ethiopia and the two locally adapted bread wheat varieties, Kingbird and Wane, were obtained from Holeta Agricultural Research Center (HARC) (Table 1).

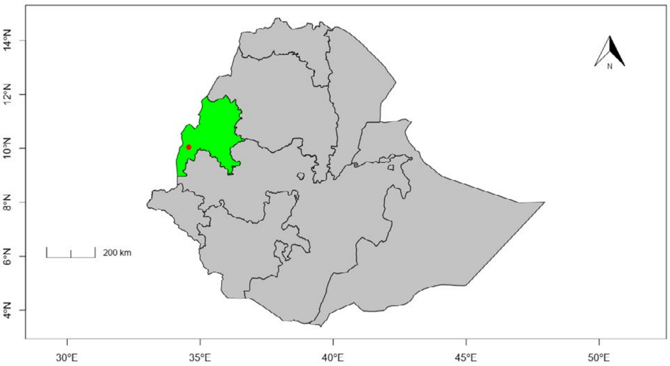

Figure 1: Map of the study area; green color is Benishangul Gumuz region, Ethiopia and the red point is the specific location where the experiment was conducted.

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Table 1: Bread whet genotypes evaluated against Fusarium head blight disease.

Genotype code	Pedigree	Genotype code	Pedigree
1	Tacupetof2001/brambling//kiritati/3/francolin#1/blouk#1/4/francolin#1/blouk #1	27	Fret2*2/shama/3/pfau/weaver//brambling*2/4/huw234+lr34/prinia*2//yanac
2	Bav92//irena/kauz/3/huites*2/4/chil/chum18/5/pbw343*2/kukuna*2//frtl/pifed/6/bav92//irena/kauz/3/huites/4/2*rolf07	28	Tacupetof2001/6/cndo/r143//ente/mexi_2/3/aegilopssquarrosa(taus)/4/weaver/5/pastor/7/rolf07/8/pbw343*2/kukuna*2//frtl/pifed
3	Kfa//pbw343/pastor/3/pbw343*2/kukuna/4/kachu#1//pi610750/sasia/3/kachu/5/kfa/3/pfau/weaver//brambling/4/pfau/weaver*2//brambling	29	Kachu#1/kiritati//kachu/5/bav92//irena/kauz/3/huites/4/2*rolf07
4	Neloki*2/4/sokoll//pbw343*2/kukuna/3/attila/pastor	30	Ciro16*2/3/muu #1/saual//muu
5	Baj #1*2/premio	31	C80.1/3*batavia//2*wbll1/5/reh/hare//2*bcn/3/croc_1/ae.squarrosa(213)//pgo/4/huites/6/francolin#1/blouk#1/7/c80.1/3*batavia//2*wbll1/5/reh/hare//2*bcn/3/croc_1/ae.squarrosa(213)//pgo/4/huites
6	Quaiu/yanac//francolin#1/blouk#1/3/francolin #1/blouk #1	32	Trch/huirivis#1/4/kachu#1//pi610750/sasia/3/kachu/5/kachu #1/kiritati//kachu
7	Pastor/3/ures/jun//kauz/4/wbll1/5/gkaron/agseco7846//2180/4/2*milan/kauz//prinia/3/bav92	33	Kinde*2/4/t.dicocconpi94625/ae.squarrosa(372)//tui/clms/3/2*pastor/5/pbw343*2/kukuna*2//frtl/pifed/6/pbw343*2/kukuna*2//frtl/pifed
8	Sseri1/chibia/4/bav92//irena/kauz/3/huites/5/kza//wh542/2*pastor/3/baceu#1/6/fret2/kukuna//fret2/3/heilo	34	Saual*2/3/wl6718//2*prl/vee#6/4/2*pbw343*2/kukuna*2//frtl/pifed
9	Baj #1*2/premio	35	Prl/2*pastor//parus/5/nac/th.ac//3*pvn/3/mirlo/buc/4/2*pastor/6/kingbird#1//inqalab91*2/tukuru
10	Norm/wbll1//wbll1/3/tnmu/4/wbll1*2/tukuru/5/pbw343*2/kukuna*2//frtl/pifed/6/pbw343*2/kukuna*2//frtl/pifed	36	Kachu#1/yunmai47//kachu/5/saual/3/c80.1/3*batavia//2*wbll1/4/site/mo//pastor/3/tilhi/6/kachu #1/kiritati//kachu
11	Kfa//pbw343/pastor/3/pbw343*2/kukuna/4/kachu#1//pi610750/sasia/3/kachu/5/kfa/3/pfau/weaver//brambling/4/pfau/weaver*2//brambling	37	Quaiu#1/3/kingbird#1//inqalab91*2/tukuru
12	Wbll1/kukuna//tacupetof2001/3/up2338*2/vivitsi/4/2*pbw343*2/kukuna*2//frtl/pifed	38	Cno79//pf70354/mus/3/pastor/4/bav92*2/5/har311/6/trch/huirivis #1
13	Pbw343*2/khvaki*2//yanac/4/muu#1//pbw343*2/kukuna/3/muu/5/chipak	39	Saual*2/6/cndo/r143//ente/mexi_2/3/aegilopssquarrosa(taus)/4/weaver/5/2*pastor*2/7/pbw343*2/kukuna*2//frtl/ pifed
14	Pbw343*2/kukuna*2//frtl/pifed*2/3/bokota	40	Kachu/sup152
15	Babax/lr42//babax/3/er2000/5/w15.92/4/pastor//hxl7573/2*bau/3/wbll1	41	Saual*2/3/wl6718//2*prl/vee#6/4/2*pbw343*2/kukuna*2//frtl/pifed
16	Kfa/3/pfau/weaver//brambling/4/pfau/weaver*2//brambling*2/5/quelea	42	Saual/3/c80.1/3*batavia//2*wbll1/4/site/mo//pastor/3/tilhi*2/5/kingbird#1//inqalab91*2/tukuru
17	Kachu#1/3/c80.1/3*batavia//2*wbll1/4/kachu/8/tacupetof2001/6/cndo/r143//ente/mexi_2/3/aegilopssquarrosa(taus)/4/weaver/5/pastor/7/rolf07/9/kfa/2*kachu	43	Cno79//pf70354/mus/3/pastor/4/bav92*2/5/har311/6/pbw343*2/kukuna*2//frtl/pifed/7/cno79//pf70354/mus/3/pastor/4/bav92*2/5/har311
18	Babax/lr42//babax/3/er2000/4/nighar	44	Saual/mutus/3/pbw343*2/kukuna*2//frtl/pifed/4/pbw343*2/kukuna*2//frtl/pifed
19	Altar84/ae.squarrosa(221)//3*borl95/3/ures/jun//kauz/4/wbll1/5/mutus/6/kingbird #1//inqalab 91*2/tukuru	45	Attila*2/pbw65*2//murga/3/francolin#1//wbll1*2/kiritati
20	Kfa/2*kachu*2/8/tacupetof2001/6/cndo/r143//ente/mexi_2/3/aegilopssquarrosa(taus)/4/weaver/5/pastor/7/rolf07	46	Bokota/3/2*kingbird #1//inqalab 91*2/tukuru
21	Trch/huirivis#1/3/pbw343*2/kukuna*2//frtl/pifed	47	Kfa/2*kachu*2/8/tacupetof2001/6/cndo/r143//ente/mexi_2/3/aegilopssquarrosa(taus)/4/weaver/5/pastor/7/rolf07
22	Kfa/2*kachu/4/wbll1*2/kuruku//kronstad f2004/3/wbll1*2/brambling	48	Pbw343*2/kukuna*2//frtl/pifed/5/kachu#1/3/c80.1/3*batavia//2*wbll1/4/kachu
23	Up2338*2/shama/3/milan/kauz//chil/chum18/4/up2338*2/shama/5/up2338*2/vivitsi/3/fret2/tukuru//fret2/4/misr 1	49	Sumai #3
24	Saual/4/croc_1/ae.squarrosa(205)//kauz/3/attila/5/saual/6/kingbird#1//inqalab91*2/tukuru/7/saual/whear//saual	50	Gamenya(kenyas117a/2*gabo//mentana/6*gabo)
25	Bokota/5/up2338*2/vivitsi/3/fret2/tukuru//fret2/4/misr1/6/babax/lr42//babax*2/3/kukuna/4/crosbill #1/5/becard	51	Localcheck[kingbird(tam200/tui/6/pvn//car422/ana/5/bow/crow//buc/pvn/3/yr/4/trap#1)]
26	Otus//wbll1*2/tukuru/3/2*pbw343*2/kukuna*2//frtl/pifed	52	Local check [wane (sokoll/excalibur)]

Experimental procedures

The experiments were laid on randomized complete block design (RCBD) having two replications. Kernels of each genotype were disinfected and air-dried under laminar flow. An autoclaved sand/peat/compost: 1:3:1 v/v mix soil had used to fill the pots. Six kernels for each genotype had sown in pot and later thinned to three plants per pot. Each pot was fertilized, with 5 g NSP at tillering and 5 g urea at booting.

Inoculum suspension had prepared from highly virulent F. graminearum and F. culmorum mixtures. The inoculum conidia concentration was 5 x 10^4 conidia per ml. A single centrally positioned floret was injected with 10 µl conidia suspension at Zadok's growth stage 65. After inoculation, the spikes were covered with polythene bags for 72 hours (Figure 2) to maintain humidity that facilitates infection.

Data collection

Bleached spikelets were carefully inspected at weekly intervals up to 28 days after inoculation to determine FHB type-II resistance. FHB severities had recorded as described by. Finally, inoculated spikes were harvested and threshed for percent Fusarium damaged kernels (%FDK) determination. The area under the disease progress curve (AUDPC) was determined as follows:

$$\text{AUDPC} = \sum_{i=1}^{n} \left\{ \left(\frac{y_i + y_{i+1}}{2} \right) \left(t_i - t_{i-1} \right) \right\}$$

Where: AUDPC is the area under disease progress curve, n is total number of observation days at the i^{th} observation, y_i is spikelet infection severity at the i^{th} observation, it is time at the i^{th} observation.

Data analysis

Analysis of variance for spikelet bleaching severity and AUDPC had done with the general linear model procedure of the SAS 9.3 version. LSD was used to separate treatment means at a probability level of 0.05 (Figures 1 & 2).

Results and Discussions

The resistant (Sumai#3) and susceptible (Gamenya) checks showed FHB severities of 34.2% and 100%, indicating the isolates were virulent. The susceptible Gamenya had the highest (100%) FHB severity and %FDK per spike (Figure 3, Tables 3 & 4). Of the genotypes evaluated, 22 (42.31%) showed resistance levels better than Sumai#3 (Table 3). This study found that three (5.8%) genotypes were exhibited less than 10% FDK (Table 4) (Table 2).

Df degree of freedom, DH days to heading, SS number of spikelets per spike, %ISS percent of infected spikelets per spike, AUDPC area under disease progress curve, %FDK percent Fusarium damaged kernels, *** highly significant ($p < 0.0001$).

According to FHB disease scores, 15.38% of the genotypes had shown R reaction (Figure 4), but most of the genotypes (51.92%) had shown MR reaction to the mixture of dominant F. graminearum and F. culmorum (Table 3). In the same way, based on diseased or bleached spikelets per spike, 9.62%, 21.15%, and 7.69% of the genotypes showed HR, R, and MR reactions, respectively (Table 4) (Figures 3 & 4).

A significant difference in the mean values for the area under the disease progress curve (AUDPC) had observed between different genotypes (Table 2). The current study found that the AUDPC of the number of Fusarium-infected spikelets for the genotypes 21, 16, 4, 31, and 29 are the lowest AUDPC of 9.7, 10.9, 13.5, 20.2, and 21.7 (Table 3), while the susceptible Gamenya recorded very high AUDPC value (662.1). In this study, 42.3% genotypes recorded lower AUDPC values than the resistant check Sumai#3 (175). It is, therefore, clearly established that genotypes 21, 16, 4, 31, and 29 behave resistant to the progression of bleaching spikelets after inoculation (Table 3).

The analysis of variance showed that there is a significant difference ($p < 0.001$) between genotypes for %FDK (Table 2). The mean %FDK values showed a variable response, with a minimum value of 6.9% recorded on genotype 31 and a maximum of 100% recorded on genotypes 7, 8, 19, 38, and Gamenya (susceptible check), meaning a 90-

Figure 2: Polythene bags covering of inoculated spikes to maintain high humidity.

Figure 3: Total spike bleached in susceptible genotype at 28 DAI.

Table 2: Analysis of variance for days to heading, number of spikelets per spike, area under disease progress curve, and percent of Fusarium damaged kernels.

Sources	**Df**	**DH**	**SS**	**%ISS**	**AUDPC**	**%FDK**
Genotypes	51	30.58***	23.19***	3381.17***	236884.01***	3710.01***
Error	103	5.63	3.58	1394.40	176825.24	1289.20
Means		**71.16**	**16.23**	**39.36**	**474.88**	**50.86**
CV		**3.33**	**11.66**	**94.86**	**88.55**	**28.55**

Table 3: Reaction of bread wheat genotypes against the mixture of dominant Fusarium head blight pathogens in Ethiopia.

Genotypes	Days to heading	Plant height (cm)	FHB severity at 28 DAI			AUDPC
			Disease scores	Resistance reaction	% infected spikelets	
16	66.5^{g-m}	65.6^{c-j}	1.0^{b}	R	3.1^{b}	10.9^{g}
21	66.5^{g-m}	68.5^{b-j}	1.0^{b}	R	2.8^{i}	9.7^{g}
29	65.0^{i-n}	72.0^{a-g}	1.0^{b}	R	6.2^{b}	21.7^{g}
31	65.0^{i-n}	79.4^{ab}	1.0^{b}	R	5.8^{b}	20.2^{g}
4	69.0^{c-m}	68.5^{b-j}	1.0^{b}	R	3.9^{b}	13.5^{g}
39	63.5^{k-n}	65.3^{c-j}	2.0^{ab}	R	10.3^{b}	49.6^{fg}
41	72.0^{c-j}	60.3^{hij}	2.0^{ab}	R	8.0^{b}	56.3^{fg}
6	72.0^{c-j}	66.3^{c-j}	2.0^{ab}	R	7.5^{b}	35.0^{fg}
12	65.0^{i-n}	67.8^{c-j}	2.5^{ab}	MR	12.8^{b}	68.1^{e-g}
18	62.0^{mn}	71.4^{a-h}	2.5^{ab}	MR	29.3^{ab}	194.4^{b-g}
25	67.0^{f-m}	72.3^{a-g}	2.5^{ab}	MR	17.8^{b}	78.2^{e-g}
3	70.5^{c-k}	69.4^{b-i}	2.5^{ab}	MR	15.4^{b}	98.8^{d-g}
34	62.5^{lmn}	70.0^{lmn}	2.5^{ab}	MR	10.0^{b}	46.7^{fg}
35	71.0^{c-j}	68.5^{b-j}	2.5^{ab}	MR	9.2^{b}	48.9^{fg}
40	75.5^{a-d}	57.9^{j}	2.5^{ab}	MR	10.1^{b}	57.1^{fg}
52	68.0^{e-m}	76.5^{abc}	2.5^{ab}	MR	11.7^{b}	55.4^{fg}
13	68.0^{e-m}	73.5^{a-e}	3.0^{ab}	MR	53.9^{ab}	289.4^{a-g}
15	66.5^{g-m}	70.5^{a-h}	3.0^{ab}	MR	20.0^{b}	105.0^{d-g}
17	72.5^{c-h}	67.5^{c-j}	3.0^{ab}	MR	53.1^{ab}	360.9^{a-g}
2	64.0^{j-n}	69.3^{b-j}	3.0^{ab}	MR	50.0^{ab}	175.0^{c-g}
20	66.0^{h-n}	65.0^{d-j}	3.0^{ab}	MR	53.9^{ab}	340.1^{a-g}
23	68.0^{e-m}	69.4^{b-i}	3.0^{ab}	MR	50.0^{ab}	229.7^{b-g}
49	81.0^{a}	81.3^{a}	3.0^{ab}	MR	34.2^{ab}	175^{c-g}
24	72.0^{c-i}	71.4^{a-h}	3.0^{ab}	MR	25.0^{ab}	165.3^{c-g}
27	72.0^{c-i}	67.3^{c-j}	3.0^{ab}	MR	53.1^{ab}	360.9^{a-g}
30	68.5^{d-m}	69.8^{b-i}	3.0^{ab}	MR	34.8^{ab}	232.8^{a-g}
36	74.0^{a-f}	71.0^{a-h}	3.0^{ab}	MR	20.2^{b}	109.7^{d-g}
37	65.0^{i-n}	71.6^{a-h}	3.0^{ab}	MR	32.5^{ab}	196.9^{b-g}
42	66.0^{h-n}	60.3^{hij}	3.0^{ab}	MR	53.3^{ab}	250.3^{a-g}
43	68.0^{e-m}	68.8^{b-j}	3.0^{ab}	MR	16.7^{b}	87.5^{d-g}
45	65.0^{i-n}	62.3^{e-j}	3.0^{ab}	MR	50.0^{ab}	262.5^{a-g}
46	75.0^{a-e}	71.5^{a-h}	3.0^{ab}	MR	19.4^{b}	106.9^{d-g}
47	67.5^{f-m}	67.3^{c-j}	3.0^{ab}	MR	12.2^{b}	64.2^{e-g}
48	65.5^{h-n}	67.1^{c-j}	3.0^{ab}	MR	53.9^{ab}	366.0^{a-g}
5	67.0^{f-m}	71.8^{a-g}	3.0^{ab}	MR	34.3^{ab}	214.4^{b-g}
10	68.5^{d-m}	76.0^{a-d}	4.0^{ab}	MS	42.2^{ab}	287.3^{a-g}
11	62.5^{lmn}	68.9^{b-j}	4.0^{ab}	MS	55.9^{ab}	240.9^{a-g}
22	59.0^{n}	68.5^{b-j}	4.0^{ab}	MS	55.9^{ab}	264.8^{a-g}
51	73.5^{b-g}	72.5^{a-f}	4.0^{ab}	MS	24.4^{b}	85.6^{d-g}
9	66.5^{g-m}	70.8^{a-h}	4.0^{ab}	MS	36.7^{ab}	186.7^{b-g}
14	68.0^{e-m}	72.0^{a-g}	4.5^{ab}	S	60.0^{ab}	309.2^{a-g}
32	71.5^{c-i}	64.0^{e-j}	4.5^{ab}	S	34.4^{ab}	200.3^{b-g}
7	71.0^{c-j}	58.5^{ij}	4.5^{ab}	S	72.2^{ab}	454.2^{a-f}
1	69.5^{c-l}	67.4^{c-j}	5.0^{a}	S	100.0^{a}	615.3^{ab}
19	68.5^{d-m}	72.4^{a-f}	5.0^{a}	S	100.0^{a}	517.0^{a-d}
26	63.5^{k-n}	75.5^{a-d}	5.0^{a}	S	71.9^{ab}	389.3^{a-g}
28	70.5^{c-k}	73.5^{a-e}	5.0^{a}	S	57.0^{ab}	308.3^{a-g}
33	68.5^{d-m}	62.0^{f-j}	5.0^{a}	S	100.0^{a}	411.8^{a-g}
38	65.0^{i-n}	69.3^{b-j}	5.0^{a}	S	100.0^{a}	584.1^{a-c}
44	69.5^{c-l}	72.3^{a-g}	5.0^{a}	S	73.8^{ab}	489.7^{a-e}
50	80.5^{ab}	60.9^{g-j}	5.0^{a}	S	100.0^{a}	662.1^{a}
8	76.0^{abc}	73.3^{a-f}	5.0^{a}	S	76.2^{ab}	371.9^{a-g}
Mean	**71.16**		**3.20**		**39.33**	**217.98**
LSD	**7.5**	**11.65**	**3.94**		**75.6**	**431.52**
CV	**5.4**	**8.32**	**61.06**		**95.5**	**88.9**

Keys: FHB is Fusarium head blight, R is resistant, MR is moderately resistant, MS is moderately susceptible, S is susceptible, and means with the same letter in the column are not statistically different.

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Table 4: Response of bread wheat genotypes to the mixture of F graminearum and F culmorum at Assosa.

Genotypes	Number of spikelets per spike	Diseased spikelets per spike	Resistance level	% of Fusarium damaged kernels per spike	Response
4	11.5^{k}	0.5^{g}	HR	20.6^{de}	S
16	17.0^{c-i}	0.5^{g}	HR	37.5^{a-e}	S
21	16.5^{d-j}	0.5^{g}	HR	14.9^{de}	MS
29	16.5^{d-j}	1.0^{g}	HR	9.3^{e}	MR
31	17.5^{b-h}	1.0^{g}	HR	6.9^{e}	R
6	20.0^{a-d}	1.5^{fg}	R	19.0^{de}	MS
34	14.5^{g-k}	1.5^{fg}	R	21.3^{de}	S
39	16.0^{e-j}	1.5^{fg}	R	16.6^{de}	MS
40	17.0^{c-i}	1.5^{fg}	R	20.0^{de}	MS
41	18.5^{a-f}	1.5^{fg}	R	26.1^{cde}	S
52	13.5^{i-k}	1.5^{fg}	R	9.2^{e}	MR
12	16.5^{d-j}	2.0^{fg}	R	13.7^{de}	MS
25	11.5^{k}	2.0^{fg}	R	30.6^{b-e}	S
35	21.0^{ab}	2.0^{fg}	R	12.9^{de}	MS
43	13.5^{i-k}	2.0^{fg}	R	72.0^{a-e}	VS
47	16.5^{d-j}	2.0^{fg}	R	14.0^{de}	MS
3	20.5^{a-c}	3.0^{efg}	MR	92.6^{abc}	VS
15	13.5^{i-k}	3.0^{efg}	MR	21.4^{de}	S
36	16.0^{e-j}	3.5^{d-g}	MR	26.0^{cde}	S
46	19.0^{a-e}	3.5^{d-g}	MR	35.1^{a-e}	S
5	13.5^{i-k}	4.5^{c-g}	MS	40.8^{a-e}	S
24	18.0^{b-g}	4.5^{c-g}	MS	91.7^{abc}	VS
51	19.0^{a-e}	4.5^{c-g}	MS	17.1^{de}	MS
18	17.5^{b-h}	5.0^{b-g}	MS	29.4^{cde}	S
9	15.0^{f-k}	5.5^{b-g}	MS	47.2^{a-e}	S
30	15.0^{f-k}	5.5^{b-g}	MS	56.0^{a-e}	VS
32	16.5^{d-j}	5.5^{b-g}	MS	73.8^{a-e}	VS
37	16.5^{d-j}	5.5^{b-g}	MS	60.9^{a-e}	VS
42	13.0^{jk}	6.0^{b-g}	MS	53.2^{a-e}	VS
2	13.0^{jk}	6.5^{b-g}	S	36.6^{a-e}	S
49	22.0^{a}	6.5^{b-g}	S	15.6^{de}	MS
10	15.5^{e-j}	7.0^{a-g}	S	58.8^{a-e}	VS
20	14.0^{h-k}	8.0^{a-g}	S	63.5^{a-e}	VS
23	14.0^{h-k}	8.0^{a-g}	S	60.6^{a-e}	VS
45	14.0^{h-k}	8.0^{a-g}	S	53.6^{a-e}	VS
11	16.0^{e-j}	8.5^{a-g}	S	54.8^{a-e}	VS
27	16.0^{e-j}	8.5^{a-g}	S	75.0^{a-e}	VS
48	14.5^{g-k}	8.5^{a-g}	S	56.4^{a-e}	VS
7	11.5^{k}	9.0^{a-g}	S	100.0^{a}	VS
13	15.5^{e-j}	9.5^{a-g}	S	62.5^{a-e}	VS
14	15.5^{e-j}	9.5^{a-g}	S	56.6^{a-e}	VS
17	17.0^{c-i}	9.5^{a-g}	S	80.4^{a-d}	VS
22	17.5^{b-h}	10.0^{a-g}	S	60.6^{a-e}	VS
28	17.5^{b-h}	10.0^{a-g}	S	92.3^{abc}	VS
26	16.5^{d-j}	12.0^{a-g}	S	79.0^{a-d}	VS
44	19.0^{a-e}	13.5^{a-f}	S	98.8^{ab}	VS
8	20.0^{a-d}	15.0^{a-e}	S	100.0^{a}	VS
38	15.5^{e-j}	15.5^{a-d}	HS	100.0^{a}	VS
1	16.0^{e-j}	16.0^{abc}	HS	94.4^{abc}	VS
19	17.0^{c-i}	17.0^{ab}	HS	100.0^{a}	VS
33	17.0^{c-i}	17.0^{ab}	HS	55.6^{a-e}	VS
50	19.0^{a-e}	19.0^{a}	HS	100.0^{a}	VS
LSD	**2.008**	**12.5**		**69.4**	

Keys: HR is highly resistant, R is resistant, MR is moderately resistant, MS is moderately susceptible, S is susceptible, HS is highly susceptible, VS is very susceptible, and means with the same letter in the column are not statistically different.

fold difference (Table 4; Figure 5). According to Agostinelli et al, %FDK reveals kernel damage and is more linked to a decrease in test weight and, somehow drops in yield. Also, kernels with less %FDK exhibited fewer toxins. Similarly, Bai et al. and Lehoczki-Krsjak et al. reported a direct correlation among %FDK and DON. Based on this, %FDK was reported as another parameter for determining FHB type-II resistance in wheat. FHB type-II resistance is ascribed to cell wall thickening of rachis nodes and mycotoxin decomposition. Based on this evidence, the present study found that genotype 31 was the most FHB type-II resistant, followed by genotypes 59 and 29 with 9.2% and 9.3% percent FDK, respectively (Table 4, Figure 5). Out of 52 genotypes of bread wheat evaluated in this study, genotype 31 had chosen as putative FHB resistant sources based on disease score, diseased spikelets per spike, and %FDK (Table 3, Table 4). In addition, genotype 29 showed good resistance to FHB under controlled condition in Ethiopia (Table 3, Table 4) (Figure 5).

Figure 4: Single spikelet bleached in resistant genotype at 28 DAI.

As illustrated in Table 2, bread wheat genotypes had shown significant differences for days to heading (DH). Sumai#3 (81 DH) and Gamenya (80.5 DH) showed the highest number of DH, respectively. In addition, the promising FHB-resistant genotypes 31 and 29 recorded 65 DH, which is almost similar to well adapted and released Kingbird (73.5 DH) and Wane (68 DH) varieties (Table 5). Thus, these promising FHB-resistant genotypes were acceptable height in Ethiopia (Table 4).

This study also found significant differences among bread wheat genotypes in plant height (Table 2). The mean values of bread wheat genotypes for plant height (PH) were shorter at Assosa than at Holeta. These could be related to higher altitude, higher rain fall, and relatively lower temperature at Holeta site, which might have increased the height of bread wheat plants at this location. Likewise, Muhder et al. reported that temperature, altitude, and precipitation meaningfully and evenly influenced the plant height of bread wheat genotypes.

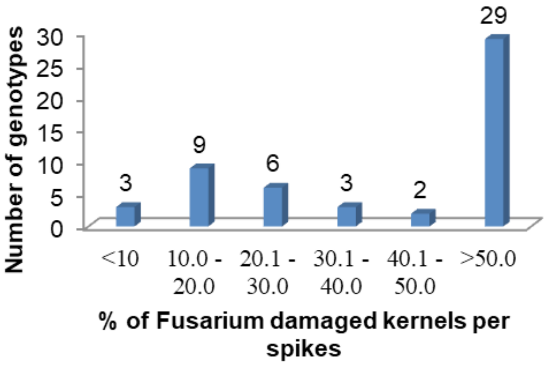

Figure 5: Reaction of 52 bread wheat genotypes against FHB disease in Assosa.

Table 5: Plant height, 1000 Kernel weight, agronomic score, and yield of bread wheat genotypes at HARC nursery.

Genotype	Height (cm)	1000 kernel (g)	Agronomic score (5=best)	Yield (g)	Genotype	Height (cm)	1000 kernel (g)	Agronomic score (5=best)	Yield (g)
1	90	32.0	2.5	598.9	26	75	38.0	2.5	275.0
2	95	37.6	2.5	682.4	27	95	30.0	2.5	431.2
3	95	36.0	2.5	555.6	28	95	23.2	2.0	278.8
4	80	32.8	2.5	558.5	29	90	26.8	2.0	313.2
5	95	40.8	3.0	677.1	30	95	19.2	2.0	368.1
6	90	26.4	2.0	481.5	31	90	31.6	2.5	587.1
7	95	30.0	2.0	442.9	32	85	27.2	2.5	444.6
8	100	28.8	2.0	548.1	33	90	24.8	2.5	359.7
9	95	42.4	3.5	695.4	34	95	35.6	3.0	520.1
10	95	38.0	2.5	485.7	35	100	31.2	3.0	467.5
11	95	36.0	2.5	618.0	36	95	27.2	2.5	377.5
12	90	20.8	2.0	401.4	37	85	30.8	2.0	298.7
13	93	39.2	3.0	589.7	38	85	34.4	2.5	517.9
14	90	31.2	3.0	590.5	39	85	28.8	3.0	507.2
15	80	30.0	2.5	358.2	40	85	23.6	2.0	361.6
16	85	26.0	2.5	441.2	41	95	25.6	2.5	528.9
17	85	25.6	2.0	346.8	42	95	26.4	2.5	417.8
18	90	40.0	3.0	484.9	43	85	38.8	3.0	458.4
19	85	24.4	2.0	193.0	44	100	28.0	2.5	582.1
20	90	26.0	2.5	375.5	45	95	27.6	2.0	366.4
21	90	30.4	2.5	475.8	46	95	24.4	2.0	257.7
22	95	31.6	2.0	361.9	47	90	30.8	2.5	458.0
23	95	30.8	3.0	528.5	48	95	35.2	3.0	587.4
24	90	20.8	2.5	312.0	49	130	34.0	4.0	558.7
25	80	25.6	2.0	305.6	50	115	18.8	2.0	276.2

Keys: HARC = Holeta Agricultural Research Center

According to Buerstmayr et al. and Khanizadeh et al. taller plants have less FHB disease than shorter ones, which indicates that plant height is a passive mechanism for FHB resistance? The promising genotypes 31 and 29 had almost the same plant height as the well-adapted and released varieties in the country (Table 5).

Conclusions

Five genotypes (4, 16, 21, 29, and 31) were highly resistant based on diseased spikelets of 0.5–1.0 (disease severity 2.8%–6.2%), eleven genotypes (6, 39, 41, 34, 40, 52, 12, 25, G35, 43, and 47) were resistant with diseased spikelets of 1.5–2.0 (disease severity 7.5%–17.8%). However, based on %FDK, genotype 31 was founded to be resistant and only produced 6.9%FDK. Next, to genotype 31, cultivar wane (with 9.2%FDK) and genotype 29 (with 9.3%FDK) showed moderate resistance against FHB disease. Undeniably, genotype 31 was founded to be highly resistant based on diseased spikelets per spike and resistant based on disease scores. Therefore, the bread wheat breeding program may introduce genotypes 31 and 29 as a source of resistance to improve the resistance of bread wheat against FHB disease in Ethiopia. Many genes control FHB disease resistance in bread wheat. Therefore, it requests a continuous screening of bread wheat genotypes to identify resistance sources and using them for evolving resistant cultivars. These can exist when there are motivated researchers and strong support from the government to have FHB-resistant cultivars that ensure safe foods.

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