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Genotype by environment interaction analysis for Fusarium head blight response and yield performance of bread wheat (*Triticum aestivum* L.) in southern Ethiopia

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Abstract

Fusarium head blight (FHB) is one of the major biotic constraints to wheat due to its direct detrimental effects on yield quality and quantity. To manage the disease, the deployment of resistant genotypes is ideal in terms of effectiveness, eco-friendliness, and sustainability of production. The study was conducted to determine the responses of different wheat genotypes to FHB, and to identify suitable and stable wheat genotype(s) regarding the FHB resistance and yield performance. A field study was carried out using eleven bread wheat genotypes in seven locations in southern Ethiopia during the 2019 main cropping season. A randomized complete block design with three-time replicates was applied in this study. The results showed that the lowest mean FHB severity (11.33%) and highest mean yield (4.54 t/ha) were recorded at Bonke. Conversely, the highest mean FHB severity (83.38%) and the lowest mean yield (0.94 t/ha) were observed at North Ari. It was also showed that maximum mean FHB severity (49.25%) and minimum mean yield (2.95 t/ha) were recorded on the genotype Hidase under crosswise assessment. Across locations, a minimum mean FHB severity (17.54, 18.83, and 21.31%) and maximum mean yield (3.92, 3.96, and 3.93 t/ha) were noted from the Shorima, Bondena, and Wane genotypes, respectively. GGE biplot analysis and various comparison tests for FHB severity revealed a higher percentage of variation concerning FHB resistance reactions due to the environment (47% as an interactive element), followed by genotype by environment interaction (21%). AMMI analysis revealed genotype, environment, and genotype by environment interaction had a total variation of 7.10, 58.20, and 17.90% for yield performance, respectively. The inconsistency between genotype responses to FHB and yield performance demonstrated that the environmental component was responsible for significant variability in FHB reaction, yield performance, and the dominance of cross-over interaction. However, the greatest level of resistance to FHB was comparatively found in the genotypes Shorima, Bondena, Wane, and Huluka across locations. Considering both FHB resistance response and yield stability, in most environments, Shorima, Bondena, Wane, and Huluka genotypes were suggested for consideration of cultivation where they are well-performed under the pressure of FHB. North Ari and Hulbareg

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were acknowledged as more discriminating environments than the others for test genotypes against FHB. Bonke and Chencha were considered ideal environments for selecting superior genotypes with good yield performance.

Keywords: AMMI and GGE-biplot analysis, Environment, Fusarium head blight, Genotype-by-environment interaction, Resistance reaction, Severity, Wheat genotype, Yield performance

Background

Cereal crops provide essential nutrients and energetic yield in daily human food through direct consumption as well as beef production as a key livestock feed (Alicia and Holopainen-Mantila 2020). Among cereals, wheat (*Triticum* spp.) is the world's leading crop, and more than one-third of the world's population consumes it as a staple food. In addition, the crop participates in food security and global market share (FAO et al. 2018; FAO 2020; USDA 2018). Ethiopia is one of the major wheat-producing countries in Africa next to Egypt and Morocco, and it has an annual grain production of 4 million tons (CSA 2018; FAOSTAT 2018). In southern Ethiopia, the crop produced on 151,584 hectares of land contributed more than 400 thousand tons of yield in 2018 (CSA 2018). However, wheat production in Ethiopia is being significantly affected by multiple abiotic and biotic factors, including climate change and those related to crop management (Zegeye et al. 2001; Ayele et al. 2008; Dunwell 2014). Due to this, the mean productivity of wheat is far below in Ethiopia (2.77 t/ha) as well as in southern Ethiopia (2.66 t/ha) compared with the world's productivity (3.77 t/ha) in 2018 (CSA 2018; FAOSTAT 2018). However, according to the Ministry of Agriculture and Natural Resources (MANR) and Ethiopian Agricultural Transformation Agency (EATA), the productivity of the crop ever reached more than 7 t/ha under research and more than 4 t/ha under farmers' field conditions (MANR and EATA 2018).

Among biotic constraints, Fusarium head blight (FHB), or head scab of wheat, is a widespread and destructive disease that damages the head/spike, limits productivity, and reduces yield worldwide, including in Ethiopia. The disease is caused by a number of *Fusarium* species, of which *Fusarium graminearum* Schwabe [teleomorph *Gibberella zeae* (Schwein.) Petch] is a well-known causal agent worldwide (Gilbert and Tekauz 2000; Dean et al. 2012; Gilbert and Haber 2013; Earecho et al. 2020; Shude et al. 2020; Mengesha et al. 2021). The disease has not been as well studied as other wheat diseases in Ethiopia (Earecho et al. 2020; Mengesha et al. 2021). The harvested grains infected with the pathogen are small, light, pre-mature, shriveled, shrunken, and sometimes covered with white or pink fungal mass and contaminated with mycotoxins (deoxynivalenol, DON) (Langseth et al. 1995; Andersen et al. 2014; Karasi et al. 2016). Grain losses range from medium to high due to complete spike failure (50–100%), depending on the severity of FHB (Windels 2000; Pirgozliev et al. 2003). A remarkable destructive outbreak occurred in southern Ethiopia during the 2017 and 2018 cropping seasons, according to the report of the Southern Regional Bureau of Agriculture and respective districts of the office of Agriculture within the region. Considerable damage has been witnessed in the study areas, especially in Adiyo, Bench, and North Ari districts. In some fields, nearly a 100% yield loss has been reported during the growing seasons. Therefore, reducing FHB pressure and associated yield loss calls for designing effective, eco-friendly, and sustainable management schemes for the study areas as well as the country.

Disease management options such as removal of crop residues, deep plowing, intercropping with legume crops, crop rotations, cultivation of moderately resistant crop varieties, seed treatment and foliar sprays of fungicides, and integrated management approaches are the main recommended practices to reduce damage/loss caused by FHB (Karasi et al. 2016; Shude et al. 2020). However, even if FHB management through a fungicidal approach is an efficient option, it has negative impacts due to the long-term use of a certain fungicide. Long-term fungicide use, on the other hand, may result in fungicide resistance in the pathogen population and the accumulation of toxic residues that endanger the environment, human health, and non-target organisms (Green et al. 1990; Mostafalou and Abdollahi 2012; Foster et al. 2017). For this reason, Agrios (2005) suggested that the use of host resistance is the most reliable, effective, and economically profitable approach among various crop disease manage approaches. Other studies have found that using resistant cultivars is the most efficient, eco-friendly, and cost-effective way to reduce the severity of FHB in different parts of the world (Gilbert and Haber 2013; Beres et al. 2018; Ghimire et al. 2020; Shude et al. 2020). This approach, host resistance, is supposed to reduce yield loss, fungicide use, and production costs, thus enhancing profitability and lessening negative impacts on the environment (Singh and Schwartz 2010; Gilbert and Haber 2013; Ghimire et al. 2020; Shude et al. 2020).

However, the identification of resistance genotypes coupled with high yield potential is significantly influenced by the environment and the genotype itself besides pathogen factors (Rubiales 2012; Sharma et al.

2015; Tekalign et al. 2017; Akan and Akcura 2018; Das 2019; Goddard et al. 2021). Moreover, many researchers reported that testing wheat genotypes for resistance to FHB in areas where the environmental conditions are favorable for the development of the disease could be a worthwhile approach that determines the effectiveness of the selection process in resistance breeding programs (Trail et al. 2002; Doohan et al. 2003; Buerstmayr et al. 2008; Karasi et al. 2016; Beres et al. 2018; Zhu et al. 2019; Hautsalo et al. 2020). Nevertheless, because of the existence of broad variability within host, environment, and pathogen population, understanding the interaction between and among these factors for a particular pathosystem can be difficult and challenging (Yan and Falk 2002). Realizing the role of the environment (mainly locations where the study was conducted, agro-ecologies, and weather conditions) and genotype-by-environment interaction (GEI) regarding the pathosystem and host genotype stability around various locations is imperative for an effective resistance breeding program. Thus, a suitable analytical model of the genotype main effect plus genotype by environment interaction biplot technique (GGE biplot) is commonly used to estimate the response of the genotypes for various reasons. It is one of the most effective tools to diagnose GEI patterns graphically for determining the GEI interaction concerning disease resistance over multi-location trials (Yan and Falk 2002; Yuksel et al. 2002; Kadariya et al. 2008; Gitonga et al. 2016; Akan and Akcura 2018).

On the other hand, pooled analysis of variance (ANOVA) can be utilized to quantify GEI and depict the main effect. This approach, however, does not adequately elucidate the interaction between test genotypes and environments for determining stable and high-yielding genotypes (Yan and Falk 2002; Yan et al. 2007; Admassu et al. 2008). As a result, the use of simple ANOVA might be failing to differentiate genotype(s) that shows specific or broad adaptation in multi-location studies. For this reason, to describe the interaction of the main effects beyond ANOVA, supplementary statistical models could be applied to meet the objective (s) of the study. Accordingly, the additive main effects and multiplicative interaction model (AMMI model) were suggested for such kinds of studies (Zobel et al. 1988). In comparison, AMMI stability and GGE biplot analysis may be preferable tools for identifying stable, high-yielding, and adaptable genotype(s) for broad or specific environments under plant disease pressure (Zhang et al. 1998; Purchase et al. 2000; Yan and Falk 2002). Moreover, the AMMI model can handle both the additive main effect and multiplicative interaction constituents by employing variance of analysis and the Interaction Principal Components Axis (IPCA), respectively (Gauch and Zobel 1996).

Therefore, the identification of stable and resistant genotype(s) of wheat against FHB and their subsequent judicious use in resistance breeding programs would be an efficient and effective approach for sustainable wheat production. In recent times, AMMI and GGE biplot analyses have been employed to assess genotypes with broad or particular adaptations associated with resistance to different plant pathogens in many crops in different parts of the world (Kadariya et al. 2008; Rubiales 2012; Sharma et al. 2015; Tekalign et al. 2017; Akan and Akcura 2018; Das 2019; Singh et al. 2020). Disease intensity could help to determine the levels of damage on the head/spike (Engle et al. 2003; Sharan et al. 2004) and is correspondingly used in AMMI and GGE biplot analysis (Yan et al. 2000; Yan and Falk 2002; Sharma et al. 2016). In addition to this, the AMMI model is effective in understanding GEI as well as in increasing the precision of making genotype recommendations for various target and testing locations. Here, we reported the results of a multi-location field study carried out in southern Ethiopia during the 2019 main cropping season, aiming to (i) determine the response of different wheat genotypes to FHB and their yield performances, (ii) identify suitable and stable wheat genotype(s) regarding the FHB resistance and potential yield, and (iii) determine the discriminating and representative ability of the test locations.

Results

Symptoms and identified Fusarium head blight-causing species

Natural occurrence of FHB disease on the evaluated wheat genotypes was observed, as shown by various symptoms that appeared on the spikes and spikelets (Fig. 1). Typical symptoms of FHB first appeared on the genotypes Hidase, Kakaba, Danda'a, Kingbird, and Ogolcho across locations, manifested with discolored (light-brown or pinkish-white) spikes and spikelets (Fig. 1b–g), and shrunken and premature kernels (Fig. 1h). The formation of black spherical structures (perithecia) was also observed on spikes and spikelets of these wheat genotypes (Fig. 1b–d). In contrast, healthy spikes and spikelets were still green in color (Fig. 1a).

On the other hand, the results obtained from the laboratory work showed that *F. graminearum, F. culmorum, F. avenaceum, F. poae, F. ussurianum, F. semitectum, F. lateritium, F. sambucinum,* and *F. heterosporum* are the major identified *Fusarium* species that infected the test genotypes across locations (Table 1), and all test genotypes were infected by *F. graminearum*. The genotypes Bondena, Shorima, and Wane were infected by all the identified *Fusarium* species, followed by the Ogolcho genotype, which was not infected by *F. lateritium*.

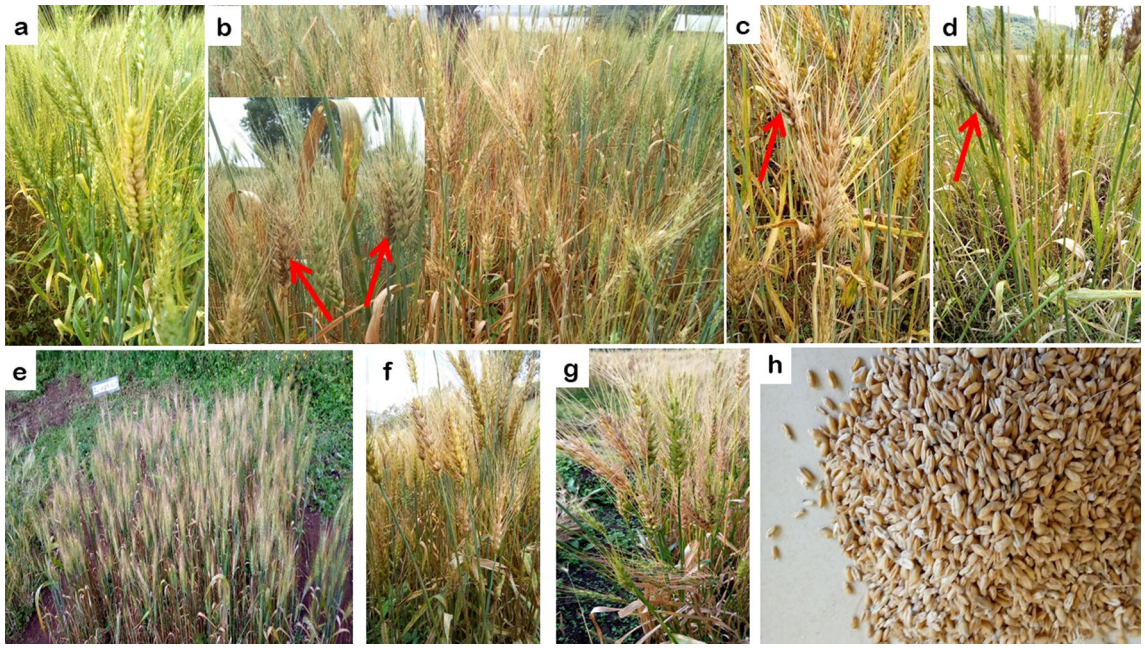

Fig. 1 Typical symptoms of Fusarium head blight on spikes of some highly-infected wheat genotypes in the experimental plots. **a** Infected spikes and spikelets with water-soaked injuries and healthy heads on Kakaba genotype. **b**–**g** Infected and complete death of spikes on Kingbird (**b**), Ogolcho (**c**), Kubsa (**d**), Huluka (**e**), Lemu (**f**), and Hidase (**g**) genotypes; black spherical structures or perithecia formation on Kingbird (**b**), Ogolcho (**c**), and Kubsa (**d**) genotypes as indicated by red arrows. **h** pre-mature, shrunken, and shriveled grains from Danda'a genotype

Table 1 Fusarium species causing Fusarium head blight isolated from the evaluated wheat genotypes

Wheat genotypes	Identified *Fusarium* species causing Fusarium head blight[a]								
	F. graminearum	*F. culmorum*	*F. heterosporum*	*F. avenaceum*	*F. ussurianum*	*F. semitectum*	*F. poae*	*F. sambucinum*	*F. lateritium*
Bondena	+	+	+	+	+	+	+	+	+
Danda'a	+	+	+	+	−	−	+	+	−
Huluka	+	+	+	+	−	−	+	−	+
Hidase	+	+	+	+	+	+	+	+	−
Kakaba	+	−	−	+	+	−	−	−	+
Kingbird	+	+	+	−	−	+	−	−	−
Kubsa	+	−	−	+	−	+	+	−	−
Lemu	+	−	−	−	−	−	−	−	−
Ogolcho	+	+	+	+	+	+	+	+	−
Shorima	+	+	+	+	+	+	+	+	+
Wane	+	+	+	+	+	+	+	+	+

[a] Positive sign (+) indicates that the wheat genotype infected by the identified *Fusarium* species in the column; Negative sign (-) indicates that the wheat genotype was not infected by that particular *Fusarium* species in the column

Other test genotypes such as Danda'a, Huluka, and Hidase were infected by *F. culmorum, F. heterosporum, F. avenaceum,* and *F. poae* besides *F. graminearum.* Overall, *F. graminearum*, followed by *F. culmorum, F. heterosporum, F. avenaceum,* and *F. poae,* was prevalent across the experimental locations (Table 1).

Analysis of variance for randomized complete block design (RCBD) of study parameters

The mean square results obtained from the combined ANOVA for disease scores and yield-related parameters over environments were presented in Table 2. The combined ANOVA over environments/locations exhibited

Table 2 Combined analysis of variance for mean squares of disease score and yield-related traits across locations in southern Ethiopia during the 2019 main cropping season

Source of variation[a]	DF[b]	Study parameters[c, d]				
		DI_f (%)	DS_f (%)	AUDPC (%/days)	TKW (g)	Yield (t/ha)
REP (within LOC or ENV)	14	35.18 ^{ns}	155.84 ^{ns}	5196.63 ^{ns}	6.67 ^{ns}	1.44 ^{ns}
LOC (or ENV)	6	24,831.51****	10,331.72****	1,381,930.24****	1196.66****	48.13****
GEN	10	1887.23*	2463.86**	19,128,338***	89.25 ^{ns}	3.74**
ENV × GEN	60	586.76****	574.12****	55,364.20****	60.70****	1.38****
Pooled error	154	59.61	69.76	6213.71	4.52	0.53
Pooled F-value		44.82****	22.84****	28.64****	34.12****	10.25****
Grand mean		41.06	32.01	304.32	36.63	3.37
CV (%)		18.80	26.09	25.90	5.80	21.54

[a] REP, replication; LOC, location; ENV, environment; GEN, genotype; ENV × GEN, interaction effect between environment and genotype

[b] DF, degree of freedom

[c] DI_f, disease incidence at a ZGS of 90, during the soft dough stage; DS_f, disease severity at a ZGS of 90, during the soft dough stage; AUDPC, area under disease progress curve; and TKW, thousand kernels weight

[d] Asterisks indicate significant difference (****$P \leq 0.0001$, *** ≤ 0.001, ** $P \leq 0.01$, and * $P \leq 0.05$); ns, not significant ($P > 0.05$); CV = Co, coefficient of variation (%)

significant ($P < 0.0001$) variations for mean squares of environments on disease incidence (DI), disease severity (DS), area under disease progress curve (AUDPC), thousand kernels weight (TKW), and yield. In addition, the combined ANOVA showed that various levels of significance ($P < 0.05$–0.001) for disease scores and yield-related traits, except for TKW, were observed for the mean squares of wheat genotypes. No significant ($P > 0.05$) difference was observed for mean squares of TKW among the tested wheat genotypes. Highly significant ($P < 0.0001$) variations were detected for the mean squares of DI, DS, AUDPC, TKW, and yield due to GEI effects (Table 2). The results exhibited the existence of significant differences among wheat genotypes and environments and their interactions, suggesting the need to carry out further GEI analysis to recognize resistance stability and yield potential of wheat genotypes across environments under FHB challenge. Overall, the highest mean square values for the genotype, environment, and GEI across all tested environments indicated that the tested wheat genotypes responded similarly across locations/environments in disease scores and yield-related traits. Conversely, the lowest mean square values for the study parameters implied that each wheat genotype responded differently to different environments as well as locations.

Genotypic response to Fusarium head blight across locations

Disease incidence (DI)

The results obtained from the ANOVA for DI across locations are presented in Table 3. Analysis of variance revealed that there were very significant ($P < 0.05$) variations for DI among evaluated wheat genotypes in the seven locations (Tables 2, 3).

At Adiyo, the highest mean DI was noted on the genotype Hidase (77.66%), statistically on par with those on Kakaba (70.07%) and Kingbird (65.25%) genotypes; conversely, the lowest mean DI was observed on Huluka (13.03%) and then on Lemu (16.61%), statistically similar to those on Shorima (28.73%) and Danda'a (27.96%) (Table 3). At both Bonke and Chencha, the highest mean DI was recorded on the genotype Danada (46.22% and 41.88%) and then on Kubsa (37.56% and 41.88%), while the lowest mean DI was recorded on Shorima (0.00% and 0.00%) and then on Wane (7.56% and 5.56%), Bondena (8.34% and 0.00%), Kakaba (10.15% and 0.00%), and Lemu (11.01% and 10.23%) genotypes, respectively (Table 3). At Gedeb and Hulbareg, the highest mean DIs were recorded on the genotypes Hidase (73.37%) and Lemu (49.05%), respectively, statistically on par with those on the genotypes Kingbird (66.33%) at Gedeb, Huluka (44.33%), Shorima (41.78%), and Kakaba (39.96%) at Hulbareg, while the lowest mean DIs were noted on Shorima (16.89%) and Hidase (25.43%) genotypes, respectively, not statistically different from those on Bondena (29.35%), Huluka (23.37%), and Lemu (22.63%) genotypes at Gedeb, and Danda'a (27.25%) and Kingbird (27.25%) genotypes at Hulbareg (Table 3).

At North Ari, 100% DI was recorded on Bondena, Danda'a, Huluka, Hidase, Kakaba, Kingbird, Kubsa, and Ogolcho genotypes. However, the value was not significantly different from those on the Lemu (96.67%) and Shorima (96.67%) genotypes in this location. Comparatively, the lowest mean DI was recorded on the genotype

Table 3 Mean disease incidence (%) of Fusarium head blight at a Zadoks growth stage of 90 (during the soft dough stage) across locations in southern Ethiopia during the 2019 main cropping season

Genotypes	Location[a]							
	Adiyo	Bonke	Chencha	Gedeb	Hulbareg	North Ari	Sodo Zuriya	LM[b]
Bondena	31.73^{d-f}	8.34^{c}	0.00^{d}	29.35^{ef}	32.70^{b-d}	100^{a}	21.91^{f}	30.47^{f}
Danda'a	27.96^{ef}	46.22^{a}	41.88^{a}	44.31^{cd}	27.25^{cd}	100^{a}	41.28^{b}	49.32^{bc}
Huluka	13.03^{f}	24.56^{b}	30.33^{bc}	23.37^{ef}	44.33^{ab}	100^{a}	29.30^{de}	39.32^{e}
Hidase	77.66^{a}	43.33^{a}	33.22^{b}	73.37^{a}	25.43^{d}	100^{a}	42.13^{b}	55.84^{a}
Kakaba	70.07^{ab}	10.15^{c}	0.00^{d}	56.94^{bc}	39.96^{ab}	100^{a}	33.36^{cd}	41.03^{de}
Kingbird	65.25^{ab}	21.66^{b}	23.11^{c}	66.33^{ab}	27.25^{cd}	100^{a}	14.32^{g}	45.57^{cd}
Kubsa	43.33^{c-e}	37.56^{a}	41.88^{a}	51.99^{c}	39.24^{a-c}	100^{a}	37.56^{bc}	51.64^{ab}
Lemu	16.61^{f}	11.01^{c}	10.23^{d}	22.63^{ef}	49.05^{a}	96.67^{ab}	28.65^{d-f}	31.37^{f}
Ogolcho	52.28^{b-d}	23.11^{b}	26.00^{bc}	44.68^{cd}	34.52^{b-d}	100^{a}	54.76^{a}	46.82^{bc}
Shorima	28.73^{ef}	0.00^{c}	0.00^{d}	16.89^{f}	41.78^{ab}	96.67^{ab}	26.12^{ef}	28.34^{f}
Wane	53.22^{b-d}	7.56^{c}	5.56^{d}	34.21^{de}	36.33^{b-d}	93.33^{b}	26.96^{d-f}	32.15^{f}
GM[c]	43.63	17.86	17.86	42.18	36.17	98.78	32.39	41.06
LSD (0.05)[d]	21.33	9.72	7.44	13.94	12.10	5.10	7.08	4.70
CV (%)[e]	28.88	32.16	24.63	28.41	19.76	3.05	12.91	18.80

[a] Means followed by the same letter within the column are not significantly different at $P < 0.05$

[b] LM, location mean

[c] GM, ground mean

[d] LSD, least significant difference at 5% probability level

[e] CV, coefficient of variation (%)

Wana (93.33%) (Table 3). The ANOVA revealed that the highest (54.76%) mean DI was recorded on genotype Ogolcho, while the lowest mean DI was observed on Kingbird (14.32%) at Sodo Zuriya (Table 3). The overall location mean results for the test wheat genotypes showed that the highest (55.84%) mean DI was recorded on the Hidase genotype, not statistically different from that on the Kubsa genotype (51.64%). On the contrary, the genotypes Shorima (28.34%), Bondena (30.47%), Lemu (31.37%), and Wane (32.15%) exhibited the lowest mean DI under crosswise assessment. Accordingly, Shorima, Bondena, Lemu, and Wane genotypes reduced DI by 49.25, 45.43, 43.82, and 43.42%, respectively, compared with the Hidase genotype. Overall, the mean DI was comparatively higher (98.78%) in North Ari than those in other locations (Table 3).

Disease severity (DS)

Analysis of variance for DS revealed significant ($P < 0.01$) differences among the tested wheat genotypes in different locations (Tables 2, 4). At Adiyo, the highest mean DS was recorded on the Hidase genotype (67.52%), statistically similar to those on the Kakaba (61.05%) and Kingbird (56.95%) genotypes. Contrariwise, the lowest mean DS was noticed on the genotype Lemu (21.94%) and then on Danda'a (24.24%), followed by those on Shorima (24.95%), Kubsa (25.13%), and Bondena (27.66%) (Table 4). There were no statistically significant differences in mean DS among the tested genotypes at Bonke and Chench, though the lowest mean DS was recorded on Shorima, Wane, Bondena, Lemu, and Kakaba genotypes with varying degrees of severity during the study. According to ANOVA, no statistically significant variations were observed among the evaluated genotypes at North Ari, though relatively the lowest mean DS was noted on the genotypes Wane (44.20%) and Shorima (49.63%) (Table 4).

At Gedeb, the maximum mean DS was recorded on the Kingbird genotype (60.72%), not statistically significantly different from those on the Danada'a (57.35%), Hidase (57.00%), and Kubsa (55.66%) genotypes. On the contrary, the lowest mean DS was noted on the Shorima genotype (4.72%), statistically on par with the Wane genotype (11.81%). At Hulbareg and Sodo Zuriya, analysis of variance revealed that the highest mean DSs were recorded on the genotypes Lemu (43.22) and Ogolcho (63.19%), respectively, not statistically varied from those on the genotypes Huluka (38.74%), Wane (34.62%), and Kakaba (34.55%) at Hulbareg and Danada'a (54.76%), Kakaba (53.25%) and Hidase (52.24%) at Sodo Zuriya. The lowest mean DS was observed on Kingbird (18.30% and 9.10%) at both Hulbareg and Sodo Zuriya (Table 4). The overall location mean results exhibited the highest mean DS on the Hidase genotype (49.25%), while the lowest mean DS

Table 4 Mean disease severity (%) of Fusarium head blight at a Zadoks growth stage of 90 (during the soft dough stage) across locations in southern Ethiopia during the 2019 main cropping season

Genotypes	Locations[a]							
	Adiyo	Bonke	Chencha	Gedeb	Hulbareg	North Ari	Sodo Zuriya	LM[b]
Bondena	27.66^{d-e}	6.85	0.00	22.94^{d}	25.73^{b-d}	66.90	10.78^{e}	18.83^{ef}
Danda'a	24.24^{ef}	16.40	18.79	57.35^{ab}	26.68^{b-d}	63.93	54.76^{b}	39.67^{bc}
Huluka	5.66^{f}	10.31	13.77	29.35^{cd}	38.74^{ab}	63.93	22.77^{d}	25.50^{e}
Hidase	67.52^{a}	20.53	19.39	57.00^{ab}	20.21^{cd}	53.80	52.24^{b}	49.25^{a}
Kakaba	61.05^{ab}	8.97	11.36	38.79^{cd}	34.55^{ab}	69.33	53.25^{b}	37.23^{c}
Kingbird	56.95^{ab}	14.20	13.31	60.72^{a}	18.30^{d}	73.87	9.10^{e}	31.96^{e}
Kubsa	25.13^{d-e}	19.36	20.35	55.66^{ab}	29.38^{b-d}	60.53	28.92^{d}	41.02^{bc}
Lemu	21.94^{ef}	8.93	9.45	29.35^{cd}	43.22^{a}	69.80	37.91^{c}	26.20^{e}
Ogolcho	45.52^{b-d}	15.56	8.80	42.84^{bc}	33.00^{a-c}	80.27	63.19^{a}	43.63^{b}
Shorima	24.95^{d-f}	0.00	0.00	4.72^{f}	32.93^{a-c}	49.63	14.83^{e}	17.54^{f}
Wane	46.38^{bc}	3.55	3.09	11.81^{ef}	34.62^{ab}	44.20	14.99^{e}	21.31^{ef}
GM[c]	37.00	11.33	11.52	37.35	30.67	63.24	32.98	32.01
LSD (0.05)[d]	20.70	ns	ns	16.33	13.26	ns	6.85	5.09
CV (%)[e]	33.05	38.01	37.82	25.81	25.55	36.16	12.28	26.09

[a] Means followed by the same letter within the column are not significantly different at $P < 0.05$

[b] LM, location mean

[c] GM, ground mean

[d] LSD, least significant difference at 5% probability level

[e] CV, coefficient of variation (%)

was noted on the Shorima genotype (17.54%), not statistically different from those on Bondena (18.83%) and Wane (21.31%) genotypes (Table 4). Shorima, Bondena, and Wane genotypes reduced mean DS by 64.39, 61.77, and 56.73%, respectively, compared with the level of mean DS noted on the Hidase genotype across locations. The overall FHB pressure was relatively higher at North Ari, followed by Adiyo and Gedeb, while comparatively the lowest FHB pressure was observed at Bonke, followed by Chencha, during the study.

Area under disease progress curve (AUDPC)

The ANOVA results for the AUDPC value exhibited considerable ($P < 0.001$) variations among the evaluated genotypes across locations (Tables 2, 5). At Adiyo, the highest mean AUDPC value was recorded on the Hidase genotype (458.48%/days), not statistically different from those on the genotypes Kingbird (403.43%/days), Kakaba (396.90%/days), and Wane (372.57%/days). Conversely, the lowest mean AUDPC value was recorded on the Huluka genotype (33.00%/days), statistically similar to that on the Lemu genotype (107.14%/days) (Table 5). At Bonke and Chench, the computed AUDPC values for tested genotypes were statistically similar to each other, although relatively the lowest mean AUDPC values were recorded on Shorima (0.00 and 0.00%/days), followed by Bondena (24.68 and 0.00%/days) and Wane (25.37 and 27.15%/days) genotypes during the epidemic period (Table 5).

At Gedeb, Hulbareg, and North Ari, the significantly highest AUDPC values were observed on the genotypes Kingbird (647.69%/days), Lemu (560.85%/days), and Ogolcho (1128.75%/days), respectively, not statistically significantly different from those on the genotypes Hidase (611.38%/days), Huluka (502.56%/days), and Hidase (988.17%/days) (Table 5); the lowest mean AUDPC values were noted on Shorima (32.86%/days), Kingbird (236.93%/days), and Wane (323.87%/days) genotypes, respectively, statistically similar to those on Wane (98.49%/days), Hidase (261.78%/days), and Shorima (445.43%/days) genotypes. At Sodo Zuriya, the highest mean AUDPC value was recorded on the Ogolcho genotype (505.50%/days), while the lowest mean AUDPC value was noted on Kingbird (72.79%/days), followed by Bondena (86.27%/days), Shorima (118.62%/days), and Wane (119.97%/days) genotypes (Table 5).

Under crosswise comparisons, Hidase genotype (453.46%/days) exhibited the highest mean AUDPC values, while Shorima (170.25%/days) showed the lowest mean AUDPC value, followed by Wane (194.85%/days), and Bondena (205.69%/days) (Table 5). Shorima, Wane, and Bondena genotypes reduced mean AUDPC values by 62.46, 57.03, and 54.64%, respectively, compared with that observed on the Hidase genotype across locations.

Table 5 Fusarium head blight mean area under disease progress curve (%/days) across locations in southern Ethiopia during the 2019 main cropping season (from the Zadoks growth stage of 59 and 61–69 to 90, from heading and post-anthesis to soft dough stage)

Genotype	Locations[a]							
	Adiyo	Bonke	Chencha	Gedeb	Hulbareg	North Ari	Sodo Zuriya	LM[b]
Bondena	220.33^{c}	24.68	0.00	263.45^{de}	333.44^{b-e}	536.32^{ef}	86.27^{e}	205.69^{e}
Danda'a	163.19^{cd}	181.76	275.12	562.38^{a-c}	345.86^{b-e}	549.03^{ef}	438.10^{b}	340.95^{bc}
Huluka	33.00^{e}	171.88	208.55	285.88^{de}	502.56^{ab}	663.48^{c-e}	182.17^{d}	258.19^{d}
Hidase	458.48^{a}	263.11	262.96	611.38^{ab}	261.78^{de}	988.17^{ab}	417.88^{b}	453.46^{a}
Kakaba	396.90^{ab}	107.04	187.25	377.28^{cd}	448.10^{a-c}	828.22^{bc}	425.97^{b}	353.78^{bc}
Kingbird	403.43^{ab}	118.70	164.37	647.69^{a}	236.93^{e}	610.05^{d-f}	72.79^{e}	311.61^{c}
Kubsa	185.83^{cd}	252.46	271.00	558.81^{a-c}	308.19^{c-e}	774.08^{cd}	309.35^{c}	375.47^{b}
Lemu	107.14^{de}	89.99	67.70	283.55^{de}	560.85^{a}	523.83^{e-g}	303.30^{c}	254.10^{d}
Ogolcho	348.81^{b}	150.66	297.40	436.94^{b-d}	428.03^{a-d}	1128.75^{a}	505.50^{a}	429.24^{a}
Shorima	167.76^{cd}	0.00	0.00	32.86^{f}	427.08^{a-d}	445.43^{fg}	118.62^{e}	170.25^{e}
Wane	372.57^{ab}	25.37	27.15	98.49^{ef}	449.06^{a-c}	323.87^{g}	119.97^{e}	194.85^{e}
GM[c]	259.77	126.88	157.59	378.07	391.08	670.11	270.90	36.63
LSD (0.05)[d]	96.51	ns	ns	193.76	172.84	202.09	57.41	48.05
CV (%)[e]	21.94	30.11	39.25	30.27	26.10	17.81	12.52	5.80

[a] Means followed by the same letter within the column are not significantly different at $P < 0.05$

[b] LM, location mean

[c] GM, ground mean

[d] LSD, least significant difference at 5% probability level

[e] CV, coefficient of variation (%)

The overall AUDPC was comparatively higher at North Ari, while relatively lower at Bonke and Chencha during the epidemic periods (Table 5).

Yield performance across locations

Analysis of variance pointed out a considerable genotypic variation ($P < 0.01$) for yield performance among the tested genotypes across locations (Tables 2, 6). At Adiyo, the highest (4.51 t/ha) mean yield was received from the Bondena genotype, not statistically different from that on the Lemu (3.82 t/ha) genotype, whlie the lowest (2.16 t/ha) mean yield was obtained from the Hidase genotype, followed by the Kubsa genotype (2.39 t/ha), which were significantly affected by FHB (Tables 4, 5, 6) among the tested genotypes (Table 6). At Bonke and Chencha, the highest mean yield was harvested from the genotype Kingbird (5.33 and 4.96 t/ha), then from Shorima (5.31 and 5.31 t/ha), Wane (5.30 and 5.59 t/ha), Hukuka (5.23 and 4.73 t/ha), Kubsa (5.19 and 4.87 t/ha), Kakaba (4.56 and 4.53 t/ha), Bondena (4.49 and 5.15 t/ha), Hidase (4.31 and 4.67 t/ha), and Ogolcho (4.14 and 4.81 t/ha), respectively (Table 6). Shorima, Wane, Bondena, and Kakaba genotypes maintained consistent high yield potential (Table 6) and low FHB intensity at Bonke and Chencha (Tables 4, 5, 6). Conversely, the lowest mean yield was recorded from the Danada'a genotype (2.56 and 2.95 t/ha) at Bonke and Chencha, respectivly (Table 6). At Gedeb, the heaviest (5.01 t/ha) mean yield was noted from the Shorima genotype, followed by the Wane genotype (4.52 t/ha), while the lightest (2.92 t/ha) mean yield was observed from the Hidase genotype, statistically similar to those from the Bondena (3.35 t/ha) and Ogolcho (3.39 t/ha) genotypes (Table 6).

At Hulbareg, a maximum (3.52 t/ha) mean yield was obtained from the Kingbird genotype, not statistically significantly different from that obtained from the genotypes Hidase (2.99 t/ha), Bondena (2.93 t/ha), Wane (2.86 t/ha), and Kubsa (2.83 t/ha), while the minimum mean yield was recorded from the Lemu genotype (2.03 t/ha). Hulbareg had consistently high production potential for Kingbird (Table 6) and low FHB pressure (Tables 3, 4, 5). At North Ari, a region significantly suffering from FHB pressure, the maximum (1.91 t/ha) mean yield was received from the Danada'a genotype, statistically similar to the Shorima genotype (1.83 t/ha), while the minimum (0.28 t/ha) mean yield was recorded from the Ogolcho genotype, followed by the Lemu (0.84 t/ha), Kakaba (0.75 t/ha), and Hidase (0.63 t/ha) genotypes (Tables 3, 4, 5). At Sodo Zuriya, a substantial yield of 5.95 and 5.58 t/ha was noted on the genotypes Bondena and Shorima, respectively, whereas the lowest mean yield of 2.34 t/ha was noted on the Kingbird genotype, not statistically significantly different from that on the Hukuka (2.60 t/ha) genotype (Table 6).

Table 6 Mean wheat genotype yield (t/ha) under Fusarium head blight pressure in southern Ethiopia during the 2019 main cropping season

Genotype	Location[a]							
	Adiyo	Bonke	Chencha	Gedeb	Hulbareg	North Ari	Sodo Zuriya	LM[b]
Bondena	4.51^{a}	4.49^{a}	5.15^{a}	3.35^{cd}	2.93^{ab}	1.38^{a-c}	5.95^{a}	3.96^{a}
Danda'a	3.56^{a-c}	2.56^{b}	2.95^{b}	3.41^{cd}	2.67^{bc}	1.91^{a}	2.67^{d-f}	2.98^{cd}
Huluka	2.29^{a-d}	5.23^{a}	4.73^{a}	4.29^{a-c}	2.48^{bc}	1.42^{a-c}	2.60^{ef}	3.43^{b}
Hidase	2.16^{d}	4.31^{a}	4.67^{a}	2.92^{d}	2.99^{ab}	0.63^{cd}	2.97^{c-e}	2.95^{cd}
Kakaba	3.12^{b-d}	4.56^{a}	4.53^{a}	3.63^{b-d}	2.58^{bc}	0.75^{cd}	2.88^{c-f}	3.16^{b-d}
Kingbird	2.63^{b-d}	5.33^{a}	4.96^{a}	3.54^{b-d}	3.52^{a}	1.17^{a-d}	2.34^{f}	3.35^{bc}
Kubsa	2.39^{cd}	5.19^{a}	4.87^{a}	3.38^{cd}	2.83^{ab}	0.98^{b-d}	3.54^{c}	3.46^{b}
Lemu	3.82^{ab}	3.58^{ab}	3.92^{ab}	4.11^{a-c}	2.03^{c}	0.84^{cd}	3.19^{cd}	2.76^{d}
Ogolcho	3.03^{b-d}	4.14^{a}	4.81^{a}	3.39^{cd}	2.75^{b}	0.28^{d}	3.02^{c-e}	3.12^{b-d}
Shorima	2.54^{b-d}	5.31^{a}	5.31^{a}	5.01^{a}	2.41^{bc}	1.83^{ab}	5.58^{a}	3.92^{a}
Wane	3.19^{a-d}	5.30^{a}	5.59^{a}	4.52^{ab}	2.86^{ab}	1.44^{a-c}	4.57^{b}	3.93^{a}
GM[c]	3.12	4.55	4.68	3.78	2.73	1.15	3.57	3.37
LSD (0.05)[d]	1.36	1.89	1.68	1.03	0.71	0.89	0.56	0.44
CV (%)[e]	25.78	24.68	21.23	16.14	15.40	46.12	9.41	21.54

[a] Means followed by the same letter within the column are not significantly different at $P < 0.05$

[b] LM, location mean

[c] GM, ground mean

[d] LSD, least significant difference at 5% probability level

[e] CV, coefficient of variation (%)

The overall location mean showed that the highest (3.96, 3.93, and 3.92 t/ha) mean yield was noted from the genotypes Bondena, Wane, and Shorima, respectively. Quite the reverse, the lowest (2.76 t/ha) mean yield was noticed on the Lemu genotype under crosswise assessment, not statistically different from those on the genotypes Danada'a (2.98 t/ha) and Hidase (2.95 t/ha). Around 30.30, 29.77, and 29.59% of the yield advantage was received from the Bondena, Wane, and Shorima genotypes, respectively, compared with the Hidase genotype. Comparatively, the overall FHB pressure was highest at North Ari (Tables 3, 4, 5), resulting in the lowest yield at this location (Table 6).

AMMI analysis for Fusarium head blight severity and yield performance

The AMMI analysis of variance for FHB severity and yield performance of the tested genotypes is shown in Table 7. The variance of the analysis revealed that FHB severity and yield performance were significantly ($P < 0.01$) affected by environment (E), genotype (G), and GEI. For FHB severity, environmental and genotypic contributions accounted for 47% and 10.60% of the total $G + E + G \times E$ to the sum of squares, respectively, whereas GEI explained 21.00% of the treatment variation in FHB severity. Most of the total sum of squares of the model was attributed to the environment and the interaction effects. The fact that the treatment contributed more to FHB severity (78.6%) than the error (18.0%) indicated the reliability of the multi-environment experiment (Table 7). The two IPCA 1 and IPCA 2 produced from the AMMI model were significantly varied for the GEI sum of squares. Accordingly, IPCA 1 and IPCA 2 explained 52.90% and 27.60% of the GEI sum of squares, respectively, with 80.50% cumulative total sum of a square for FHB severity (Table 7).

Concerning yield performance, in the AMMI variance of analysis, the main effect of environment contributed 58.20% to the sum of square, whereas genotypes and $G \times E$ interactions explained 7.10% and 17.90% of the total yield difference, respectively (Table 7). This indicated that most of the total sum of squares was accredited to the environment and $G \times E$ interaction effect. The greater contribution of the treatment (83.2%) than the error (15.60%) argues for the reliability of the multi-environment experiment (Table 7). The AMMI model further partitioned the $G \times E$ interaction sum of a square into IPCAs and residual terms, and the values for the mean squares of the two IPCAs were highly significant. The two IPCAs of $G \times E$ interactions accounted jointly for 73.33% of the total sum of square of GEI (IPCA 1 and IPCA 2 accounted for 40% and 33.33% of the observed variation due to GEI, respectively), indicating their significant effects on the total difference in yield performance (Table 7).

Table 7 Additive main effects and multiplicative interaction variance of analysis for disease severity and yield of eleven genotypes tested across different environments during the 2019 main cropping season

Source of variation[a]	AMMI analysis of variance for disease severity (%)						AMMI analysis of variance for yield (t/ha)					
	Interactions[b]			Sum of square explained			Interactions[b]			Sum of square explained		
	DF	TSS	MS[c]	Total (%)	G × E (%)	G × E cumulative (%)	DF	TSS	MS[c]	Total (%)	G × E (%)	G × E cumulative (%)
Total	230	131,819	573**				230	494.30	2.149**			
TRT	76	103,587	1363**	78.60			76	411.20	5.411**	83.20		
G	10	13,956	1396**	10.60			10	35.00	3.50**	7.10		
E	6	61,990	10,332**	47.00			6	287.70	47.95**	58.20		
Block	14	4456	318**	3.40			14	6.00	0.43**	1.20		
G × E	60	27,641	461**	21.00			60	88.50	1.48**	17.90		
IPCA 1	15	14,615	974**	11.10	52.90		15	35.40	2.36**	7.20	40.0	
IPCA 2	13	7638	588**	5.80	27.60	80.50	13	29.50	2.27**	5.97	33.30	73.33
Residuals	32	5388	168**	23.43			32	23.70	0.74 ns	4.80		
Error	140	23,777	170**	18.00			140	77.10	0.55	15.60		

[a] TRT, treatments; G, genotype, E, environment, G × E, genotype by environment; and IPCA, interaction principal component axis

[b] DF, degree of freedom; TSS, total sum of square; and MS, mean squares for disease severity and yield

[c] **Indicates significant difference at $P < 0.01$ for disease severity and yield

Genotype and environmental stability as determined by AMMI stability values

A set of AMMI-based stability parameters (ASV, IPCA 1, and IPCA 2) were computed based on the first two IPCAs to generate a well-balanced measure for evaluation of FHB severity and yield performance (Table 8). The lowest IPCA 1 and IPCA 2 values are near zero, elucidating the high resistance of the genotypes to FHB at best in the biplot. Contrary to commonly used approaches in agronomic data for AMMI stability analysis, the genotypes Ogolcho, Lemu, Kubsa, Bondena, and Danda'a were considered unstable due to higher FHB severity

Table 8 AMMI stability values for disease severity and yield of the tested wheat genotypes across environments during the 2019 main cropping season

Genotype	Disease severity (%)				Yield (t/ha)			
	Pooled means over seven environments[a]	AMMI model stability parameter			Pooled means over seven environments[a]	AMMI model stability parameter		
		IPCA 1[b]	IPCA 2[b]	ASV[c,d]		IPCA 1[b]	IPCA 2[b]	ASV[c,d]
Bondena	22.98 (2)	− 1.892	− 1.11	3.79 (4)	3.97 (1)	− 0.91	− 0.62	1.26 (10)
Shorima	19.96 (1)	− 3.56	1.17	6.91 (10)	3.93 (2)	− 0.29	− 0.95	1.02 (8)
Wane	23.16 (3)	− 3.08	0.58	5.93 (8)	3.93 (3)	0.09	− 0.48	0.49 (4)
Danda'a	40.53 (9)	2.43	0.07	4.65 (5)	2.80 (11)	− 0.95	1.06	1.55 (11)
Huluka	26.36 (4)	− 3.00	0.09	5.75 (7)	3.43 (4)	0.39	0.36	0.59 (5)
Hidase	41.58 (10)	4.39	− 0.28	8.40 (11)	2.95 (10)	0.40	− 0.03	0.48 (3)
Kakaba	36.80 (8)	2.91	2.50	6.11 (9)	3.15 (9)	0.19	0.19	0.30 (1)
Kingbird	33.00 (6)	0.25	− 5.23	5.25 (6)	3.36 (5)	0.84	0.38	1.08 (9)
Kubsa	36.40 (7)	0.92	− 2.09	2.73 (3)	3.30 (6)	0.47	− 0.26	0.62 (6)
Lemu	28.86 (5)	− 0.03	2.49	2.49 (2)	3.10 (8)	− 0.50	0.34	0.69 (7)
Ogolcho	42.52 (11)	0.67	1.81	2.22 (1)	3.13 (7)	0.27	0.03	0.32 (2)
Mean	32.01				3.37			

[a] Numbers in the parenthesis indicates rank of genotypes for disease severity and yield

[b] IPCA, interaction principal component axis for disease severity and yield

[c] ASV, AMMI stability values for disease severity and yield

[d] ASV rank of genotypes in descending and ascending order for disease severity and yield

(above the grand mean), although they were committed to relatively lower ASV values. These genotypes can be used as discriminating genotypes for the FHB resistance reaction study in some or across environments. Similarly, Kingbird, Huluka, Wane, Kakaba, Shorima, and Hidase genotypes were identified as somewhat stable with relatively moderate to higher disease severity even if they had higher ASV values (Table 8). Although Shorima, Bondena, Wane, Huluka, and Lemu genotypes were unstable across environments (according to ASV values), they showed comparatively lower mean FHB severity compared to the overall grand mean of the genotypes and consistency in most of the environments. This suggests that these genotypes can be used as resistance or moderate-resistance for some or most of the environments, as supported by their yield potential for those environments. In this study, genotypes with lower FHB severity had higher ASV values and vice versa, implying an inconsistency in the reactions of the genotypes to FHB across environments.

AMMI stability analysis revealed negative or positive values for both IPCA 1 (environmental influence) and IPCA 2 (genotypic response to FHB), by which to evaluate the adaptability of the genotypes and their reactions to FHB across environments. For instance (Bondena), the genotype with both negative IPCA 1 and IPCA 2 is unadaptable and therefore unstable for the test environments, although it showed higher resistance to FHB. The genotypes Shorima, Wane, Huluka, and Lemu exhibited negative IPCA 1 and positive IPCA 2, suggesting that they are unadaptable in some specific environments, with lower to moderate reactions to FHB across environments. The other genotypes, such as Danda'a, Kakaba, and Ogolcho, had both positive values of IPCA 1 and IPCA 2, which pointed out that the genotypes are adaptable and highly susceptible in specific as well as across environments. These genotypes are significantly affected by the change in the environments, in addition to the magnitude of FHB pressure. Whereas Hidase, Kingbird, and Kubsa genotypes had positive IPCA 1 and negative IPCA 2 values, signifying that they are adaptable in some specific environments with lower reactions to FHB (Table 8). The genotypes showing low response to FHB and becoming stable across environments are not enough for selection. Considering lower to higher disease reactions coupled with high yield potential is a prerequisite in testing genotypes across environments.

On the other hand, there was a broad range of variation in ASV values among the genotypes for yield performance (Table 8). Most of the genotypes had an ASV of less than 1 for yield performance. Among the test genotypes, Kakaba (0.30), Ogolcho (0.32), Hidase (0.48), Wane (0.49), Huluka (0.59), Kubsa (0.62), and Lemu (0.69) had lesser ASV values. These genotypes were stable with various levels (low to high) of yield potential based on the genotype ASV values, which takes both the overall genotypes' mean yield performance and lower ASV into consideration. The genotypes Wane and Huluka were stable (found above the grand mean values of the genotypes) and had relatively lower ASV values. Shorima, Kingbird, Bondena, and Danda'a genotypes were unstable due to their highest ASV values, although they exhibited the highest yield performance and were found above the grand mean values of the genotypes. Compared with those having higher IPCA 2, the genotypes having lower IPCA 1 would produce lesser GEI effects and become more stable across environments.

The genotypes Bondena and Shorima exhibited the same sign (negative) of IPCA 1 and IPCA 2 scores, indicating their inadaptability to stress environments, including FHB epidemic pressure. These genotypes cannot be cultivated under stress conditions, although they had a lower reaction to the FHB. Wane, Hidase, and Kubsa were adaptable under unfavorable environmental conditions with opposite signs of IPCA 1 (positive) and IPCA 2 (negative) scores and could be considered for cultivation across environments under stress conditions, even under the high pressure of FHB epidemics. The production of other genotypes, including Danda'a and Lemu, is unsuitable due to their lower yielding potential even if there are favorable environmental conditions and low FHB pressure. The genotypes Huluka, Kakaba, Kingbird, and Ogolcho had the same sign (positive) of IPCA 1 and IPCA 2 scores, and are adaptable and suitable for production in unfavorable environmental conditions, including high-pressure FHB epidemics. Overall, the genotypes Wane, Hidase, Kubsa, Huluka, Kakaba, Kingbird, and Ogolcho could be considered for cultivation across environments based on IPCA 1 and IPCA 2 scores. However, AMMI stability analysis cannot be considered the only approach for determining adaptable and suitable genotypes in wheat production. Thus, identifying genotypes coupled with high-yield performance via GGE biplot analysis and observing consistent results across environments is of paramount importance.

GEI analysis of mean performance and stability using GGE biplot model

The GGE biplot analysis for FHB severity and yield performance provides a graphic expression of the association between IPCA 2 (averages of genotype) and the environment (main effects, IPCA 1) (Fig. 2). The wheat production per environment was significantly ($P < 0.01$) affected by the treatment effects as held in the environment, genotype, and interaction components. Accordingly, these variables together captured 57.86%

of the total sum of squares for FHB severity (Fig. 2a) and 33.47% for yield performance (Fig. 2b), whereas the IPCA 2 accounted for 27.60% of FHB severity and 33.30% of yield performance for the total variation of the GEI. The genotype and interaction portions were 11.10% (IPCA 1) and 5.80% (IPCA 2) for FHB severity, and 7.20% (IPCA 1) and 5.97% (IPCA 2) for yield performance (Table 7). The two axes (IPCA 1 and IPCA 2) together explained the significance of the interaction sum of squares for FHB severity of 80.50% and yield performance of 73.33% (Table 7). The genotypes, as well as environments on a similar parallel line compared to the y-axis, have similar FHB and yield responses. And also, the genotype as well as the environment on the right side of the midpoint of the y-axis has lower FHB severity and higher yield performance than those on the left side. For FHB severity and yield performance, the treatment explained about 78.60% and 83.20% of the total variation of the sum of squares in that order of appearance. The genotype, environment, and GEI effects explained about 10.60% and 7.10%, 47.00% and 58.20%, and 21.00% and 17.9% of the total variation in FHB severity and yield performance, respectively (Table 7).

Mean performance and stability of the test genotypes across environments were graphically depicted through AEC for FHB severity (Fig. 2a) and vectors for yield performance on the scatter plots (Fig. 2b). Concerning FHB severity, the individual arrowhead-line on the diagram cognized with AEC abscissa, passing through the biplot origin, points to the higher FHB severity and thus indicates fewer resistance reactions of the tested genotypes to FHB. In this regard, it could be said that the genotypes Bondena (G1), Shorima (G10), and Wane (G11) exhibited low FHB severity, suggesting that these genotypes exhibited resistance to FHB by having lower main effects (IPCA 1) and negative IPCA 2. The genotypes Danda'a (G2), Hidase (G4), Kubsa (G7), and Ogolcho (G9) exhibited the highest FHB severity, implying susceptibility to FHB. The remaining tested genotypes were found to have intermediate FHB severity and were considered moderately resistant to FHB (Fig. 2a).

Genotypic stability for levels of resistance is generally assessed based on the absolute length of the projection of a genotype. That is, the reaction of genotypes to FHB varied based on their projection length from the AEA on the GGE biplot. According to GGE biplots, the projection line of the tested genotype to the AEC abscissa indicates stability. Accordingly, the test genotypes closer to the AEC line are more stable. In the mean vs. stability biplot, the higher projection of the test genotypes from the AEC abscissa denoted their lower stability and vice versa. The best performing genotypes could be those with minimum FHB severity, a relatively greater negative projection line on AEC, and the highest stability, that is, a projection line on AEC near zero. In this regard, the short and/or long projection line indicates the stability of the genotypes across environments as well as locations. Consequently,

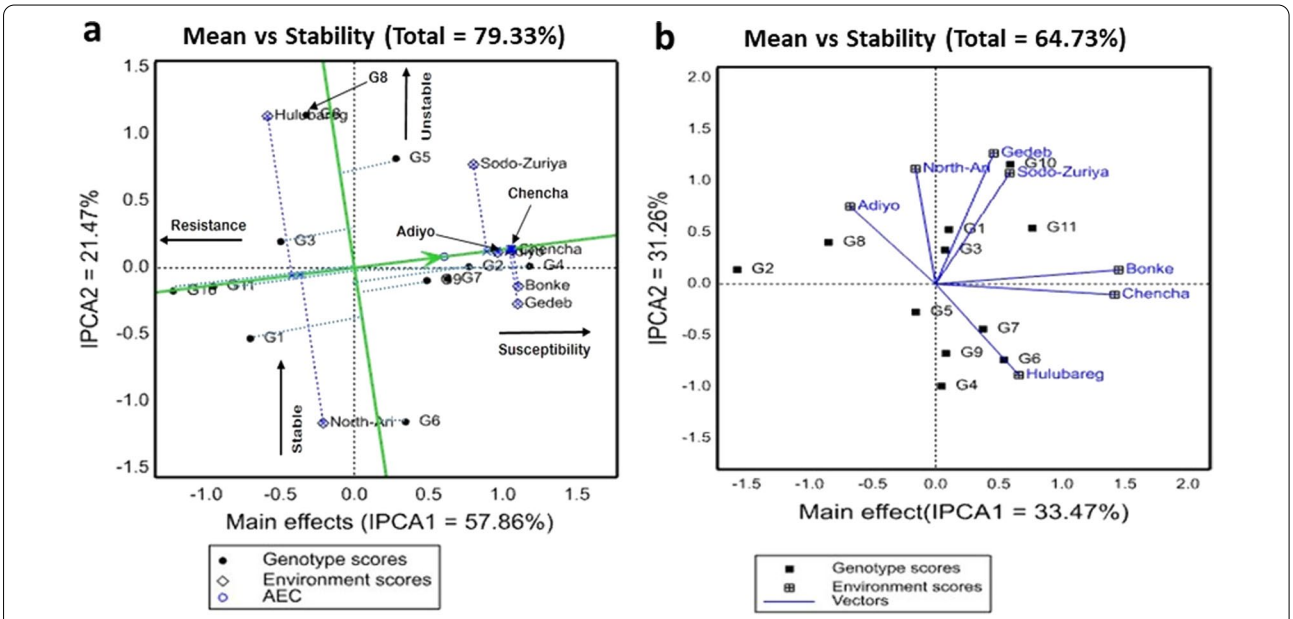

Fig. 2 Average Environment Coordination (AEC) views of the GGE biplot based on the environment-focused scaling for the mean performance and stability of genotypes for disease severity (**a**) and a discriminating power vs. representativeness view of the GGE biplot for yield performance (**b**). G1, Bondena; G2, Danda'a; G3, Huluka; G4, Hidase; G5, Kakaba; G6, Kingbird; G7, Kubsa; G8, Lemu; G9, Ogolcho; G10, Shorima; and G11, Wane

the Lemu genotype (G8) was the supreme "ideal genotype" among the tested genotypes, having the shortest projection line from AEC abscissa along with moderate resistance against FHB. Genotypes situated nearer to the "ideal genotype" are more suitable than other genotypes. These genotypes, Kakaba (G5), followed by Huluka (G3), were reckoned as desirable because of their nearer position to the "ideal genotype" (Lemu (G8)), with a moderate FHB score as well as having steady performance across environments. However, the overall observation indicated that the FHB resistance reaction for the test genotypes is unstable across environments and responds differently to the specific environment. Generally, low IPCA 2 (negative values) means better resistance to FHB. The resistance levels for FHB increased away from the AEC abscissa line on the biplot; however, the test genotypes became unstable. Susceptible genotypes were located faraway on the right side, while resistant genotypes were on the faraway left along the AEC abscissa. Genotypes located away from the AEC abscissa exhibited less stability across environments (Fig. 2b).

As regards the test environments (locations), North Ari and Hulbareg were similar with higher main effects and negative (North Ari) and positive (Hulbareg) IPCA 2, representing more discriminating environments for FHB resistance due to their longer projection line. This suggests better information concerning the differences in levels of resistance reaction for the test genotypes against FHB since they exhibited higher main effects and negative IPC 2. However, North Ari could be suggested as choosing superior genotypes against FHB resistance reaction than Hulbareg due to higher main effects and negative IPC 2. The environments include Adiyo, Bonke, Chencha, and Gedeb, followed by Sodo Zuriya, which exhibited a relatively shorter projection line and was near to origin, although the test genotypes responded differently to FHB. Thus, these environments provide scanty or no information about the test genotype disparities for FHB resistance reactions and cannot be test environments, even though there are pathogen diversities in this dynamic *Fusarium* species. Thus, the projection lines linking each test environment to the biplot origin give a clear comparison of the test environments for study genotypes. In the mean vs. stability, the biplot exhibited that the genotypes Danda'a (G2), Hidase (G4), Kubsa (G7), and Ogolcho (G9) were found in most of the environments, including Adiyo, Bonke, Chencha, and Gedeb, with fewer main effects (IPCA 1) and positive IPCA 2, but near-zero, IPCA 1. The genotypes Bondena (G1), Shorima (G10), and Wane (G11) exhibited negative IPCA 1 and IPCA 2 and below-average main effects (Fig. 2). The genotypes, Kakaba (G5) and Kingbird (G6), had positive (Kakaba (G5)) and negative (Kingbird (G6)) IPCA 2, far from the mean main effect (Fig. 2). The genotypes Huluka (G3) and Lemu (G8) showed above average main effects (had lower effects) and positive IPCA 2.

On the other hand, the GGE biplot analysis showed that the environments (or locations) Bonke and Chencha, followed by Gedeb, Sodo Zuriya, and Hulbareg, were high-yielding environments with high additive genotypic main effects, with a longer vector and larger angle on the biplot. This provides more information about the disparities of the test genotypes across environments. The environments of Adiyo and Noth Ari exhibited comparatively shorter vectors and relatively lower yield performance than the environmental mean, and they cannot be used in selecting supreme genotypes (Fig. 2a). However, they can be useful in removing unstable test genotypes. In this regard, the smaller the vector angle, the stronger the representativeness and/or discriminating power of the environment for the test genotypes. The scatter plot of the test genotypes exhibited that the genotype Danda'a (G2), followed by Shorima (G10) and Kingbird (G6) were high-yielding but unstable genotypes across environments. The genotypes Huluka (G3), Kakaba (G5), Bondena (G1), and Kubsa (G7) were positioned near the origin and verified as highly stable. However, the average yield values of Kakaba (G5) and Kubsa (G7) were found on the lower side of the origin, and therefore, they should not be suggested for production. Two sectors were observed, and the genotype Shorima (G10) clustered with Bonke, Gedeb, and Sodo Zuriya, representing repeatable performance. The genotype Danda'a (G2) clustered with Adiyo and Noth Ari, indicating the winning genotype in these environments. The genotype Kingbird (G6) was comparatively closer to the origin on the biplot and could be good enough for Hulbareg (Fig. 2a).

Overall, any test genotypes for FHB reaction and yield performance dropping close to the origin of the multiplicative axis (IPCA 1) on the biplot had lower interaction effects with most of the test environments and were stable. The test genotypes placed beyond ± 1 indicated high interactive propriety with environments adjacent to them and were typically unstable. Correspondingly, environments with IPCA 2 scores close to zero had few interaction effects with genotypes and exhibited low discrimination power and representativeness of the test genotypes. Those with IPCA scores outside of ± 1 discriminated against the genotypes more effectively than the others. Most of the test genotypes had IPCA 1 scores of ± 1 for both disease severity and yield performance. The rest of the genotypes, including Kingbird (G6) and Lemu (G8), and environments (Hulbareg and North Ari) were grouped beyond IPCA 1 scores ± 1 and below the mean, except for genotype Kingbird for FHB severity (Fig. 2a, b).

GEI analysis for "which-won-where?" using GGE biplot model

The GGE biplot was used to separate the genotype by GEI effects for FHB reactions and performance, and it revealed highly significant ($P<0.01$) G × E interactions mean squares for disease severity and yield performance across environments. The "which-won-where?" of GEI was examined using GGE biplots, in which crossing over GEI, mega-environment distinction, and specific genotype acclimation are diagrammatically shown for the test genotypes and environments (Fig. 3). Accordingly, the symmetrical singular value decomposing technique was utilized to exhibit the GGE biplot of the main effect (IPCA 1 score) plotted against the IPCA 2 score of study parameters for both test genotypes and environments. The biplot was partitioned into six (A–F) and five (A–E) sectors by perpendicular lines against each side of the polygon view of FHB severity (Fig. 3a) and yield performance (Fig. 3b) in that order. Sector A, Sector B, and Sector D exhibited not only test genotypes but also test environments for FHB severity (Fig. 3a), whereas Sector A, Sector C, and Sector D were formed with both test genotypes and environments for yield performance (Fig. 3b).

For FHB severity and yield performance on GGE biplots, parameters like the main effect (IPCA 1), IPCA 2, convex hull, and environmental scores were utilized for FHB severity and yield performance on GGE biplots to identify the paramount genotype for a specific environment and mega-environment and appraise the stability of the genotypes. Thus, the main effects (IPCA 1) accounted for 57.86% and 33.47% of the total variation, and IPCA 2 explained 21.47% and 31.26% of FHB severity and yield performance, respectively. Cumulatively (GGI), FHB severity, and yield performance were explained for about 79.33% and 64.73% of the total variation on the GGE biplots, respectively (Fig. 3a).

In this study, it was observed that Bondena (G1), Hidase (G4), Kakaba (G5), Kingbird (G6), Lemu (G8), and Shorima (G10) had the lowest FHB susceptibility in most environments and were found on the vertex furthest away from the GGE biplot origin, which showed inconsistency in the FHB resistance reaction. The remaining genotypes were constituted within the polygon. In the reverse to a common assessment of GGE biplot analysis of agronomic data, Bondena (G1), Shorima (G10), and Wane (G11) were placed below the mean main effect (IPCA 1) and negative IPCA 2 on the biplot and considered resistant to FHB. The other genotypes, including Kingbird (G6), Kubsa (G7), and Ogolcho (G9) with an above mean main effect and negative IPCA 2 of the biplot, were assessed as moderately resistant (Fig. 3a). The genotypes Danda'a (G2), Huluka (G3), Hidase (G4), Kakaba (G5), and Lemu (G8) were considered susceptible to FHB since they had

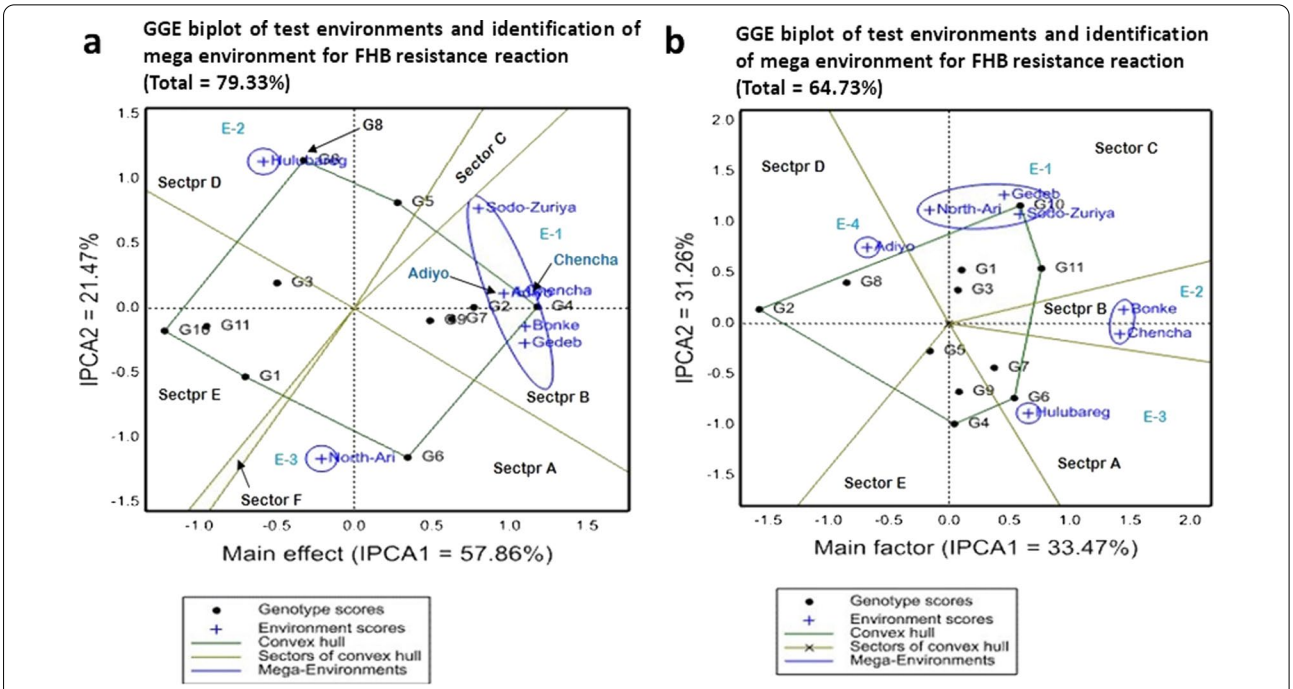

Fig. 3 GGE biplot of environments showing classifications of environments (agro-ecologies): a showcase for suitability studies in wheat genotypes for disease severity (**a**) and yield performance (**b**). G1, Bondena; G2, Danda'a; G3, Huluka; G4, Hidase; G5, Kakaba; G6, Kingbird; G7, Kubsa; G8, Lemu; G9, Ogolcho; G10, Shorima; and G11, Wane

above-mean main effect and positive IPCA 2 values on the biplot. Generally, test genotypes that are located to the left of the mean line (main effect, IPCA 1) are considered paramount in terms of resistance reactions. However, no consistent resistance genotype was observed across environments. Moreover, GGE biplot analysis revealed three groups of mega-environments, including E1 (Adiyo, Bonke, Chencha, Gedeb, and Sodo Zuriya), E2 (Hulbareg), and E3 (North Ari) (Fig. 3a).

Environments (or locations) Adiyo, Chencha, and Sodo Zuriya had a higher mean main effect (IPCA 1) and positive IPCA 2 values and were placed on the right side of the GGE biplot. Hulbareg, with a positive IPCA 2 value, and North Ari, with a negative IPCA 2 value, lower than the mean of the main effect, are located on the left side of the biplot. Among the test environments, Bonke and Gedeb exhibiting higher mean main effect (IPCA 1) and negative IPCA 2 values were located on the right side of the GGE biplot (Fig. 3a); North Ari (E3) is the best environment for testing wheat genotypes against FHB since it had a lower mean main effect and negative IPCA 2 score, exhibited the highest FHB pressure, and was located far from the biplot origin. The AEC aspect of the GGE biplot supported by environment-focused scaling for the mean performance and stability of genotypes was used to identify the "ideal genotypes" with consistent resistance genotypes across environments. However, GGE biplot analysis revealed inconsistency in resistance levels of the test genotypes across environments, indicating the instability of the genotypes across environments and their potential for high resistance or susceptibility to FHB for a specific environment (Fig. 3a).

Accordingly, the genotypes Danda'a (G2), Hidase (G4), Kubsa (G7), and Ogolcho (G9) had the highest FHB severity and exhibited susceptibility at Adiyo, Bonke, Chencha, Gedeb, and Sodo Zuriya. The genotypes Lemu (G8) at Hulbareg, Kakaba (G5) at Sodo Zuriya, and Kingbird (G6) at North Ari showed high FHB reactions and are representative of susceptible check for that particular environment (Fig. 3a). Conversely, all genotypes far away from specific environments had moderate to high resistance against FHB depending on the magnitude of FHB severity scores. For instance, Bondena (G1), Shorima (G10), and Wane (G11) exhibited resistance to FHB at Adiyo, Bonke, Chencha, Gedeb, and Sodo Zuriya; these genotypes are located in the negative of IPCA 1 and IPCA 2 and have lower mean main effects. However, these genotypes, besides Kingbird (G6), Kubsa (G7), and Ogolcho (G9), are susceptible to FHB at North Ari, with both genotypes and environment placed at negative IPCA 2 and left of the mean main effect on the biplot (Fig. 3a). At Hulbareg, Bondena (G1), Shorima (G10), and Wane (G11) exhibited resistance to FHB because they had negative IPCA 1 and IPCA 2 and were located on the left side of the biplot. The genotypes, including Kingbird (G6), Kubsa (G7), and Ogolcho (G9), had moderate resistance with negative IPCA 2 and were placed above the mean main effect (IPCA 1) on the biplot around Hulbareg. These uncertainties, that genotypes responded inconsistently across environments, were confirmed by the sectoring of the GGE biplot; for example, no environment dropped into "Sector E" with Bondena (G1), Huluka (G3), Shorima (G10), and Wane (G11) genotypes, signifying that the genotypes were not best performing in terms of low FHB severity with the same reaction levels across environments (Fig. 3a).

Concerning yield performance, the genotypes Danda'a (G2), Hidase (G4), Kingbird (G6), Shorima (G10), and Wane (G11) were the vertex genotypes, furthest from the biplot origin, so that all the remaining genotypes are contained within the polygon (Fig. 3b). The vertex genotypes are regarded as the high-yielding genotypes in all environments that are portioned into the sectors. Vertex genotypes with any test environment falling in their respective sectors had poor performance. The genotypes located near the biplot origin would respond the same across environments and they would not be sensitive to the change in environments. However, to determine "which-won-where?", the biplot was divided into different mega-environments and sectors. Accordingly, the biplot was divided into five sectors made by perpendicular lines with arrays of the respective sides of the polygon (Fig. 3b). In addition, four groups of mega-environments are formed on the biplot. Moving in a clockwise way, E1 (Gedeb and Sodo Zuriya), E2 (Bonke and Chencha), E3 (North Ari), and E4 (Hulbareg) were displayed on the biplot (Fig. 3). Most environments (E1, E2, and E4) exhibited positive IPCA 2 values and were situated on the right-wing side of the biplot, except E4, which was placed on the left side of the biplot. The environment Hulbareg (E3) had a negative IPCA 2 and was located on the right side of the biplot and exhibited a lower mean main effect (IPCA 1) on yield performance (Fig. 3b).

All environments fell into different sectors in which Shorima (G10) and Wane (G11) were the best-performed genotypes at Gedeb and Sodo Zuriya (E1), followed by Bonke and Chencha (E2) under the pressure of the FHB epidemics. The Kingbird genotype (G6) was the high-yielding genotype at Hulbareg, while Danda'a (G2) was the highest-yielding genotype at Adiyo under the influence of the FHB epidemics. "No environment" fell into sector E. The genotypes within the polygon, notably Bondena (G1), Huluka (G3), Kakaba (G5), Kubsa (G7), Lemu (G8), and Ogolcho (G9), were less responsive to yield performance than the vertex genotypes and comparatively stable across environments than the vertex

genotypes (Fig. 3b). Overall, genotypes near the biplot's origin are not responsive to environmental changes and are relatively stable across environments.

Spearman correlation coefficients among study parameters

The results obtained from correlation analysis between disease (DI, DS, and AUDPC) and yield-related (TKW and yield) parameters were displayed in Additional file 1: Table S1. The results showed that variable levels of relationships (positive and negative associations) were observed among DI, DS, AUDPC, TKW, and yield across locations. Positive and highly significant ($P<0.0001$) associations between and among mean values of disease parameters (DI, DS, and AUDPC) were found across locations. In this regard, the correlation analysis showed that positive and high associations were observed between DI_f and DS_f ($r=0.94^{****}$), DI_f and AUDPC ($r=0.92^{***}$), and DF_f and AUDPC ($r=0.99^{***}$) (Additional file 1: Table S1). The correlation results revealed a highly negative correlation and varying levels of significance ($P<0.05$–0.001) association between DS_f and TKW ($r=-0.65^{*}$), DS_f and TKW ($r=-0.74^{***}$), TKW and AUDPC ($r=-0.78^{**}$), yield and DS_f ($r=-0.70^{*}$), and yield and AUDPC ($r=-0.70^{*}$). The results pointed out that the observed values of FHB intensity had considerable adverse effects on the yield of genotypes. In this study, no significant ($P>0.05$) association was observed between DI_f and yield. But, the two parameters, DI_f and yield, exhibited a strongly negative association ($r=-0.56$). On the other hand, yield-related parameters apparently showed a positive and strong association between them. A strongly positive correlation ($r=0.88^{***}$) and highly significant ($P<0.01$) association was observed between TKW and yield (Additional file 1: Table S1).

Association of Fusarium head epidemics and yield of wheat

The relationships between disease severity and yield were examined using linear regression analysis to see the yield loss due to FHB pressure for each location. The mean values of final disease severity were used to predict the yield loss, and significant ($P<0.0001$) relationships were observed for yield loss across locations (Fig. 4). The graphs showed that as the effect of disease severity got higher, the yield obtained from test genotypes became lower. As a result, the higher the FHB pressure is, the more susceptible wheat genotypes are in that environment. In addition, the distance between the points and the line on the diagrams inferred whether the regression analysis caught a weak or strong relationship. The closer the dots on the graphs are to the line, the better the relationship, and vice versa (Fig. 4). The regression analysis equation attempted to find out the yield losses in every unit of disease severity progression. That means, for every one-unit progression of disease severity, there was 0.8780, 0.3475, 0.1772, 0.0455, 0.0438, 0.0326, and 0.0264 units of total yield loss in wheat genotypes tested at North Ari, Chencha, Adiyo, Bonke, Hulbareg, Sodo Zuriya, and Gedeb, respectively (Fig. 4). Similarly, the coefficient of determination (R-square) value indicated that 0.7590, 0.6750, 0.870, 0.3090, 0.2480, 0.2240, and 0.1120 of the variation in yield loss was explained by disease severity at Hulbareg, Gedeb, Adiyo, Chencha, North Ari, Sodo Zuriya, and Bonke, respectively (Fig. 4). In Bonke, Chencha, and Sodo Zuriya, the yield losses were significantly associated with other factors rather than FHB pressure, as indicated by R-square values during the growing periods (Fig. 4).

Discussion

Fusarium head blight is a devastating disease that is responsible for quantitative and qualitative losses (50–100%) of wheat yield worldwide (Windels 2000; Pirgozliev et al. 2003; Shude et al. 2020). Even if there are suggested fungicides to decrease the FHB pressure, this approach is neither safe nor economically feasible. Green et al. (1990), Mostafalou and Abdollahi (2012), and Foster et al. (2017) suggested that chemical control of plant diseases is not sustainable because of high cost and undesirable consequences on the environment, human health, non-target organisms, and resistance development in the pathogen population. Hence, the use of disease-resistant genotypes is ideal in terms of cost-effectiveness, eco-friendliness, and sustainability for managing any plant disease, including FHB (Campbell and Madden 1990; Gilbert and Haber 2013; Agrios 2005; Bolanos-Carriel 2018). Accordingly, in this study, eleven wheat genotypes were evaluated for their resistance reaction against FHB, yield performance, and stability regarding FHB resistance and potential yield across locations in southern Ethiopia. Just like agronomic characters, the response of wheat genotypes to FHB varies in various locations or environments due to that the difference in weather conditions and the *Fusarium* species complex influences the interaction between FHB and wheat genotypes (Buerstmayr et al. 2008; Kadariya et al. 2008; Beres et al. 2018; Shude et al. 2020).

During the study, FHB symptoms were first observed on Hidase, Kakaba, Danda'a, Kingbird, and Ogolcho genotypes at the Zadok's growth stage (ZGS) of 59 at Adiyo, Gedeb, North Ari, Sodo Zuriya, Hubareg, Chencha, and Bonke. FHB symptoms observed on the test wheat genotypes were in agreement with its typical symptoms reported by other scholars in different parts of the world (Gilbert and Tekauz 2000; Murray et al. 2009; Dill-Macky

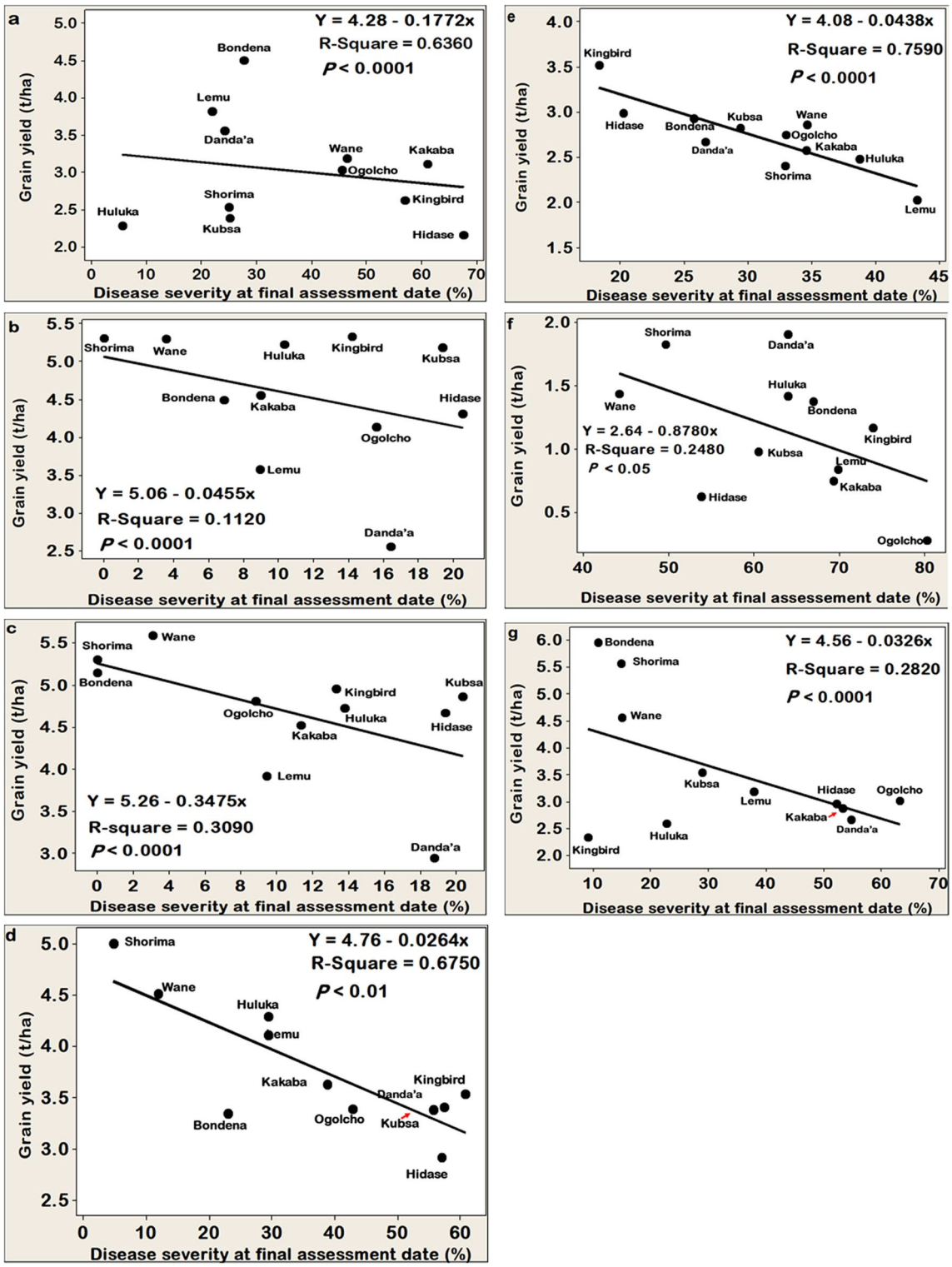

Fig. 4 Estimation of the relationship between yield loss and disease severity in Adiyo (**a**), Bonke (**b**), Chencha (**c**), Gedeb (**d**), Hulbareg (**e**), North Ari (**f**), and Sodo Zuriya (**g**) districts in southern Ethiopia during the 2019 main cropping season

2010; Ghimire et al. 2020; Mengesha et al. 2021, 2022). On the other hand, the identified *Fusarium* species such as *F. graminearum, F. culmorum, F. avenaceum, F. poae, F. ussurianum, F. semitectum, F. lateritium*, *F. sambucinum*, and *F. heterosporum* were in line with the reports of Earecho et al. (2020), Getachew et al. (2022), and Mengesha et al. (2021, 2022) in Ethiopia.

The pooled ANOVA for RCBD of disease and yield parameters demonstrated that the test genotypes were significantly different across locations/environments. Regarding the response of genotypes to FHB intensity, various degrees of disease incidence, disease severity, and AUDPC were noted for the test genotypes across locations. In addition, inconsistent results for these parameters on the test genotypes were recorded across locations. Accordingly, the highest mean disease incidence was noted for the genotype Hidase at Adiyo, Bonke, and Gedeb. At Chencha, Hulbareg, and Sodo Zuriya, the highest mean incidence was registered from Danda'a, Lemu, and Ogolcho genotypes, respectively. Conversely, the lowest mean incidence was noted for the genotype Shorima at Bonke, Chencha, and Gedeb. The genotypes Huluka, Hidase, and Kingbird exhibited the lowest mean incidence at Adiyo, Hulbareg, and Sodo Zuriya, respectively. However, more than 93% FHB incidence was recorded for all test genotypes at North Ari. Overall, the highest mean disease incidence was observed on Hidase, followed by Kubsa, while the lowest mean was recorded from Bondena, followed by Lemu, Shorima, and Wane genotypes under crosswise assessments.

During the study, field recorded data indicated that the development of FHB incidence initially showed slow progression (especially at Adiyo, Bonke, and Chencha), and eventually became higher at the final assessment date (at the ZGS of 90), especially at Gedeb, Hulbareg, and North Ari. Berger (1988), Campbell and Neher (1994), Jones (2001), Bolanos-Carriel (2018), and Cazal-Martínez et al. (2020) reported that disease incidence progression, including FHB, between and among different genotypes with various resistance reactions to the disease was variable and increased with time, and eventually the maximum disease incidence for numerous pathosystems is close to 100%. It was true in the study areas, especially in North Ari. A 100% FHB incidence was reported in southern Ethiopia (Getachew et al. 2022). Comparable tendencies in FHB severity and AUDPC were also observed between and among test genotypes across locations. However, the highest mean severity and AUDPC were noted from genotypes Hidase and Lemu, and the lowest mean severity and AUDPC were perceived from Huluka and Kingbird genotypes at Adiyo and Hulbareg, respectively. The genotypes Hidase, Kubsa, and Kingbird exhibited the highest mean severity and AUDPC (for Ogolcho) at Bonke, Chencha, and Gedeb Ari, respectively. In the listed locations, the lowest mean severity and AUDPC were noticed in the Shorima genotype. In both North Ari and Sodo Zuriya, the highest mean severity and AUDPC were observed on the Ogolcho genotype, while the lowest mean severity and AUDPC were noted on the Wane and Kingbird genotypes, respectively. The overall results exhibited that the genotype Hidase had the highest mean severity, and the genotype Shorima, followed by Bondena and Wane, showed the lowest severity under crosswise assessments.

However, variable responses between and among the tested genotypes were observed for FHB epidemic development across locations. A given genotype showing lower FHB intensity in a specific location might not exhibited the same result in other locations. The phenomenon could be attributed to an abundance of inoculum load in the environment, the presence of the *Fusarium* species complex, and favorable environmental conditions (primarily temperature and precipitation) for infection. Trail et al. (2002), Kriss et al. (2010), McMullen et al. (2012), and Karasi et al. (2016) reported that the outbreak of FHB in wheat genotypes oscillates depending on the pathosystems, or interactions among host, pathogen, and environment. Furthermore, Campbell and Madden (1990), Jeger (2004), and Madden et al. 2017a) suggested that the interaction among suitable environments (optimal for infection), available hosts, and virulent pathogens during the epidemic period has a strong influence on disease epidemic or intensity. Thus, the current study suggests that each location requires specific wheat genotypes under FHB pressure. For instance, the genotypes Shorima, Bondena, Wane, and others could be produced depending on yield potential under FHB pressure at Adiyo, Bonke, Chencha, and Gedeb.

Among the experimental sites, symptoms of FHB first appeared at Adiyo in the growing season. However, the overall FHB pressure was relatively higher in North Ari, while the lowest FHB pressure was noted at Bonke and Chencha. Variation in FHB intensity could be due to conducive weather conditions, genotype susceptibility, inoculum load, and viability within or around the host in the areas for epidemic development. Although there was the convenience of host tissue and optimum temperature and moisture for the outbreak of FHB, the FHB intensity in Bonke and Chencha could be mainly associated with lower inoculum load or viabilities within the surroundings, time of disease onset, genotype resistance levels, and environmental adaptability. Shaner (2003), Brown et al. (2011), Shah et al. (2013), Lenc (2015), and Reis et al. (2016) reported that the existence of auspicious environmental conditions (especially temperature and sufficient moisture) and abundance of viable inoculum

before, during, and post-anthesis ensued in severe epidemic development of FHB on small grain cereals worldwide. Furthermore, while the pathogen is capable of causing disease in a variety of conditions, variations in climatic requirements, genetic background, and environmental adaptations within the FHB complex species have been shown to have a significant impact on disease epidemic development, according to previous studies (Parry et al. 1995; Akinsanmi et al. 2006; Muthomi et al. 2008; Lenc 2015; Lenc et al. 2015). The authors also reported that the auspicious conditions for FHB infection included frequent precipitation, prolonged periods (48–72 h) of high moisture, and a pretty temperatures (15–30 °C) with available air currents. Such optimal conditions were authentic in the study areas during the study period (Additional file 2: Figure S1).

However, disease intensity in any situation is associated with inoculum density and viability, suitable environmental conditions (mainly optimum weather conditions), and susceptibility of the crop in the pathosystems, and therefore, the intensity of individual diseases differs from year to year and place to place for these reasons (Campbell and Madden, 1990; Agrios, 2005; Madden et al. 2017a, 2017b). In this study, the low levels of FHB intensity might be due to the resistance capability of the genotypes to the disease. However, no wheat genotype bestows a resistance gene for FHB; resistance is conferred through quantitative trait loci (QTLs) (Mesterházy et al. 2005; Dweba et al. 2017; Ghimire et al. 2020; Shude et al. 2020). In addition, Zhou et al. (2002), Buerstmayr et al. (2009), and Giancaspro et al. (2016) reported that the resistance to *Fusarium* species is a quantitative trait and, intrinsically, is expected to be controlled by the collective effects of a number of QTLs, epistasis (the interaction between QTLs), environment (mainly weather conditions), and interaction between QTLs and the test environment. Accordingly, several commonly utilized QTLs for FHB incidence and severity were mapped on wheat chromosomes 2AS and 3AL, and 2AS, 2BS, and 4BL (Ban 2000; Cuthbert et al. 2006; Buerstmayr et al. 2009; Giancaspro et al. 2016).

The variance of analysis for RCBD also pointed out significant genotypic variation for yield across experimental sites. Like that of FHB intensity, the variable and inconsistent results of yield performance were also observed across locations. That is, a genotype performing well in a given location might not perform well in another location and vice versa. For instance, the genotype Bondena gave the highest yield at Adiyo but the lowest yield at North Ari. At Bonke and Chencha, all genotypes exhibited comparatively high yield performance with statistically similarity, except for the Danda'a genotype, which was the lowest yielding genotype in the two locations. The genotypes Shorima, Kingbird, Denda'a, and Bondena displayed the highest mean yield performance, whereas Hidase, Lemu, Ogolcho, and Kingbird genotypes brought forth the lowest mean yield performance at Gedeb, Hulbareg, North Ari, and Sodo Zuriya, respectively. Genotype Bondena at Adiyo, Bonke, Chencha, and Sodo Zuriya, genotype Shorima at Bonke, Chencha, Gedeb, and Sodo Zuriya, and genotype Wane at Bonke, Chencha, Gedeb, and Hulbarege maintained consistent yield potential and FHB reaction. In this study, low-yielding genotypes were severely affected by FHB in all locations. The overall mean results also confirmed that Bondena, Shorima, and Wane genotypes maintained comparatively higher yield and the lowest FHB intensity across locations.

Several earlier pieces of research also confirmed the existence of genotypic variations among wheat genotypes for agronomic parameters at various experimental conditions for a number of reasons (Purchase et al. 2000; Wiśniewska et al. 2004; Buerstmayr et al. 2008; Šíp et al. 2011; Cazal-Martínez et al. 2020). Furthermore, tested genotypes produce a comparatively higher overall mean yield at Bonke and Chencha than others. This might be elucidated by the auspicious environmental conditions for growth and low FHB pressure in these areas. Contrarily, genotypes produce a comparatively lower overall mean yield potential at North Ari. The low yield attained from North Ari could not be linked only to the FHB pressure, the environmental adaptability of genotypes to the area could also be an additional contributing factor. Chrpová et al. (2010), Steiner et al. (2017), Steiner et al. (2018), and Cazal-Martínez et al. (2020) reported that differences in yield performance among evaluated wheat genotypes resulted from environmental adaptability of the genotype in addition to FHB constraints under production. In addition, a GEI study also indicated the existence of noteworthy effects due to genotype, environment, and their interactions for agronomic traits of wheat (Yuksel et al. 2002; Buerstmayr et al. 2008; Mohammadi et al. 2010, 2015; Akan and Akcura 2018).

For various reasons, several studies indicate that simple ANOVA of RCBD is not enough for multi-location experimental studies to determine the study genotypes. This is because it does not exhibit the contribution of the genotypes to the environmental interaction and which genotype was stable for yield performance across environments under the pressure of plant disease (Yan and Falk 2002; Yan and Tinker 2005; Yan et al. 2007). In this regard, the AMMI and GGE analyses were better options for the identification of promising genotype on disease resistance and yield potential under specific or across environments and for the determination of the stability of the test genotypes in multi-location studies (Yan et al.

2000, 2007; Yan and Tinker 2005, 2006). For FHB severity, the AMMI analysis exhibited that 47% of the total sum of squares was ascribable to environmental influence, while only 10.60% to genotype and 21% to G × E interaction. A huge sum of squares for test environments pointed out that the test environments were diverse with big alterations among environmental means, triggering most of the disparity in FHB severity. This indicates that environment plays a strong influence on disease epidemic development (Yan and Tinker 2006; Buerstmayr et al. 2008; Beres et al. 2018). The degree of the GEI sum of squares was more than 1.50 folds higher over the genotype, indicating that there were considerable variations in genotypic response across environments. These findings were in line with earlier reports for various crop diseases, including FHB (Yan and Falk 2002; Yuksel et al. 2002; Yan et al. 2007; Buerstmayr et al. 2008; Gitonga et al. 2016; Akan and Akcura 2018; Beres et al. 2018). In addition, the AMMI analysis of variance of the treatment sum of squares due to interaction was partitioned into two significant IPCAs. The two IPCAs explained 80.50% of the total variation due to G × E commutative interaction, in which the contribution of IPCA 1 was 52.90% and that of IPCA 2 was 27.60%. A substantial percentage of GEI was elucidated by the two IPCAs. Some researchers also suggested the importance of comprehending most of the GEI sum of square in the first two IPCAs to get accurate information on the role of the environment on disease development (Yan and Tinker 2006; Yan et al. 2007; Gitonga et al. 2016; Das et al. 2019).

Genotype stability as ascertained by ASV exhibited a wide range in ASVs among genotypes across environments. All the test genotypes had an ASV of greater than one, indicating the instability of the genotypes for consistent FHB resistance responses across environments. Hidase was the most unstable genotype, having the highest ASV of 8.40. It was trailed by Shorima (6.91) and Kakaba (6.11), while Ogolcho, Lemu, and Kubsa had the lowest ASVs of 2.22, 2.49, and 2.73, respectively. In this study, the genotypes having the lowest FHB severity showed the highest ASVs compared with those having the highest FHB severity but lowest ASVs, indicating inconsistency of the genotypes' resistance response to FHB across environments. That is, the response of genotypes to FHB varies in various environments. This could be due to the variation in environmental conditions and the existence of various *Fusarium* species, which affect the interaction between FHB and wheat genotype for epidemic development. Variation in genotypic response to FHB has been known to result from variations in climate conditions and *Fusarium* species (Buerstmayr et al. 2008; Beres et al. 2018; Earecho et al. 2020; Mengesha et al. 2021).

In this study, the wheat genotypes with the lowest FHB reactions typically have lower IPCA 1 and IPCA 2 scores. According to Yan and Falk (2002), Yan and Tinker (2006), and Yan et al. (2007), genotypes with lower IPCA 1 scores have a lower GEI effect than those with higher IPCA 1 and have less variability for disease reaction across environments. The genotypes with a negative score for both IPCA 1 and IPCA 2 were unsuitable even if in the presence of lower pressure of FHB, and therefore are not recommended for cultivation across locations. The genotypes exhibiting positive IPCA 1 and negative IPCA 2 scores could be considered for cultivation in all environments depending on their yield potential since these genotypes are adaptable and less susceptible to FHB. The remaining genotypes could be advised for cultivation in environments where they are well-performed. The results pointed out the inconsistency in genotypes' response to FHB, and a single genotype could not be advised for cultivation across environments. In wheat resistance breeding for FHB, tests of genotype performance across a broad range of agro-ecologies (environments) are considered to lessen the influence of GEI, ensuring that the nominated genotypes keep stable resistance against FHB coupled with high-yield performance across many environments (Buerstmayr et al. 2008; Šíp et al. 2011; Beres et al. 2018; Cazal-Martínez et al. 2020).

In the end, variations in climate variables between and among the testing environments, along with the genetic difference of wheat genotypes under the pathosystem, brought forth variable genotypic responses to FHB across environments. Accordingly, none of the test genotypes exhibited resistance to FHB across environments, indicating the difficulties in FHB-resistant breeding program. However, some genotypes were found to be resistant to FHB in specific environments. Earlier studies also confirmed that there were inconsistent genotypic responses with varying disease reactions in various crops across environments, including wheat for FHB reaction (Yan and Falk. 2002; Buerstmayr et al. 2008; Kadariya et al. 2008; Sandhu et al. 2015; Sharma et al. 2016; Parihar et al. 2017; Miedaner et al. 2022). Breeders want to specify genotypes with high yields as well as wide adaptation in the overall breeding program for the agronomic character. Unfortunately, in resistance breeding work, the specification of genotypes is occasionally influenced by the complexity of host–pathogen-environment interactions, resulting in disease resistance variability for the test genotypes (Yan and Falk 2002; Yan et al. 2007). Multi-location genotype evaluation facilitates the determination of genotypes with less spatial variation and consistent performance across environments (Kang 2002; Yan and Falk 2002).

In the "mean vs. stability" view of the GGE biplot, the AEC ordinates suggest a higher GEI effect in both directions and signify instability against resistance reaction to the disease (Yan and Falk 2002; Yan and Tinker, 2006), while the resultant projections of the tested genotype to the AEC abscissa denote the mean performance (Yan and Falk 2002). Rubiales et al. (2014), Akan and Akcura (2018), and Das et al. (2019) also reported that genotypes that show up to the left of the AEC line are considered paramount in terms of resistance. In this study, Shorima (G10), Wane (G11), and Bondena (G1) showed greater negative projection on the ATC abscissa, indicating less FHB reaction or higher resistance. Lemu (G8) was identified as a stable and winning genotype with the lowest vector projection onto the AEC abscissa. Moreover, Kakaba (G5) and Huluka (G3) were recognized as desirable genotypes and were located nearer to the ideal genotype, Lemu (G8). Like the ideal genotype, Huluka (G3) similarly has the resistance response to FHB, which is a higher negative projection on the ATC abscissa with less projection on AEC ordinates, implying high stability (Yan et al. 2007; Parihar et al. 2018). Such strategies have been successfully used to identify stable and resistant genotypes in a variety of crops for a variety of diseases (Yan and Falk 2002; Sharma et al. 2015; Parihar et al. 2017; Sillero et al. 2017; Tekalign et al. 2017).

In the current study, the integration of a GGE biplot, accompanied by a statistical hypothesis, enhanced the precision of the visual observation toward genotype recommendation. Accordingly, the GGE biplot provides a graphical presentation of the "which-won-where" configuration and makes it easy to ascertain the assemblage of environments with the same winners. The vertex genotypes in the sectors exhibited susceptibility to all environments inside that sector, attributable to the amount and direction of their distance from the origin of the GGE biplot. The genotypes are distant from the environments on the opposite sides and are considerably assessed as the most resistant to these environments. For example, resistance genotypes around Adiyo, Bonke, Chencha, Gedeb, and Sodo Zuriya include Shorima (G10), Wane (G11), Bondena (G1), Huluka (G3), and Lemu (G8); however, cultivation of these genotypes should be considered for adaptability and yield potential. In the aforementioned environments, Danda'a (G2), Hidase (G4), Kubsa (G7), and Ogolcho (G9) were susceptible genotypes. Earlier reports confirmed the role of GGE biplot and GEI in an assortment of genotypes with resistance to various crop diseases (Kadariya et al. 2008; Rubiales et al. 2014; Akan and Akcura 2018; Das et al. 2019). In the current study, it was observed that the vertex genotypes exhibited the lowest FHB susceptibility and were located far from the origin, thereby portraying inconsistency in the resistance performance across environments. Yan and Falk (2002), Akan and Akcura (2018), and Das et al. (2019) reported that the vertex genotypes exhibited inconsistency for some reasons and were the most responsive to resistant reactions or susceptible in specific or across environments.

Separating testing environments into different mega-environments and identifying representative test environments are the only approaches to acquire consistent genotype performance against FHB within that specific sector. In this regard, Yan and Falk (2002) and Yan et al. (2007) stated that representativeness in various mega-environments is the main factor to identify how a test environment should be utilized in genotype testing under suitable pathosystems, presuming satisfactory discriminating ability. In the current study, North Ari and Hulbareg were identified as the most discriminating ("ideal") environments for testing genotype resistance to FHB. However, in the multi-location genotype evaluation, data from multiple years are required to determine the repeatability of the environments and to properly examine the repeatability in GEI (Yan et al. 2000, 2007, 2011; Yan and Rajcan 2002; Yan and Holland 2010). Locations inside each mega-environment assembled in the current study revealed the same conclusions concerning genotypic response toward FHB. The judicial arrangement of study locations and joining breeding attempts in a location-specific mode holds great relevance for bettering the precision of the resistance breeding plan. A similar approach was made with GGE biplot for various diseases, including FHB and powdery mildew in wheat (Kadariya et al. 2008; Lillemo et al. 2010), Ascochyta blight in faba bean (Rubiales et al. 2012), Ascochyta blight and Fusarium wilt in chickpea (Pande et al. 2013), and Fusarium wilt in pigeon pea (Sharma et al. 2016).

On the other hand, the yield performance of various wheat genotypes is frequently influenced by environmental conditions (Dabi et al. 2016; Ashebr et al. 2020). The GEI study can be constructed based on stability analysis to identify high-yield potential suitable for resource-poor growers to produce wheat in various stress-prone environmental conditions, including FHB epidemic pressure. The results of GEI in the pooled analysis might be the contribution of the environment's sum of the squares to the total disparity in yield as indicated by the wide variation in yield attained per environment. Additionally, most examined genotypes' outrank positions have changed both within and across settings. Accordingly, the environment, genotype, and GEI explained 58.20, 7.10, and 17.90% of the total variation, respectively, signifying the existence of significant environmental variation. The first IPCA managed over 40% of the G × E sum of squares, while the

second IPCA revealed 33.30% of the interaction, and the remaining 26.70% is due to residual, which is hard to interpret and needs to be removed. A substantial percentage of G × E interaction was elucidated by the first two IPCAs. Purchase et al. (2000) and Kaya et al. (2002) also suggested the prominence of comprehending most of the G × E sum of squares in the first two IPCAs to realize accurate information.

The test genotypes with lesser IPCA 1 scores would bring forth a lesser GEI effect than those with higher IPCA 1 scores and are more stable across test environments (Zhang et al. 1998; Yan et al. 2007; Singh et al. 2019). Bondena and Shorima exhibited the same sign (negative) of IPCA 1 and IPCA 2 scores, and are suitable for production under stress conditions in specific environments since they are significantly influenced by the change in environments. Whereas genotypes with opposite signs of IPCA 1 and IPCA 2 are suitable in unfavorable environmental conditions because they are significantly affected by environmental change. The results suggested that a genotype having the same sign of IPCA 1 and IPCA 2 scores could not be deliberated for cultivation across environments. The genotypes Wane, Hidase, Kubsa, Huluka, Kakaba, Kingbird, and Ogolcho could be advised for cultivation across environments as indicated by the opposite sign of IPCA 1 and IPCA 2 scores. The other genotypes could be considered for production in environments where they accomplish well under stress conditions. Zhang et al. (1998) and Yuksel et al. (2002) suggested instability infers for stable genotypes concerning yield performance, always corresponding to the mean response of the test environments, close to zero in the GEI study. In crop improvement programs, tests of genotype performance for agronomic traits across a broad range of environments are carried out to minimize the GEI effect and to assure that the nominated genotypes have a high yield and stable performance across many environments (Stanley et al. 2005; Yan et al. 2007). In the current study, variations in yield performance and stability perceived among the test genotypes might also have been due to variations in their genetic background, environmental adaptability, biotic constraints, and other factors. Inconsistent genotypic responses to environmental factors such as weather conditions, soil type, fertility status, biotic restraints, and others from place to place and year to year are a function of GEI (Ceccarelli et al. 1994).

The genotypes Bondena and Shorima were the highest yielding genotypes with comparatively highest ASV values, but they are not stable. In this regard, Farshadfar (2008) reported that stability alone cannot be regarded in crop production, and therefore, identifying genotypes with extraordinary yield potential coupled with consistent stability across environments is of great importance. Accordingly, Kakaba, Ogolcho, Hidase, Wane, Huluka, Kubsa, and Lemu were regarded as stable genotypes as indicated by the lowest ASV values, whereas genotype Danda'a was the smallest stable genotype across environments. Thus, these findings emphasize the significance of multi-location studies when advocating genotypes having good yield stability under diverse environments with FHB epidemic pressure. The estimated values of ASV verified that most study environments were normally stable and might hold more than one restraining factor influencing the performance of the tested genotypes. Yan et al. (2007), and Benard et al. (2018) further suggested that no meaningful evidence of test genotype performance can be found in such environments.

Environmental potential decides the threshold at which a genotype has to perform well (Ceccarelli et al. 1994). The GGE biplot and environment mean yield suggest that Adiyo and Noth Ari can be regarded as low potential environments, whereas Gedeb, Sodo Zuriya, and Hulbareg could be considered as moderate potential environments, and Bonke and Chencha as high potential environments for test genotypes. Khaliq et al. (2004), Dabi et al. (2016), and Ashebr et al. (2020) reported that wheat yields are low if produced in low-potential environments and vice versa. Bonke and Chencha discriminated environments with longer vectors, which can be used in choosing superior genotypes with high yield since these environments provide more information about variances among test genotypes. Adiyo and Noth Ari took comparatively short vectors, which provide little information about variations in yield among the genotypes, and thus, they cannot be utilized as test environments for wheat genotypes. However, Yan et al. (2007) reported that the identification and elimination of non-informative trial environments as well as distinguishing of test environments for yield potential appraisal trials requires several years of data. Yan and Hunt (2001) and Yan et al. (2007) suggest that an ideal environment ought to be a highly discriminating factor for the testing genotypes and simultaneously representative of the target environment. Representativeness of the study environment is portrayed by an angle made between the environment vector and the abscissa of the average environment axis. In this regard, the more representative the environment is, the smaller the angle presents on the graph. While environments having longer vectors are more suitable for discriminating of the test genotypes, environments with short vectors have little or no informative variation among the tested genotypes (Yan et al. 2007).

On the polygon view, the vertex genotypes found at a distance from the GGE biplot origin are more responsive to changes in the environment and provide higher yields, except for the Danda'a and Hidase genotypes. The vertex

test genotypes in each sector are the best genotypes in environments whose markers fall into the respective sector. Environments within a similar sector partake of similar winning genotypes, whereas environments found in different sectors hold different winning genotypes. In this regard, Yan and Hunt (2001) and Yan and Tinker (2006) mentioned that the test genotypes inside the polygon view and closer to the GGE biplot origin were less responsive than vertex genotypes. Accordingly, the genotypes Bondena, Hukuka, Kakaba, Kubsa, Lemu, and Ogolcho were positioned within a polygon, and they are less responsive. Previous researchers described the polygon view of the GGE biplot as the best method for identifying winning test genotypes by visualizing interaction patterns between test genotypes and study environments (Yan et al. 2000; Yan and Kang 2003). Therefore, the GGE biplot has been used in genotype trials to efficiently distinguish the superior genotype(s) across environments, identify the superlative genotypes for specific environments, whereby specific genotypes can be suggested for specific environments, and can be used to assess the yield and stability of genotypes (Yan and Kang 2003; Yan and Tinker 2006).

The association study connoted a highly significant and positive correlation among epidemiological parameters. During outbreak periods, the epidemiological parameters are significantly interconnected, according to Campbell and Madden (1990) and Agrios (2005). Yield and yield-related parameters also exhibited a positive association between them. Previous research findings also confirmed that thousand kernels' weight and other agronomic traits had a significant positive association with yield (Khaliq et al. 2004; Dabi et al. 2016; Ashebr et al. 2020). However, the association between epidemiological and yield and yield-related parameters held negative and highly significant associations among themselves. For instance, highly affected test genotypes due to FHB exhibited higher severity scores, which resulted in severe yield reductions, figured out to be cut by half compared with a genotype having low levels of severity (resistant genotypes) across locations. Plant disease and agronomic parameters had negative relationships on various grounds, according to Campbell and Madden (1990) and Agrios (2005), and this could result in noticeable yield reductions. In this study, the negative relationship between FHB severity and yield suggests that epidemiological parameters are important components in estimating yield losses of wheat. That is, the FHB commonly accelerates kernel desiccation and harvested grains become small, light, pre-mature, shriveled, shrunken, and sometimes covered with a white or pink fungal mass and contaminated with mycotoxins, leading to heavy yield losses in wheat production (Andersen et al. 2014; Karasi et al. 2016; Shude et al. 2020).

Accordingly, a regression analysis was conducted to examine how much the relationship between FHB severity and yield influenced the predicted yield losses in each location. The relationship graph showed that as the magnitude of FHB severity becomes higher, the yield gets lower, inferring that the higher the FHB severity, the more losses in yield. Several researchers reported that plant diseases had a strong link to crop growth retardation and yield losses in all stages of disease development (Wheeler 1969; Campbell and Madden 1990; Guant 1995; Agrios 2005). The coefficient of determination found on the graph suggested that 0.7590, 0.6750, 0.870, 0.3090, 0.2480, 0.2240, and 0.1120 of the disparity in yield loss were explained by FHB severity at Hulbareg, Gedeb, Adiyo, Chencha, North Ari, Sodo Zuriya, and Bonke, respectively, during the growing season. However, the R-square values found on the relationship graph indicated that environmental factors and other biotic constraints played more significant roles than FHB epidemics in the variation of yield loss in Sodo Zuriya, Chencha, and Bonke. That is, in the aforementioned locations, the contribution of FHB pandemic to higher values in yield loss estimation was less than that of environmental variables and other biotic restrictions. Overall, considering the medium intensity of wheat rusts and Septoria leaf blotch, environmental factors, and other variables could also be responsible for variation in yield loss besides FHB. The effects of these factors were not amply elucidated by this study. However, their influence cannot be undervalued in the yield loss in wheat production.

Conclusions

The current study investigated resistance responses and yield potentials of eleven wheat genotypes to FHB in seven locations. Evidence obtained from the present study exhibited the existence of wide variability in resistance to FHB and yield performance among the test wheat genotypes across locations. AMMI and GGE biplot analysis also confirmed the inconsistent results concerning resistance reaction levels and yield stability of the test genotypes across environments. The variations observed in test genotypes across different environments were regarded as an indication of the existence of GEI. North Ari and Hulbareg were found as discriminating settings for selecting superior wheat genotypes in the face of FHB pressure, whereas Bonke and Chencha were indicated as discriminating environments for testing wheat genotypes against FHB. The "Mega-environment" determination helped in rearranging the agro-ecological region and location of the specific breeding site. Accordingly, the

identification of non-redundant testing sites would accelerate optimal resource use in future work. As a result, the winning genotype(s) in a particular or other environment can be produced using appropriate cultural practices for reducing FHB harms and yield losses during production.

Methods

Characteristic features of the study sites

The wheat genotypes were tested at seven locations (Adiyo, Bonke, Chencha, Gedeb, Hulbareg, North Ari, and Sodo Zuriya) in southern Ethiopia during the 2019 main production season. These locations were selected for the study based on the history of FHB and the production potential of wheat. The experimental locations and their respective geographic positions are depicted in Fig. 5. The experimental sites of Sodo Zuriya, Gedeb, Hulbareg, North Ari, Adiyo, Chencha, and Bonke were situated at an altitude of 2116, 2245, 2304, 2391, 2400, 2667, and 2786 m above sea level, respectively. The locations experienced rainfall two times, a bimodal pattern, within a production season. March to May is known as the short rainy season, and July to November is known as the long rainy season, the main production season. As reported by Belay et al. (1998), the short and long rainy season constitutes 25% and 45% of the annual rainfall, respectively, in Ethiopia. Mean monthly minimum and maximum temperatures, total rainfall, and relative humidity for experimental locations during the production season were presented in Additional file 2: Figure S1. The meteorological data was obtained from the Ethiopian Meteorological Agency at Hawassa Branch for the 2019 cropping year. The soil is characterized by diversified physical and chemical properties in the experimental sites.

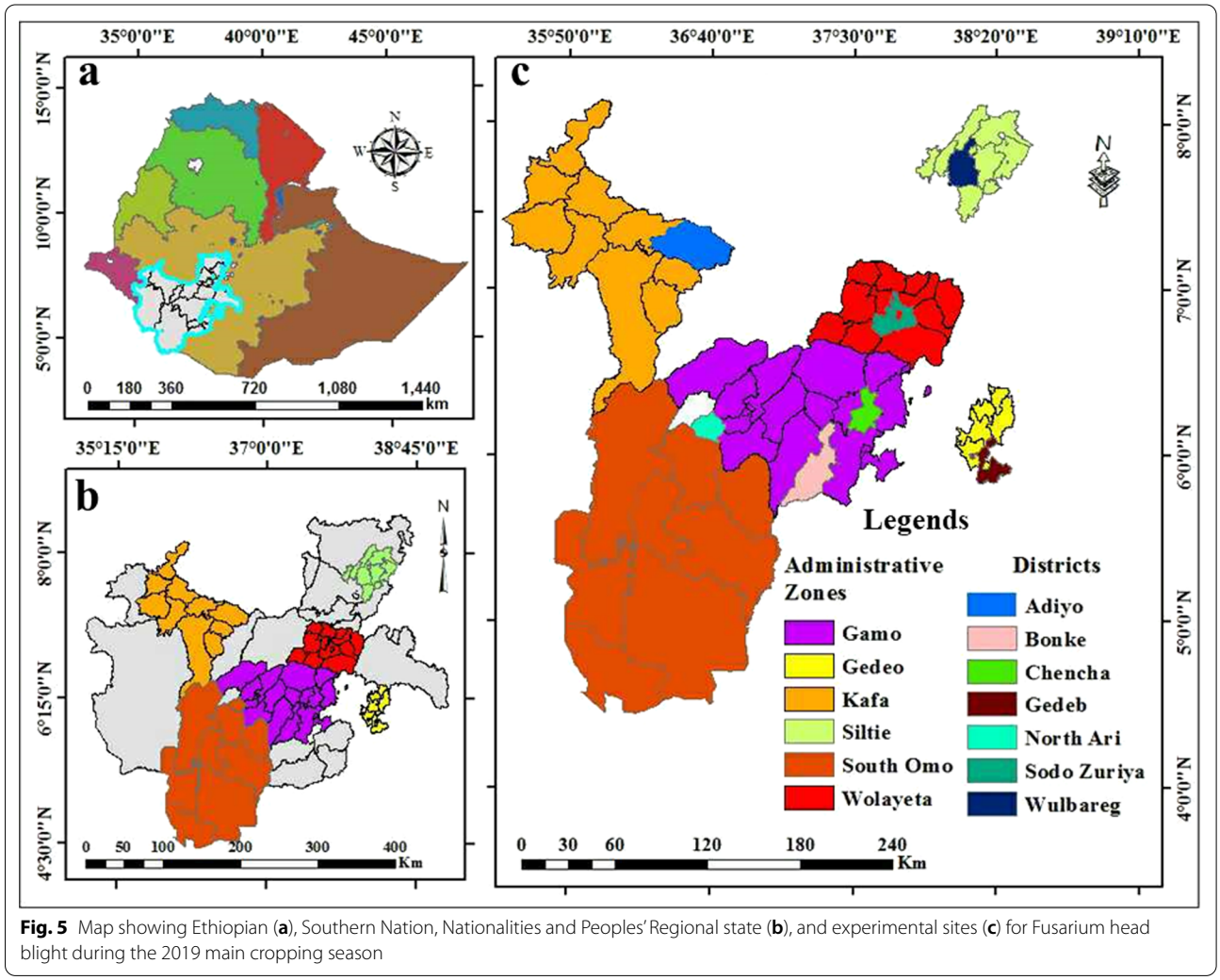

Fig. 5 Map showing Ethiopian (**a**), Southern Nation, Nationalities and Peoples' Regional state (**b**), and experimental sites (**c**) for Fusarium head blight during the 2019 main cropping season

Plant materials, trial design and management

Eleven wheat genotypes, which were obtained from the Kulumsa Agricultural Research Center and Areka Agricultural Research Center, Ethiopia, were used to achieve the objectives of the study. Previous information on responses of these wheat genotypes to major wheat diseases, such as wheat rusts (*Puccinia* spp.) and Septoria leaf blotch (*Septoria tritici*) in major wheat-producing areas of the country, was also obtained (MoANR and EATA 2018; Getachew 2020). However, these genotypes were not tested for their reaction to FHB in the study areas or the country as well. The genotype Kubsa (HAR 1685) was used as a susceptible control based on the suggestion from MoANR and EATA (2018). The details of pedigree, suitable agro-ecologies, and other information regarding all wheat genotypes are presented in Additional file 1: Table S2. The trials were set up with a randomized complete block design (RCBD) with three-time replicates. Each treatment combination was delegated at random to experimental plots within a block.

The experiment was arranged with a gross area of 8.4 m × 27.0 m in each location. The total field size was 226.80 m^2. A unit plot size was 1.8-m width × 2.0-m length and consisted of seven rows with an inter-row of 0.25 cm. Each of the adjacent replications and plots was spaced at 0.5 and 1.5 m, respectively. Sowing was achieved on July 27th (Sodo Zuriya) and August 5th (at North Ari), 2019. Sowing dates were performed between these dates for the other locations during the growing season. The seeds were drilled along the rows at a soil depth of 3 cm during sowing time. An inorganic NPS blended fertilizer at the rate of 100 kg/ha was applied in rows during sowing. In addition, N-fertilizer of 200 kg/ha was applied, of which 1/3 was used during sowing and 2/3 was added at 35 days after sowing. All other necessary field management practices were accomplished uniformly for all plots as per the recommendations to produce a strong and healthy crop, as suggested by MoANR and EATA (2018). Rex® Duo [Epoxiconazole + Thiophanate-methyl] at the rate of 0.5 L/ha with diluting water of 300 L was used for the management of wheat rusts and Septoria leaf blotches regardless of the control plots in all locations during the 30–39 Zadoks growth stage (ZGS) (Zadoks et al. 1974).

Disease monitoring and pathogen identification

Disease monitoring began when the first symptoms of FHB were observed on the spikelet of the genotypes Hidase, Kakaba, Danda'a, Kingbird, and Ogolcho at the ZGS of 59 (heading completed) at Adiyo, followed by Gedeb, North Ari, Sodo Zuriya, Hubareg, Chencha, and Bonke (at the ZGS of 61–69, during post-anthesis). For *Fusarium* species identification, disease samples of infected spikes having characteristic symptoms of FHB were taken from each genotype in each location. The collected samples were bagged individually with sterile paper bags and brought to Hawassa Agricultural Research Center, Areka Agricultural Research Center, and Arba Minch Crop Protection Clinic, Ethiopia, to identify and confirm the causal pathogen and species. Pathogen identification was performed following standard procedures for fungi isolation (Agrios 2005).

Fusarium head blight incidence (DI) and severity (DS) were assessed at a 10-day interval. Subsequently, the area under the disease progress curve (AUDPC) was computed to determine the response of wheat genotypes to FHB under natural epiphytotic conditions during the epidemic period. The disease score ceased with the crop reaching physiologically mature, which was approximately at a ZGS of 90, during the soft dough stage. To ascertain FHB incidence and severity, 20 wheat plants per plot were randomly selected from the middle five rows and marked for subsequent data assessment. As suggested by Wheeler (1969) and Campbell and Madden (1990), the incidence was determined as the mean percentage of the number of diseased spikes per total number of spikes and rated within the plot.

$$\text{Disease incidence (\%)} = \frac{\text{Number of plants showing disease symptoms}}{\text{Total number of plants sampled and rated}} \times 100$$

The FHB severity was assessed on a rating scale of 1 to 100% following Robert and Marcia's (2011) scale. A total of five assessments were made per location during the growing period. The mean values of disease severity obtained from the 20 assessed plants of each plot were used for data analysis. The area under the disease progress curve (AUDPC), which means the progression and buildup of disease on the whole spike or part of the spike during the epidemic periods, was determined from disease severity data assessed on a different day after sowing for each plot, using the following formula designated by Campbell and Madden (1990).

$$\text{AUDPC} = \sum_{i=1}^{n-1} 0.5(X_i + X_{i+1})(t_{i-1} - t_i)$$

where n is the total number of disease assessments, t_i is the time of the *ith* assessment in days from the first assessment date and x_i is the disease severity of FHB at the *ith* assessment. The AUDPC value was expressed in %/days since severity (x) is expressed in percent and time (t) in days.

Yield and yield-related parameters

The thousand kernels' weight and harvested yield were considered among the crop parameters for this study. The yield was collected from the central five rows of each plot in each location. The two border rows of the plot were avoided to reduce their effects in all locations during harvesting. Harvesting of yield was conducted on 140 and 160-days after sowing (at a ZGS of 100) at Sodo and Bonke, respectively. Harvesting dates were fall between 135 and 159 days after sowing for the remaining locations. The yield weight (kg) was assessed by weighing the total harvested yield per plot. The plot-wise harvested yield was transformed into t/ha. Thousand seed weight was assessed by weighing 1000 kernels from randomly sampled kernels taken from the total harvested yields. A thousand kernels' weight was assessed in grams (g). The moisture of the kernels was checked using the standard moisture tester device for cereal crops during the study. The moisture content of kernels was adjusted to 12.5% following the method described by Taran et al. (1998). A seed counter and sensitive balance devices were used to measure thousands of seed weights as a random sample of the total adjusted yield.

Data analysis

The collected disease incidence, severity, AUDPC, thousand kernels' weight, and yield data were subjected to ANOVA. It was employed following the generalized linear model procedure of SAS version 9.2 (SAS Institute 2009). Significant treatment means were separated using a Fisher-protected least significant difference test at a 0.05 probability level designed for RCBD (Gomez and Gomez 1984). ANOVA for the study parameters was employed separately for each environment and under a combination of the whole environments. The GEI effects were detected by ANOVA, which led to the GEI analysis using AMMI stability and GGE biplot models. Accordingly, only disease severity and yield data were considered for the GEI analysis.

The AMMI stability analysis was utilized to determine the stability of resistance reaction and yield performance of the genotypes across environments, mainly representing study locations, agro-ecologies, surrounding weather conditions, and other factors that affect the genotype adaptability and disease development in the pathogen population in the areas (Zobel et al. 1988; Yan 2001, 2002, 2006; Yan et al. 2007). In the AMMI stability analysis, the mean separation among genotypes that significantly differed was separated using the Duncan Multiple Range Test (DMRT) at a 5% probability level. The AMMI analysis was used to assess the relationships between genotypes, environments, and GEI for the study parameters, using the model proposed by Zobel et al. (1988), Crossa (1990), Gauch and Zobel (1996), and Yan et al. (2000). The following AMMI model was used to determine the adaptability and phenotypic stability of the test genotypes across environments.

$$\overline{Y}_{ij} = \mu + g_i + e_i + \sum_{k=1}^{n} \lambda_k \alpha_{ik} \gamma_{ij} + r_{ij} + \rho_{ij}$$

where Y_{ij} is the yield of the *ith* genotype in the *jth* environment; μ is the grand mean; g_i and e_j are the genotype and environment deviations from the grand mean, respectively; λ_k is the square root of the eigen value of the *kth* IPCA analysis axis; α_{ik} and γ_{ij} are the principal component scores for IPCA axis *k* of the *ith* genotypes and the *jth* environment; *n* is the number of principal components retained in the model; r_{ij} is the effect of the jth block nested in ith replica; and ρ_{ij} is the deviation from the model.

An AMMI stability value (ASV) was computed using the procedure suggested by Purchase et al. (2000). As stated by Zobel et al. (1988), AMMI analysis with only two IPCAs could be the paramount prognostic model. Thus, in this study, the first two IPCAs were adopted for AMMI analysis.

$$\text{AMMI stability value} = \sqrt{\left[\left(\frac{SS_{IPCA1}}{SS_{IPCA2}}(IPCA1)\right)^2 + (IPCA2)^2\right]}$$

where $SS_{IPCA\,1}/SS_{IPCA\,2}$ denotes the weighted value allotted to the IPCA 1 score due to its high contributions in the genotype by environment model; SS IPCA 1 and SS IPCA 2 are the sum of squares for IPCA 1 and IPCA 2, respectively; and IPCA 1 and IPCA 2 are the first and second IPCA scores for each genotype.

The GGE-biplot method was employed to generate a genotype-focused GGE biplot diagram to assess the responses of genotypes to identify the resistant and high-yielders. Yan and Falk (2002), Yan and Tinker (2006), and Yan (2014) explained the details of the statistical theory of GGE biplot methodology in host–pathogen-environment interaction analysis for evaluating genotypes for various environments as well as locations. The following GGE model was used to determine the resistance levels (Yan 2002; Yan et al. 2007) and yield performance (Yan 2006) of the wheat genotypes across environments, respectively, based on the singular value breakdown of *t* principal components.

$$\overline{Y}_{ij} = \mu_i + \beta_i + \sum_{k=1}^{t} \lambda_k \alpha_{ik} \gamma_{jk} + \varepsilon_{ij}$$

where $\bar{Y}_{ij}$ is the performance of genotype i in environment *j*; μ is the grand mean of all genotypes-environment combinations; β_j is the main effect of environment *j*; *k* is the number of the principal component; λ_k is the singular values of the *kth* principal components; α_{ik} and γ_{jk} are the scores of *ith* genotype and *jth* environment, respectively, for principal component *k*; and ε_{ij} is the residual associated with genotype *i* in environment *j*.

$$Y_{ij} = \lambda_1 \gamma_{1i} \delta_{1j} + \lambda_2 \gamma_{2i} \delta_{2j} + \rho_{ij}$$

where λ_1 and λ_2 are singular values of the first and second IPCA associated with the matrix of the effects of genotypes added to effects of GEI; γ_{1i} and γ_{2i} are eigenvectors of the first and second IPCA associated with the effect of the genotype *i*; δ_{1j} and δ_{2j} are eigenvectors of the first and second IPCA associated with the effect of the environment *j*; ρ_{ij} is the residual of the model associated with the genotype *i* in the environment *j*.

For genotype valuation as well as deciding stability against resistance reactions, an average environment coordination (AEC) or Average Environment Axis (AEA) view of the GGE biplot was constructed, which simplifies the genotype comparisons based on the mean disease score and stability across environments (Yan 2001, 2002). A performance line passing via the GGE biplot origin was utilized to decide the mean performance and stability of the genotype in terms of FHB severity scoring. For the evaluation of the test environments, the "discriminating power vs. representativeness" view of the GGE biplot was constructed where the "ideal" test environment ought to both discriminate the genotypes and be representative of the "mega-environment" (Yan et al. 2007). Moreover, to determine the dominance of the genotypes in various test environments as well as the assemblage of test environments into various "mega-environments," a "which-won-where?" view of the GGE biplot, was prepared following the method described by Yan and Rajcan (2002). The GGE biplot package in GenStat statistical software version 17th edition was utilized for the analyses (Payne et al. 2014).

A Spearman correlation analysis was employed to examine associations between and among disease and yield-related parameters. In addition, the relationship between the disease pressure and yield was estimated using linear regression of the disease severity and yield of wheat to determine the greater contribution of yield reduction due to either FHB or environmental conditions for the evaluated wheat genotypes. MINITAB® software version 14 (Release 14.20 for Windows® 2007) was used to calculate statistical regression.

Supplementary Information

The online version contains supplementary material available at https://doi.org/10.1186/s42483-022-00152-y.

Additional file 1. **Table S1**: Correlation coefficients between disease scores of Fusarium head blight and yield-related traits of wheat genotypes across locations in southern Ethiopia during the 2019 main cropping season. **Table S2**: Descriptions of the tested bread wheat genotypes for Fusarium head blight across locations in southern Ethiopia during the 2019 main cropping season.

Additional file 2. **Figure S1**. Total rainfall (mm), mean monthly minimum and maximum temperatures (oC), and relative humidity (%) in Adiyo (a), Bonke (b), Chencha (c), Gedeb (d), Hulbareg (e), North Ari (f), and Sodo Zuriya (g) districts of southern Ethiopia during the 2019 cropping season.

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Author contributions
GGM, SMA, and MMS designed the research; All authors conducted the experiment and collected the data; GGM and TSD analyzed the data; GGM interpreted the data and wrote the full manuscript. All authors read and approved the final manuscript.

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Availability of data and materials
All datasets generated from the current study are included and cited in the manuscript. Further datasets used and/or analyzed during the current study are available from the corresponding author upon reasonable request.

Declarations

Ethical approval and consent to participate
Not applicable.

Consent for publication
Not applicable.

Competing interests
The authors declare that they have no competing interests.

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