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Multi-Environment Evaluation of Bread Wheat Genotypes under Terminal Moisture Deficit in Eastern Amhara, Ethiopia

Agegnehu Mekonnen Tessema[1]

agymak2004@gmail.com

Sirinka Agricultural Research Center

Arega Gashaw Yimam

Sirinka Agricultural Research Center

Akalu Gebru Habteselasie

Sirinka Agricultural Research Center

Getachew Yimam Feleke

Sirinka Agricultural Research Center

Tesfaye Alemayehu Abebe

Sekota Dry Land Agricultural Research Center

Research Article

Keywords: Triticum aestivum, bread wheat, genotype evaluation, yield stability, moisture stress tolerance, disease resistance, early maturity, variety release

Posted Date: March 11th, 2026

DOI: https://doi.org/10.21203/rs.3.rs-8813601/v1

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Additional Declarations: No competing interests reported.

Abstract

Wheat productivity in moisture-deficient environments is constrained by terminal drought and disease pressure, necessitating the identification of high-yielding, early-maturing, and resilient varieties. Sixteen bread wheat genotypes, including the standard checks *Kakaba, Sorra, and Danda'a*, as well as a local farmer variety, were evaluated across multiple locations to identify adaptable genotypes for such environments. Field trials were conducted at Geregera, Kon, Jamma, Dehana, and Woleh during the 2016 and 2017 main cropping seasons using a randomized complete block design. Among the tested genotypes, ETBW 6753, later named "Netsanet," demonstrated superior performance in grain yield, earliness, disease resistance, and adaptability across environments. Netsanet exceeded the mean grain yield of the standard checks by 7% and the local farmer variety by 15%, while also meeting key bread-making quality standards, including protein content, wet gluten, and thousand-kernel weight. The previously released variety *Kakaba* remained well adapted to areas experiencing severe terminal drought, particularly Dehana and Woleh. Based on its overall performance, *Netsanet* was officially released in 2020 for cultivation in moisture-stressed agroecological zones of Eastern Amhara. The release of *Netsanet* contributes to improved wheat productivity and resilience under variable rainfall conditions.

1. Introduction

The cultivation of wheat stands as a cornerstone in Old World agriculture, marking its status as the principal cereal crop globally [1, 2]. Present-day wheat varieties primarily align with two major species: hexaploid bread wheat (*Triticum aestivum*: 2n = 6x = 42, AABBDD) and tetraploid durum wheat (T. turgidum subsp. durum: 2n = 4x = 28, AABB). Ranked as the third most vital source of caloric intake worldwide, wheat (0.8 billion tonnes) trails behind sugar cane (1.9 billion tonnes) and maize (1.1 billion tonnes), asserting its significant role in global food supplies [3]. China assumes the lead in wheat production, yielding 134 million metric tonnes [3].

In Ethiopia, wheat commands the third-largest crop coverage, following teff and corn, respectively [4]. Notably, wheat and its derivatives contribute 14% to the nation's total caloric intake, positioning it as the second most crucial staple food after corn (20%) and surpassing teff (10%) and sorghum (11%) [4]. Ethiopia stands out as the primary wheat producer in Sub-Saharan Africa, harvesting 5.3 million tonnes on 1.8 million hectares of cultivated land [3]. Optimal wheat cultivation in Ethiopia typically occurs between 6° and 16°N and 35° and 42°E, at altitudes spanning 1500 to 3000 meters, with the most suitable areas for production falling between 1900 and 2700 meters [5].

Within Ethiopia, the Amhara National Regional State (ANRS) emerges as a pivotal wheat-growing region, contributing around 33.8% (641,170.34 ha.) and 31.4% (1.82 million tonnes) of the nation's total wheat production (6). However, the wheat productivity in this region, averaging 2.8 tons per hectare, falls below the national average. The North and South Wollo zones within the eastern part of the Amhara region account for 23% (147,428 ha) of wheat production, yielding approximately 2.68 million tons, but exhibit a lower productivity of around 2.5 t ha-1 compared to the regional average [6].

Several factors contribute to the decreased wheat productivity in this region. Terminal moisture deficit, due to delayed rainfall onset and early cessation, poses a significant challenge. Additionally, prevalent wheat rust diseases, such as yellow rust and stem rust, have historically affected yields, while Septoria has emerged as a prevalent disease in recent times. Furthermore, poor soil fertility and inadequate management practices, compounded by limited access to inputs like improved seeds, fertilizers, and pesticides, collectively contribute to reduced yields.

Consequently, addressing the low productivity of wheat in the Amhara region necessitates recommending improved bread wheat varieties capable of delivering satisfactory yields under existing conditions, emerging as a primary priority for enhancing productivity in this critical agricultural sector.

2. Materials and methods

2.2. Description of the study area

The research covered five locations (Dehana, Geregera, Kon, Jamma, and Woleh) over the main cropping seasons of 2016 and 2017, comprising a total of 10 distinct environments (Table 1). Rainfall patterns exhibited erratic distribution, typically commencing later

(from the first to the middle of July) and concluding earlier (by the first week of September; Fig. 1). Predominantly, substantial rainfall was concentrated in July and August, with minimal precipitation recorded during the other months.

Table 1
Geographical coordinates and the average minimum and maximum temperatures of experimental locations

Locations	Years	E	Geographical coordinates			Temperature(°C)	
			Altitude (m)	Latitude	Longitude	Min.	Max.
Dehana	2016	E1	2400	12°40'00"	38°30'00"	14	24
	2017	E2					
Geregera	2016	E3	2872	11°35'00"	38°45'00"	17	23
	2017	E4					
Jamma	2016	E5	2622	10°27'18"	39°16'01"	9	24
	2017	E6					
Kon	2016	E7	2872	11°37'34"	38°55'05"	4	21
	2017	E8					
Woleh	2016	E9	2000	13°05'00"	39°03'00	14	26
	2017	E10					

E(environments), Temperature (2016 and 2017) sourced from the National Meteorological Agency, Kombolcha, Ethiopia.

2.2. Plant materials and experimental procedures

Sixteen bread wheat genotypes, comprising standard checks and farmers' varieties, were selected for the experimentation (Table 2). Among the tested bread wheat genotypes, seeds of twelve new genotypes and two standard checks (Danda'a and Kakaba) were obtained from Kulumsa Agricultural Research Center, while one standard check (Sorra) and the farmers' variety were sourced from Sirinka Agricultural Research Center. The experimental layout followed a Randomized Complete Block (RCB) design, organized into three replications. Each plot consisted of six rows, spaced 20 cm apart and 2.5 meters in length. The harvestable plot size was set at 2 square meters (4 rows of 2.5 meters in length) for data measurement purposes.

Table 2
Bread wheat genotypes included in the experiment

Code	Genotypes name
G1	ETBW 8477
G2	ETBW 8469
G3	BECARD/FRNCLN
G4	ETBW 6753 (CROC_1/AE.SQUARROSA (224) //OPATA/4/TC14/2*HTG//DUCULA/3/PRINIA)
G5	ETBW 6768
G6	ETBW 6761
G7	KACHU#1/4/CROC_1/AE.SQUARROSA(205)//BORL95/3/2*MILAN/5/KACHU
G8	ETBW 7081
G9	ETBW 8472
G10	ETBW 8303
G11	ETBW 8263
G12	ETBW 8268
G13	Kakaba (standard check)
G14	Sorra (standard check)
G15	Farmers' variety
G16	Danda'a (standard check)

2.3. Field Management

The experimental plots underwent thorough preparation, involving three plowings before sowing. Sowing was timed in accordance with rainfall onset and soil moisture availability, occurring during the initial and second weeks of July in both years. Each location utilized a seed rate of 125 kg ha-1. Uniform application of fertilizer, including Diammonium phosphate (DAP) and Urea at rates of 69/46 kg ha^{-1}, was implemented across all experimental plots during each cropping season. Half of the recommended nitrogen fertilizer was applied at planting, and the remaining half at tillering. All prescribed phosphorus fertilizer was applied during planting. Agronomic practices adhered to location-specific recommendations. Hand weeding and removal of off-types were carried out as needed, varying by weed and off-type intensities in each location. Manual harvesting occurred when 90% of plants reached physiological maturity, covering the designated net plot area for each experimental plot.

2.4. Phenotyping

Phenotyping involved the examination of seven quantitative traits associated with yield, yield components, and phenology. These traits were assessed from the central four rows of each experimental plot, excluding the two outermost rows. The studied agronomic and phenological traits encompassed days to heading (HDT) and maturity (MDT), number of kernels per spike (NKPS), plant height (PHT), above-ground biomass yield (BYLD), grain yield (GYLD), and 1000 kernels weight (TKW). Additionally, data on wheat diseases, including yellow rust, stem rust, leaf rust, Septoria, and wheat grain quality traits such as protein content, wet gluten, Zeleny value, and starch content, were investigated. Data collection varied, with certain aspects gathered on a plot basis: HDT, MDT, BYLD, GYLD, TKW, and grain quality traits. Conversely, for data collected on a plant basis, five plants per plot were randomly selected for PHT, KPS, and wheat diseases (rusts and Septoria).

GYLD and TKW data were assessed in the laboratory using an analytical balance, subsequently adjusted to the standard moisture content of cereal crops (12.5%) through a specific formula: Adjusted X = Actual X measure × [(100%-Actual moisture content %)/(100%-standard moisture content %)], where X represents either grain yield or thousand kernels weight.

Grain quality parameters were analyzed at the Amhara Agricultural Research Institute (ARARI) lab utilizing the InfratecTM 1241 grain analyzer model employing Near-Infrared Reflectance Spectroscopy (NIRS). The grain quality data were standardized to the standard moisture at a dry base (12%).

Wheat disease severity and reactions were evaluated through visual observations following the modified Cobb scale procedures [7)]. Severity was quantified in percentage, while disease reactions, depicting the genotype's response, were categorized as follows at the field level: no infection (0), resistant (R), moderately resistant (MR), moderately susceptible (MS), and susceptible (S). The coefficient of infection (CI) for rust was calculated by multiplying Disease Severity by specific constant values (CI = Disease Severity * Constant value). These assigned constants (R, 0.2; MR, 0.4; MS, 0.8; and S, 1) were originally defined by Peterson et al.[7].

Assessment of Septoria disease in wheat utilized a double-digit 00–99 scale [8]. The first digit (D1) indicated the relative height of disease occurrence using the Saari and Prescott 0–9 scale, while the second digit 0–9 (D2) represented disease severity (necrotic leaf area) on plants. For each score, the percentage of Septoria Disease Severity (SDS) was computed using the formula established by Sharma and Duveiller [8].

$$SDS = \left[\left(\frac{D1}{9}\right)\left(\frac{D2}{9}\right]\right. * 100$$

2.5. Statistical analysis

The statistical analysis encompassed the measurement of various variables for each genotype, undergoing an analysis of variance (ANOVA) using Genstat 18th edition. To ensure the validity of the combined ANOVA and homogeneity of error variance across environments for the measured traits, Bartlett's chi-square test was employed [9].

For grain yield and related traits, a combined ANOVA was performed to assess the influences of genotype (G), environment (E), and their interaction (GE). The statistical model used for ANOVA was as follows:

$$Y_{ijk} = \mu + G_i + E_j + GE_{ij} + B_{k(j)} + \epsilon_{ijk}$$

Where, Y_{ijk} = observed value of genotype i in block k of environment (location*year) j, μ = grand mean, G_i = effect of genotype i, E_j=effect of environment j, GE_{ij} = the interaction effect of genotype i with environment j, $B_{k(j)}$ = the effect of block k in environment j, ε_{ijk} = error (residual) effect of genotype i in block k of environment j.

Following ANOVA, Duncan's Multiple Range Test (DMRT) was employed for the mean separation of measured agronomic and quality traits among tested genotypes. Subsequently, stability analysis was conducted to examine the genotypic stability across environments for grain yield. Utilizing R software, GGE (genotypic main effect plus genotype-by-environment interaction) biplot analysis was performed, providing a graphical representation aiding in the visualization of genotype performance and stability across diverse environments.

3. Results

3.2. Analysis of variance (ANOVA) for wheat traits across environments

The ANOVA across ten environments for wheat traits (HDT, MDT, TKW, PHT, NKPS, BMYLD, and GYLD) showed significant variations ($p < 0.05$) among genotypes (G), environments (E), and their interactions (GE). This highlights diverse environmental exposure for tested genotypes, revealing significant genotypic variability, particularly in GYLD and other yield-related traits in wheat (Table 3). The high values of the coefficient of determination (R2) recorded for each trait suggested that the model effectively explained most of the variations (HDT = 0.97, MDT = 0.99, PHT = 0.89, NKPS = 0.81, BMYLD = 0.86, TKW = 0.85, GYLD = 0.85), affirming the model's goodness of fit (Table 3). The total sum of squares was segregated into three components (G, E, and GE interactions) to assess the contributions of genotypes, environments, and their interaction with the observed variations (Table 3). Across all measured traits (HDT, MDT, PHT, NKPS, BMYLD, TKW, and GYLD), E accounted for the largest source of variation (45-96.7%), followed by G and GEI, respectively (Table 3). Specifically, genotype by environment interactions (GEI) explained 8.5% for DHT, 1.5% for DMT, 14.5% for PHT, 27% for NKPS, 19.7% for BMYLD, 33.2% for TKW, and 20.2% for GYLD. Notably, for grain yield, the most critical economic trait,

environment (E), and GEI collectively accounted for the largest portion of the total sum of squares (91%), underscoring the substantial impact of environment and interaction effects in evaluating bread wheat genotypes, particularly for grain yield.

Table 3
ANOVA for grain yield and yield component traits across ten environments

Sources of variation	Degree of freedom	Mean square variations						
		HDT	MDT	PHT	NKPS	BMYLD	TKW	GYLD
Blocks /E	E(R-1) = 20	ns	14.4**	99**	69.6*	6311820**	9.6*	1077683**
Genotype (G)	G-1 = 15	271**	290**	929**	460.3**	9752057**	142**	2284716**
Environment(E)	E-1 = 9	2952**	25376**	2590**	2546**	191874918**	492**	30163952**
G*E	(G-1)(E-1) = 135	21**	26**	46.7**	81.5**	3408239**	24.1**	572670**
Pooled error	E(R-1)(G-1) = 300	3.64	3.2	19	33.5	1332914	5.7	203342
R^2		0.97	0.99	0.89	0.81	0.86	0.85	0.85
% of total variance	E	79	96.7	53.5	56	74	45	71
	G	12	1.8	32	17	6	22	9
	GEI	9	1.5	14.5	27	20	33	20

*, ** significant at 0.05 and 0.01 probability levels, respectively. ns, non−significant, SS (Sum square), R(Blocks or replications), R2 (coefficients of determination), HDT(days to heading), MDT (days to maturity), PHT(plant height; cm), NKPS(number of kernels per spike), BMYLD(biomass yield; kg ha−1), TKW (Thousand kernels weight; g) and GYLD(grain yield; kg ha−1), SS(sum−square).

3.3. Mean performances of wheat genotypes across ten environments

Table 4 illustrates the mean performances of wheat genotypes concerning six quantitative traits (days to heading, days to maturity, plant height, number of kernels per spike, biomass yield, and thousand kernels weight) across ten different environments.

3.3.1. Days to heading (HDT)

The days to heading ranged between 66 to 76 days among different wheat genotypes, with an average of 70 days (Table 4). Three genotypes, namely Kakaba, KACHU¹1/4/ CROC_1/AE.SQUARROSA(205)//BORL95/3/2*MILAN/5KACHU, and ETBW 8303, exhibited earlier heading at 66 days, while ETBW 6768 and Danda'a headed later at 76 and 74 days, respectively.

3.3.2. Days to maturity (MDT)

Days to maturity ranged from 119 to 132 days among the wheat genotypes, with a mean of 123 days (Table 4). Notably, KACHU¹1/4/ and Kakaba were the early-maturing genotypes at 119 days, while ETBW 6768 exhibited delayed maturity at 132 days.

3.3.3. Plant height (PHT)

The plant height of the wheat genotypes varied from 74 to 96 cm, with an average of 78 cm (Table 4). The tallest plant was observed in the farmers' variety at 96 cm, followed by ETBW 6753 and ETBW 8469 at 82 cm. Conversely, the shortest plants (74 cm) were noted in BECARD/FRNCLN, KACHU11/4/CROC_1/AE.SQUARROSA(205)BORL95/3/2*MILAN/5KACHU, ETBW 8263, and Kakaba genotypes.

3.3.4. Above-ground biomass (BMYLD)

Measured above-ground biomass ranged from 9488 to 7514 Kg ha-1, averaging at 8629 Kg ha-1 (Table 4). Some genotypes, including ETBW 8263, ETBW 6753, and the farmers' variety, exhibited the highest biomass yields, while ETBW 8477 displayed the lowest biomass yield at 7514 Kg ha-1.

3.3.5. Number of Kernels per Spike (NKPS)

The number of kernels per spike (NKPS) ranged from 34 to 50, with an average of 42 across the tested wheat genotypes (Table 4). BECARD/FRNCLN and the farmers' variety had the highest and lowest NKPS at 50 and 34, respectively.

3.3.6. Thousand kernels weight (TKW)

The majority (94%) of the tested wheat genotypes displayed a TKW above 40 grams, averaging 42 grams (Table 4). Genotypes like ETBW 6761, KACHU11/4/CROC_1/AE.SQUARROSA(205)BORL95/3/2*MILAN/5KACHU, and Danda'a had the highest mean TKW at 45 and 44 grams, while ETBW 7081 showed the smallest mean TKW at 37 grams.

Table 4
Mean values of phenological, yield, and some yield components across ten testing environments

Code	Genotypic mean						Code	Environmental mean					
	HDT	MDT	PLH	NKPS	BMYLD	TKW		HDT	MDT	PLH	NKPS	BMYLD	TKW
G1	68^{c}	122^{d}	78^{cd}	39^{f}	7514^{h}	41^{ef}	E1	67^{c}	101^{b}	71^{e}	38^{e}	7281^{e}	40^{d}
G2	68^{c}	122^{d}	82^{b}	39^{f}	8658^{cd}	41^{ef}	E2	61^{b}	106^{c}	81^{c}	40^{d}	9521^{c}	41^{d}
G3	70^{d}	122^{d}	74^{f}	50^{a}	8583^{cd}	40^{g}	E3	77^{f}	131^{d}	83^{c}	51^{b}	5958^{g}	39^{e}
G4	72^{f}	124^{e}	82^{b}	43^{cd}	9441^{ab}	43^{cd}	E4	72^{d}	136^{e}	86^{b}	54^{a}	12531^{a}	40^{d}
G5	76^{h}	132^{g}	78^{cd}	45^{bc}	8049^{ef}	40^{g}	E5	74^{e}	146^{h}	70^{ef}	35^{f}	7152^{ef}	49^{a}
G6	71^{e}	124^{e}	77^{de}	48^{ab}	9170^{ab}	45^{a}	E6	74^{e}	140^{f}	71^{e}	32^{g}	6667^{f}	46^{b}
G7	66^{a}	119^{a}	74^{f}	42^{cd}	8533^{cd}	45^{a}	E7	78^{g}	143^{g}	88^{a}	43^{c}	8531^{d}	42^{c}
G8	67^{b}	121^{cd}	75^{ef}	43^{cd}	8033^{fg}	37^{h}	E8	77^{f}	145^{h}	85^{b}	51^{b}	8615^{d}	40^{d}
G9	69^{d}	123^{e}	75^{ef}	42^{cd}	8750^{ab}	41^{ef}	E9	60^{ab}	91^{a}	69^{f}	42^{cd}	10760^{b}	40^{d}
G10	66^{a}	120^{bc}	75^{ef}	42^{cd}	8371^{de}	42^{de}	E10	57^{a}	91^{a}	78^{d}	40^{d}	9275^{c}	41^{d}
G11	69^{d}	123^{e}	74^{f}	43^{cd}	9488^{a}	44^{bc}							
G12	72^{f}	123^{e}	79^{cd}	42^{cd}	8793^{ab}	43^{cd}							
G13	66^{a}	119^{a}	74^{f}	39^{f}	7798^{gh}	41^{ef}							
G14	69^{d}	123^{e}	80^{bc}	41^{de}	8735^{bc}	43^{cd}							
G15	73^{f}	126^{f}	96^{a}	34^{g}	9200^{ab}	40^{g}							
G16	74^{g}	126^{f}	79^{bc}	47^{ab}	8950^{ab}	44^{bc}							
Mean	70	123	78	42	8629	42							
CV(%)	2.7	1.5	5.6	13.6	13.4	5.7							

HDT(days to heading), MDT (days to maturity), PHT(plant height; cm), NKPS(number of kernels per spike), BMYLD(biomass yield; kg ha−1), TKW (Thousand kernels weight; g), Environmental code (E1 to E10) and genotypic code (G1 to G16) located at Tables 1 and 2 respectively

3.3.7. Mean performances of grain yield (GYLD)

The mean grain yield performance of the tested bread wheat genotypes across ten different environments is summarized in Table 5. The yields varied significantly across these environments, ranging from 2197 Kg ha-1 (E1) to 4812 Kg ha-1 (E4) (Table 5). The overall mean grain yield of the tested genotypes across all environments ranged from 2414 Kg ha-1 (G1) to 3298 Kg ha-1 (G6). Notably, there was no significant difference in the mean grain yields of six genotypes: ETBW 6753 (G4), ETBW 6761 (G6),

KACHU11/4/CROC_1/AE.SQUARROSA(205)BORL95/3/2*MILAN/5KACHU (G7), ETBW 8263 (G11), ETBW 8268 (G12), and Danda'a(G16).

Specific genotypes exhibited adaptability and high performance in particular environments (Table 5). For instance, at E1 (Dehana 2016), Kakaba (G13), an early maturing variety, displayed the best performance. In E2 (Dehana 2017), most tested genotypes, except G16 (Danda'a) and G2 (ETBW 8469), performed well. Similarly, in E9 (Woleh2016) and E10 (Woleh2017), four genotypes (G4, G12, G2, and G3) demonstrated the highest grain yield, indicating their suitability for those specific environments. However, due to seasonal variability at Dehana and Woleh, singling out a single genotype per environment was challenging.

At E3 (Geregera 2016), relatively high grain yields were recorded from G6 (ETBW 6761), G12 (ETBW 8268), and G14 (Sorra). In E4 (Geregera 2017), nearly all tested genotypes performed exceptionally well, with a maximum mean grain yield of 4812 Kg ha-1 observed, ranging from 3809 Kg ha-1 to 6143 Kg ha-1 across genotypes. Notably, several genotypes, including G12, G10, G16, G6, G2, G7, and G4, displayed high performance at E4 (Geregera 2017).

In two environments (Jamma 2016; E5 and Jamma 2017; E6), ETBW 6753 (G4), Danda'a (G16), and ETBW 8263 (G11) exhibited the highest mean grain yields of 3585, 3484, and 3325 Kg ha-1, respectively. Moreover, at E1 (Kone 2016) and E2 (Kone 2017), G4 (ETBW 6753) recorded the highest average grain yield of 3983 Kg ha-1, followed by G6 (ETBW 6761), G14 (Sorra), G10 (ETBW 8303), G7 (KACHU¹1/4/CROC_1/AE.SQUARROSA(205)//BORL95/3/2*MILAN/5KACHU), and G16 (Danda'a) with performances ranging from 3610 to 3824 Kg ha-1.

Table 5

Mean grain yield (kg ha^{-1}) across ten environments

Genotype	Environments										Mean
	E1	E2	E3	E4	E5	E6	E7	E8	E9	E10	
G1	1752^{e}	3097^{ab}	1506^{ef}	4059^{d-f}	2385^{d}	2086^{ef}	2230^{ef}	2909^{g}	1865de	2252^{ef}	2414^{f}
G2	2095^{d}	2664^{bc}	2573^{b-d}	5105^{b-d}	2693^{cd}	2105^{ef}	2861^{bc}	3267^{f}	2805^{ab}	2827^{ab}	2900^{cd}
G3	2417^{c}	3310^{ab}	2488^{b-d}	4511^{c-f}	2451^{cd}	2421de	2868^{bc}	3419^{ef}	2903^{a}	2677^{ab}	2946^{cd}
G4	1607^{ef}	3187^{ab}	2376^{b-d}	4987^{b-e}	3960^{a}	3209^{ab}	3630^{ab}	4336^{a}	3008^{a}	2340de	3264^{ab}
G5	1389^{f}	3535^{a}	1160^{f}	3809^{f}	2983^{b-d}	2685^{cd}	2032^{f}	3568de	1968^{c-e}	1704^{h}	2483^{f}
G6	2375^{c}	3563^{a}	3251^{a}	5193^{a-c}	3442^{a-c}	2495^{cd}	3692^{a}	3956^{bc}	2445^{a-d}	2563^{bc}	3298^{a}
G7	2537^{bc}	3627^{a}	2051de	5039^{b-e}	3081^{a-d}	2872^{bc}	3177^{ab}	4131^{ab}	2083^{b-e}	2600^{bc}	3120^{a-c}
G8	2698^{b}	2973^{ab}	2590^{b-d}	3965^{ef}	2610^{cd}	2149^{ef}	2612de	2724^{g}	1853de	1965^{fg}	2614^{ef}
G9	2408^{c}	2493^{cd}	1945de	4337^{c-f}	2361^{d}	3170^{ab}	2365^{ef}	3290^{ef}	1687^{e}	2275^{ef}	2633^{ef}
G10	1787^{e}	3373^{ab}	2126^{c-e}	5740^{ab}	3754^{ab}	2062^{ef}	3389^{ab}	4013^{bc}	2068^{b-e}	1980^{fg}	3029^{b-d}
G11	2317^{cd}	3608^{a}	2544^{b-d}	4776^{b-f}	3132^{a-d}	3517^{ab}	3465^{ab}	3478^{ef}	2503^{a-d}	3062^{a}	3240^{ab}
G12	2060^{d}	3083^{ab}	2824^{ab}	6143^{a}	2748^{cd}	2391^{ef}	3205^{ab}	3348^{ef}	2702^{a-c}	2915^{ab}	3142^{a-c}
G13	3337^{a}	3638^{a}	2024de	4823^{b-f}	2347^{d}	1927^{f}	2856^{bc}	3794^{cd}	3087^{a}	2440^{cd}	3027^{b-d}
G14	1387^{f}	3298^{ab}	2395^{b-d}	4792^{b-f}	2759^{cd}	2356^{ef}	3523^{ab}	3984^{bc}	3033^{a}	2773^{ab}	3030^{b-d}
G15	2400^{c}	2882^{ab}	2108de	4568^{c-f}	2429^{d}	2391de	2789^{cd}	3598de	2458^{a-d}	2545^{bc}	2817de
G16	2583^{bc}	2278^{d}	2778^{a-c}	5139^{a-d}	3320^{a-d}	3647^{a}	3151^{ab}	4068^{ab}	1985^{c-e}	1878^{gh}	3083^{a-c}
Mean	2197	3163	2296	4812	2904	2592.7	2990	3617.7	2403	2425	2940
Genotype (5%)	**	*	**	**	**	**	**	**	**	**	**
CV (%)	6.7	13.7	15	11.6	17.6	16	13.4	4.6	16.4	9.6	15.3

E1(Dehana2016), E2(Dehana2017), E3(Geregera2016), E4(Geregera2017), E5(Jamma2016), E6(Jamma2017), E7(Kon2016), E8(Kon2017), E9(Woleh2016), E10(Woleh2017).

3.4. Genotypic stability analysis for grain yield

3.4.1. Average-environment coordination (AEC) view

Figure 2 depicts the GGE biplot analysis using the tester-centered (G + GE) table, providing an AEC view. The AEC abscissa represented the higher mean yield across environments, while the AEC ordinate denoted increased genotype-environment (GE) interaction and stability. Genotypes were arranged along the AEC axis. G6 exhibited the highest mean yield, followed by G4 and G12. Conversely, G5 displayed the lowest mean yield. Stability analysis revealed that G13 was unstable due to its longest vector, while G6 was considered stable due to its shortest vector length.

3.4.2. Which-won-where pattern (polygon view)

Figure 3 showcases the polygon view constructed based on the tester-centered (G + GE) system without scaling and preserved genotype metric. Vertex genotypes, located farthest from the biplot origin, were identified as the most responsive genotypes. Lines

perpendicular to the sides of the polygon divided the biplot into sectors, determining winning genotypes for each sector. Genotypes G4, G6, G12, G13, G1, and G5 were positioned at the vertices of the polygon sectors, signifying their high responsiveness across specific environments.

3.5. Bread-making quality traits

The evaluation of bread wheat genotypes included vital bread-making quality traits—Protein Content (PC), Starch Content (SC), wet gluten (WG), and Zeleny Value (ZV)—in addition to grain yield. This comprehensive assessment aimed to encompass essential traits crucial for breeders and producers. Significant genotype-specific variations were detected across different environments for the four quality traits assessed (Table 6). These findings emphasized the influence of genotype and environmental interactions on these key traits, showcasing their diverse responsiveness to varying environmental conditions.

3.5.1. Protein content (PC)

Variations in protein content (PC) among tested genotypes across diverse environments were statistically significant. All genotypes, except G16 (PC; 9.9%), exhibited PC levels within the acceptable range (> 10%). The genotype G1 displayed the highest PC content, recording 11.5%.

3.5.2. Starch content (SC)

Significant variations in starch content were observed among wheat genotypes, ranging from 62% (G3 and G12) to 65.2% (G5). The general mean performance for starch content across genotypes averaged 63.2%.

3.5.3. Wet gluten (WG) and Zeleny value (ZV)

Wet Gluten Content (WG) values ranged from the smallest recorded value of 21.3% (G16) to the highest values of 26.7% (G9 and G1). G1 showcased the highest WG at 36.5%, whereas G15 (28.7%), G16 (28.8%), and G14 (28.9%) recorded the lowest ZV, indicating substantial variability among genotypes regarding whole grain formation.

Table 6
Genotypic performance in quality traits and disease reactions

Genotype	Quality traits				Diseases reactions						
	PC(%)	SC(%)	GC(%)	ZV(%)	Geregera		Kon		Jamma		
					YR	STB	YR	STB	YR	SR	LR
G1	11.5^{a}	62.6^{fg}	26.3^{ab}	36.5^{a}	5R	74	tR	65	trR	0	0
G2	10.9^{b-d}	63.7^{cd}	25.0^{a-d}	33.8^{b}	5R	64	5R	35	0	0	0
G3	11.0^{a-c}	62.0^{h}	23.9^{c-e}	33.1^{b}	tR	55	0	24	0	0	0
G4	10.5^{cd}	62.7^{fg}	22.9^{ef}	31.2^{bc}	0	53	5R	32	10MR	tR	20MS
G5	10.3^{de}	65.2^{a}	25.6^{a-c}	31.2^{bc}	5R	00	5MR	22	30MS	20S	30MS
G6	10.4^{cd}	64.0^{bc}	25.0^{a-d}	32.1^{bc}	0	55	0	65	10MR	0	0
G7	10.8^{b-d}	63.6^{cd}	25.3^{a-c}	33.5^{b}	tR	63	0	33	tR	tR	tR
G8	10.7^{cd}	63.4^{d}	24.9^{a-e}	31.6^{bc}	5MR	65	60MS	45	20MR	0	0
G9	11.4^{ab}	63.3^{de}	26.7^{a}	33.7^{b}	5R	65	tR	23	tR	0	0
G10	10.4^{cd}	62.3^{gh}	23.1^{d-f}	31.8^{bc}	0	34	5MS	53	tR	0	0
G11	11.0^{a-c}	63.5^{d}	26.0^{ab}	33.1^{b}	0	22	0	23	0	0	0
G12	10.8^{b-d}	62.0^{h}	23.2^{d-f}	29.7^{cd}	5R	54	tR	43	tR	0	0
G13	10.7^{cd}	62.6^{fg}	23.1^{d-f}	32.8^{b}	tR	63	5MS	54	5R	tR	40MR
G14	10.9^{a-d}	62.4^{gh}	24.6^{b-e}	28.9^{de}	5MS	54	40S	33	5MR	5MS	20MS
G15	10.9^{a-d}	64.2^{b}	24.7^{a-e}	28.7^{e}	5MR	44	70S	65	30S	10MS	30S
G16	9.9^{e}	62.9^{ef}	21.3^{f}	28.8^{e}	tR	43	10MR	33	10MR	5MS	20MS
Mean	10.8	63.2	24.5	31.9							
CV(%)	6.1	0.8	8.7	9.3							

PC (protein content), SC (starch content), GC (Gluten content), ZV (Zeleny value), YR (Yellow rust), STB (Septoria Bloch), SR (Stem rust), LR (Leaf rust), Genotype code (G1 to G16) presented in Table 2

3.6. Genetic responses to wheat diseases

3.6.1. Yellow rust

Yellow rust incidences were observed at three locations - Geregera, Kon, and Jamma - with respective incidence rates of 75%, 75%, and 81% (Table 6). At Geregera, immune responses (no visible infection) were noted in plants of ETBW 6753, ETBW 6761, ETBW 8303, and ETBW 8263. Most of the other tested wheat genotypes displayed low severities of yellow rust with a resistant response. In Kon, four genotypes (BCARD/FRNCLN, ETBW 6761, KACHU#1/4, and ETBW 8263) showed no incidence of yellow rust. At Jamma, zero-level infections of yellow rust were observed on three genotypes (ETBW 8469, BCARD/FRNCLN, and ETBW 8263). The farmer's variety and ETBW 6768 genotypes showed susceptibility to yellow rust (30% incidence) and moderately susceptible responses. However, the remaining genotypes exhibited lower severity levels (5–10%) with resistant to moderately resistant responses.

3.6.2. Stem rust

Stem rust incidences were solely observed at the Jamma location, affecting seven genotypes (Table 6). ETBW 6768 displayed a high severity level of stem rust (20%) with a susceptible response. Conversely, lower severity levels were observed in three check genotypes: Sorra (5%), Danda'a (5%), and the Farmers' variety (10%), indicating moderately susceptible responses. Kakaba, ETBW 6753, and KACHU#1/4/CROC_1/AE.SQUARROSA(205)//BORL95/3/2*MILAN/5/KACHU exhibited low stem rust infection levels (< 5%) with a resistant response (Table 6).

3.6.3. Leaf rust

Leaf rust incidence varied across locations, with Geregera and Kon showing no occurrences while Jamma exhibited leaf rust in nearly 44% of the tested genotypes (Table 6). The severity of leaf rust on the Farmers' variety and ETBW 6768 was high (30%) with susceptible and moderately susceptible reactions, respectively. Meanwhile, Sorra, Danda'a, and ETBW 6753 displayed a moderately susceptible response with moderate severity (20%). Kakaba exhibited a moderately resistant reaction but had high severity (40%) concerning leaf rust. The remaining genotypes showed no signs of leaf rust infection.

3.6.4. Septoria tritici blotch (STB)

The incidence of septoria tritici blotch (STB) at Kon and Geregera was recorded as 100% and 93.8%, respectively, while Jamma showed zero incidences (Table 6). This indicated the substantial prevalence and significance of STB as a disease at Kon and Geregera. The coefficient of infection (CI) of STB for different genotypes (Fig. 4) revealed variable interaction effects with the pathogen, ranging from 2% to 36%. The results clustered genotypes into categories: high (> 25%; G1, G6, G8, and G15), intermediate (between 25% and 20%; G12, G2, G13, and G9), and low (less than 20%; G3, G14, G10, G7, G4, G11, G5).

4. Discussion

4.2. ANOVA and mean performance of wheat traits across different environments

The analysis of variance (ANOVA) conducted across various environments revealed significant differences among genotypes (G), environments (E), and their interactions (GE) for multiple wheat traits [10–13]. This underscores the exposure of genotypes to diverse environmental conditions, highlighting substantial genetic variability, particularly in traits associated with grain yield (GYLD) and other yield-related attributes. High coefficients of determination (R2) for each trait indicate the model effectively captured and explained most observed variations, affirming its suitability. The breakdown of the total sum of squares into G, E, and GE interactions offered insights into their respective contributions to observed variations. Notably, environmental factors (E) significantly contributed to variations across all traits, emphasizing their substantial influence on trait expression. Genotype-by-environment interactions (GEI) notably affected various traits, especially grain yield, emphasizing the intricate relationship between genotypes and different environmental conditions in determining yield outcomes. The predominance of environmental influence, particularly in grain yield, aligns with previous research emphasizing the dominance of environmental factors over genotype and their interactions in wheat traits [10–13].

Differences in days to heading (HDT) among wheat genotypes highlight genetic diversity, leading to varied maturity periods. This corresponds with studies emphasizing genetic influence on wheat heading dates [4]. Early-heading genotypes offer quicker maturation, potentially advantageous in specific environments, while late-heading genotypes might extend growth periods [15]. Similarly, variations in days to maturity (MDT) among genotypes are crucial for adapting wheat cultivars to specific environments, as noted in previous research [14]. Early-maturing genotypes may suit shorter growing seasons, while late-maturing types could thrive in longer periods [15].

Significant variation in plant height among wheat genotypes suggests diverse growth habits influencing crop performance across environments, echoing the importance highlighted in previous studies [16]. Additionally, substantial diversity in above-ground biomass (BMYLD) among wheat genotypes is vital in understanding productivity potential, aligning with the significance of biomass yield in crop performance and potential (16). Variability in the number of kernels per spike (NKPS) among wheat genotypes indicates potential grain yield, crucial in improving wheat productivity [14].

Moreover, diverse thousand kernel weight (TKW) among genotypes is essential for potential flour extraction and yield estimation in wheat, impacting overall yield potential [4, 16].

These discussions collectively underscore the importance of genetic variability in various wheat traits and their implications for crop adaptability, productivity, and quality. Studies by Muhsin et al. [14], Baril (15), and(16) offer valuable insights into the genetic influences and agronomic importance of these traits in wheat breeding and improvement strategies.

The significant variability in mean grain yield among different environments emphasizes the influence of genotype-environment interaction on crop performance [17]. Specific genotypes demonstrated adaptability and superior performance in certain environments, highlighting the importance of selecting appropriate genotypes for specific environmental conditions to achieve optimal yields.

Several genotypes consistently emerged as top performers in certain environments. For example, in highly favorable conditions (E4 - Geregera 2017), genotypes like ETBW 8268 (G12), ETBW 8303 (G10), Danda'a (G16), ETBW 6761 (G6), ETBW 8469 (G2), KACHU¹1/4/CROC_1/AE.SQUARROSA(205)//BORL95/3/2*MILAN/5KACHU (G7), and ETBW 6753 (G4) exhibited exceptional grain yield performances.

Similarly, environments like E3 (Geregera 2016) highlighted superior performance of genotypes such as ETBW 6761 (G6), ETBW 8268 (G12), and Sorra (G14). In E1 (Kone 2016) and E2 (Kone 2017), ETBW 6753 (G4) consistently displayed the highest mean grain yield, indicating its adaptability across different conditions.

Challenges arose in selecting a single superior genotype per environment due to diverse seasonal conditions observed in Dehana and Woleh, as noted in prior research [17]. However, certain genotypes like Kakaba (G13) in E1 (Dehana 2016) and Sorra (G14) in E10 (Woleh 2017) demonstrated adaptability and remained among the best-performing genotypes in their respective environments.

These findings stress the importance of identifying top-performing genotypes for specific environments and facilitating targeted breeding programs and cultivation practices. Understanding genotype-environment interactions remains crucial in maximizing grain yield and ensuring sustainable crop production strategies.

4.3. Genotypic stability analysis for grain yield

The AEC view from Fig. 2 provided valuable insights into stability and mean yield performance across environments. G6 emerged as the most stable genotype with the highest mean yield, followed by G4 and G12. Conversely, G13 exhibited instability, indicating its susceptibility to varying environments. This observation aligns with prior studies emphasizing stability's significance, especially when associated with high-yielding genotypes [18].

The polygon view (Fig. 3) elucidated genotype responsiveness and environmental associations. Vertex genotypes, including G4, G6, G12, G13, G1, and G5, were identified as the most responsive across different sectors of the polygon. These genotypes showcased adaptability in specific environmental conditions, allowing for strategic breeding or selection decisions.

The genotype-environment associations inferred from the analyses presented in Figs. 2 and 3 hold practical implications for agriculture. For instance, the identification of Kakaba (G13) as the winning genotype in E1, known for terminal drought issues, suggests its suitability for such environments. Similar studies across varied crops, such as Pinus Radiata, maize, wheat-barley disomic lines, bread wheat, and barley by different researchers, underscore the importance of understanding genotype-environment interactions for crop improvement strategies [12, 19–22]. In conclusion, Figs. 2 and 3 depict the results of the GGE biplot analysis, offering a comprehensive understanding of complex genotype-environment interactions. They facilitate the identification of stable, high-yielding genotypes and enable tailored recommendations for specific agroecological zones, thus enhancing agricultural productivity and sustainability [23–25].

4.4. Bread-making quality traits

The evaluation expanded beyond grain yield, emphasizing the critical role of bread-making quality traits in bread wheat varieties. These quality traits are pivotal for consumer acceptance, as varieties lacking in these attributes may face rejection in the market [26].

The analysis highlighted the importance of assessing bread wheat genotypes for PC, SC, WG, and ZV. The significant variability observed among genotypes across diverse environments, as outlined in Table 4, elucidates the genotype-environment interaction's impact on these crucial quality traits.

Understanding these variations is imperative for breeders and producers. It facilitates the selection and development of wheat varieties that not only exhibit high grain yield but also possess superior bread-making qualities. Such varieties are more likely to meet consumer preferences, ensuring market acceptance and commercial success in the bread-making industry.

The observed significant variations in protein content (PC), starch content, wet gluten (WG), and Zeleny Value (ZV) among the tested wheat genotypes across different environments underline the substantial impact of both genetic variability and environmental factors on these quality traits. Notably, with the exception of G16 falling below the acceptable range for PC at 9.9%, the majority of genotypes exhibited PC levels meeting or surpassing the recommended threshold of > 10%. G1 particularly stood out with the highest PC content at 11.5%, suggesting its potential as a genotype with superior protein content compared to others [26].

Similarly, the significant variations in starch content, ranging from 62% to 65.2% among different genotypes, underscore the genetic diversity affecting starch accumulation. The observed general mean performance of starch content (63.2%) across genotypes aligns with prior research findings, indicating a consistent trend in starch composition among the evaluated wheat genotypes [27].

In terms of Wet Gluten content (WG) and Zeleny Value (ZV), the range of values among the genotypes implies substantial genetic disparities influencing whole grain formation and gluten strength. The considerable range observed in WG, from 21.3% to 26.7%, suggests varying genetic influences on nutritional aspects and end-use qualities of wheat. Notably, G1 demonstrated exceptionally high WG at 36.5%, indicating its potential as a desirable genotype for the production of whole grain-based products. Moreover, the differences in ZV scores among genotypes highlight variations in gluten strength and protein quality, with G1 exhibiting the highest ZV among the evaluated genotypes, potentially indicating superior gluten strength compared to G15, G16, and G14 [26–28].

Overall, these findings underscore the significance of genetic diversity in influencing quality traits in wheat. The observed variability in protein content, starch content, whole grain formation, and Zeleny Value among different genotypes emphasizes the importance of selecting and breeding wheat varieties with desired traits tailored to specific end-use applications in the agricultural and food industries. Understanding the genetic basis behind these variations can aid in developing improved wheat cultivars with enhanced nutritional value and better suitability for various industries.

4.5. Yellow Rust, Stem Rust, Leaf Rust, and Septoria Tritici Blotch (STB)

Variations in yellow rust incidence across locations indicate distinct genotypic responses to the disease. Certain genotypes displaying immunity at Geregera and Jamma suggest promising resistance potential. Conversely, susceptibility in farmers' varieties and ETBW 6768 underscores the need for enhanced resistance in these genotypes. Lower severity levels in most genotypes imply favorable resistance or tolerance against yellow rust, advocating for the selection of resistant genotypes for cultivation to mitigate disease impact, aligning with previous studies [29].

The occurrence of stem rust solely at Jamma suggests localized prevalence, highlighting environmental favorability for the disease. ETBW 6768's high-severity signals susceptibility, urging enhanced resistance strategies. Moderate susceptibility in Sorra, Danda'a, and the Farmers' variety suggests vulnerability with lower severity. Meanwhile, low infection rates and resistant responses in other genotypes like Kakaba, ETBW 6753, and KACHU#1/4/CROC_1/AE.SQUARROSA demonstrates promising resistance, emphasizing the importance of identifying and utilizing inherently resistant genotypes to ensure more resilient wheat cultivation.

The absence of leaf rust at Geregera and Kon suggests less favorable conditions for its development than at Jamma. High susceptibility in the Farmers' variety and ETBW 6768 underscores vulnerability, emphasizing the need for improved resistance. Moderate susceptibility in Sorra, Danda'a, and ETBW 6753 highlights the importance of monitoring and managing leaf rust in these genotypes. The discrepancy in reaction and severity in Kakaba reveals the complexity of host-pathogen interactions. The absence of leaf rust in other genotypes reinforces the significance of inherent resistance for combating this disease in wheat crops.

The high incidence of STB at Kon and Geregera emphasizes its threat to wheat crops. Variable genotypic responses, highlighted by the coefficient of infection (CI), underscore the importance of genotype-specific susceptibility or resistance in managing STB effectively. Categorizing genotypes based on infection levels shows the potential for identifying and utilizing resistant genotypes against STB. The impact of Septoria tritici blotch (STB) on wheat production underscores its substantial economic importance. A 1% reduction in wheat yield has been observed for each 1% increase in disease severity on the flag leaf, highlighting the critical need for effective and sustainable disease management strategies [30]. Research has revealed variations in STB incidence and severity concerning diverse environmental factors, accentuating the necessity for a comprehensive approach to managing it [31]. Integrating

knowledge about resilient genotypes and understanding the factors influencing STB's incidence and severity are crucial for effective disease management strategies. Implementing this understanding in breeding programs and agricultural practices is essential for sustaining wheat productivity amidst STB challenges [30, 31].

5. Conclusions

Throughout diverse environments, the wheat genotype ETBW 6753, or "Netsanet," emerged as a standout choice. Its impressive lineage features CROC_1/AE.SQUARROSA (224) //OPATA/4/TC14/2*HTG//DUCULA/3/PRINIA, equips it with vital traits for thriving in moisture-deficient regions like Kon, Geregera, and Jamma.

Netsanet embodies early maturation, robust disease resistance, high yield potential, and coveted white seed color. Its soft, palatable straw provides an advantage for animal feed. Across varied environments, Netsanet consistently outperformed standard checks Kakaba, Sorra, and Danda'a as well as the farmers' variety, boasting substantial yield advantages of 8.3%, 8%, 6%, and 15%, respectively.

Additionally, it meets stringent bread-making quality standards (10.5% protein content, 22.9% wet gluten, 62.7% starch content, Zeleny value of 31.2%, and 1000 kernels weight of 43g), further enhancing its appeal. In drought-prone areas like Dehana and Woleh, Kakaba's early maturation remains optimal.

Recognized for its exceptional attributes, ETBW 6753, now officially "Netsanet," earned approval from the Ethiopian National Variety Releasing Committee for cultivation in moisture-deficient zones like Kon, Geregera, and Jamma. Its multifaceted advantages position Netsanet as a beacon of promise and a vital asset for sustainable wheat farming in such environments.

Declarations

Authors Contributions

A.M.T. contributed to conceptualization, study design, data curation, data analysis, drafting the manuscript, software use, supervision, and preparation of the full manuscript. A.G.Y, A.G.H., G.Y.F., and T.A.A. equally contributed to data collection, field supervision, and support in data management and preliminary analyses. All authors reviewed and approved the final manuscript.

Funding

This research was supported by the Amhara Agricultural Research Institute (ARARI), Ethiopia, which provided financial support for experimentation and facilitated the preparation of the research fields.

Competing interests

The author(s) declare(s) that they have no competing interests.

Clinical trial number

Not applicable.

Ethics declaration

All plant materials used were cultivated bread wheat genotypes obtained with official permission for research use from the Kulumsa Agricultural Research Center under the Ethiopian national wheat breeding program. The seeds were supplied through formal institutional channels by the National Wheat Research Coordinator. No additional permits or collection licenses were required.

Consent to participate

Not applicable.

Consent for publication

Not applicable.

Data availability

The datasets generated and analyzed during this study are available from the corresponding author upon reasonable request

References

1. Zohary D, Hopf M. Domestication of plants in the Old World. Annuals of Botany. New York: Oxford University Press; 2000. p. 316.
2. Gustafson P, Raskina O, Ma X, Nevo E. Wheat Evolution, Domestication, and Improvement. 2121 State Avenue, Ames, Iowa 50014 – 8300 U, editor. Wheat Science and Trade. First. Willy-Blackwell; 2009. pp. 5–30.
3. Food and Agriculture Organization of the United Nations (FAO). (2021). *The State of Food and Agriculture 2021: Making agrifood systems more resilient to shocks and stresses* (ISBN 978-92-5-134329-6). Rome, Italy: FAO.
4. USDA-GAIN. USDA-GAIN (United States Department of Agriculture-Global Agricultural Information Network). Grain and Feed Annual. Addis Ababa. Ethiopia; 2022.
5. Hailu G. Bread wheat breeding and genetics research in Ethiopia. In: HailuGebre-Mariam, Tanner DG and MH, editors, editor. Wheat research in Ethiopia: A Historical Perspective. IAR/CIMMYT, Addis Ababa, Ethiopia; 1991. pp. 73–93.
6. CSA CSA. Agricultural sample survey report on area and production of major crops. Volume 1. Addis Ababa, Ethiopia; 2021.
7. Peterson RF, Campbell AB, Hannah AE. A diagrammatic scale for estimating rust intensity on leaves and stems of cereals. Can J Res. 1948;26:496–500.
8. Sharma RC, Duveiller E. Advancement toward new spot blotch resistant wheats in South Asia. Crop Sci Soc Am. 2007;47:961–8.
9. Steel RGD, Torrie JH. Principles and procedures of statistics. 2nd edition. New York, America: McGraw-Hil; 1980.
10. Bacha T, Alemerew S, Tadesse Z. Genotype x Environment Interaction and yield stability of bread wheat (Triticum eastivum L.) genotype in Ethiopia using the AMMI analysis. J Biol Agric Healthc. 2015;5(11):129–40.
11. Gurum F, Mohammed H, Alemaw G, Gurmu F, Mohammed H, Alemaw G. Genotype X environment interactions and stability of soybean for grain yield and nutrition quality. Afr Crop Sci J. 2009;17(2):87–99.
12. Jalata Z. GGE-biplot Analysis of Multi-environment Yield Trials of Barley (Hordeium vulgare L.) Genotypes in South eastern Ethiopia Highlands. Int J Plant Breed Genet. 2011;5(1):59–75.
13. Mohammadi R, Armion M, Sadeghzadeh D, Amri A, Nachit M, Mohammadi R, et al. Analysis of Genotype-by-Environment Interaction for Agronomic Traits of Durum Wheat in Iran Analysis of Genotype-by-Environment Interaction for Agronomic Traits of Durum Wheat in Iran. Plant Prod Sci. 2011;14(1):15–21.
14. Muhsin M, Nawaz M, Khan I, Chattha MB, Khan S, Aslam MT, et al. Efficacy of Seed Size to Improve Field Performance of Wheat under Late Sowing Conditions. Pakistan J Agricultural Res. 2021;34(1):247–53.
15. Baril CP. Factor regression for interpreting genotype-environment interaction in bread-wheat trials. Theor Appl Genet. 1992;83:1022–6.
16. Ponce-García N, Ramírez-Wong B, Escalante-Aburto A, Torres-Chávez PI, Serna-Saldivar SO. Grading Factors of Wheat Kernels Based on Their Physical Properties. Wheat Improvement, Management and Utilization, 275(2017).
17. Agegnehu M, Yosef G, Arega G, Mekonnen A, Yosef G, Gashaw A, et al. Evaluation of bread Wheat (Triticum aestivum L.) Genotypes under Moisture Deficit Conditions. Abyssinia J Sci Technol. 2017;2(2):38–48.
18. Yan W, Tinker NA. Biplot analysis of multi-environment trial data: Principles and applications. Can J Plant Sci. 2006;86:623–45.
19. Ding M, Tier B, Yan W, Wu HX, Powell MB, McRae TA. Application of GGE biplot analysis to evaluate genotype (G), environment (E) and GxE interaction on Pinus radiata: A case study. N Z J Sci. 2008;38(1):132–42.
20. Fan Xming, Kang MS, Chen H, Zhang Y, Tan J, Xu C. Yield Stability of Maize Hybrids Evaluated in Multi-Environment Trials in Yunnan, China. Agron J. 2007;99:220–8.
21. Farshadfar E, Mohammadi R, Aghaee M, Vaisi Z. GGE biplot analysis of genotype × environment interaction in wheat-barley disomic addition lines. Aust J Crop Sci. 2012;6(6):1074–9.
22. Temesgen M, Alamerew S. GGE Biplot Analysis of Genotype by Environment Interaction and Grain Yield Stability of Bread Wheat Genotypes in South East Ethiopia. World J Agricultural Sci. 2015;11(4):183–90.

23. Yan W. GGE Biplot vs. AMMI Graphs for Genotype-by-Environment Data Analysis. J Indian Soc Agricultural Stat. 2011;65(2):181–93.
24. Yan W, Rajcan I. Biplot Analysis of Test Sites and Trait Relations of Soybean in Ontario. Crop Sci. 2002;42:11–20.
25. Yan W, Hunt LAA, Sheng Q, Szlavnics Z. Cultivar Evaluation and Mega-Environment Investigation Based on the GGE Biplot. Crop Sci. 2000;40(3):597–605.
26. Blakeney AB, Cracknell RL, Crosbie GB, Jefferies SP, Miskelly DM, O'brien L, et al. A basic introduction to Australian wheat quality. Kingston, Australia: Wheat Quality Objectives Group and GRDC; 2009. pp. 1–39.
27. Erekul O, Kautz T, Ellmer F, Turgut I. Yield and bread-making quality of different wheat (Triticum aestivum L.) genotypes grown in Western Turkey. Arch Agron Soil Sci. 2009;55(2):169–82.
28. Korkut KZ. OB. Determination of Some Bread Quality and Grain Yield Characters in Bread Wheat (Triticum aestivum L). Int J Agricultural Biology. 2005;7(1).
29. Shiferaw W, Abinasa M, Tadesse W. Evaluation of Bread Wheat (Triticum Aestivum L.) Genotypes for Stem and Yellow Rust Resistance in Ethiopia. Comput biology Bioinf. 2020;8(2):43–51.
30. King jE, jenkins jEE. The estimation of yield losses in wheat from severity of infection by Septoria species. Plant Pathol. 1983;32:239–49.
31. Hailemariam BN. Identification and characterization of sources of genetic resistance to wheat diseases in Ethiopian landraces and in the Ethiopian durum wheat NAM (EtNAM) population.

Figures

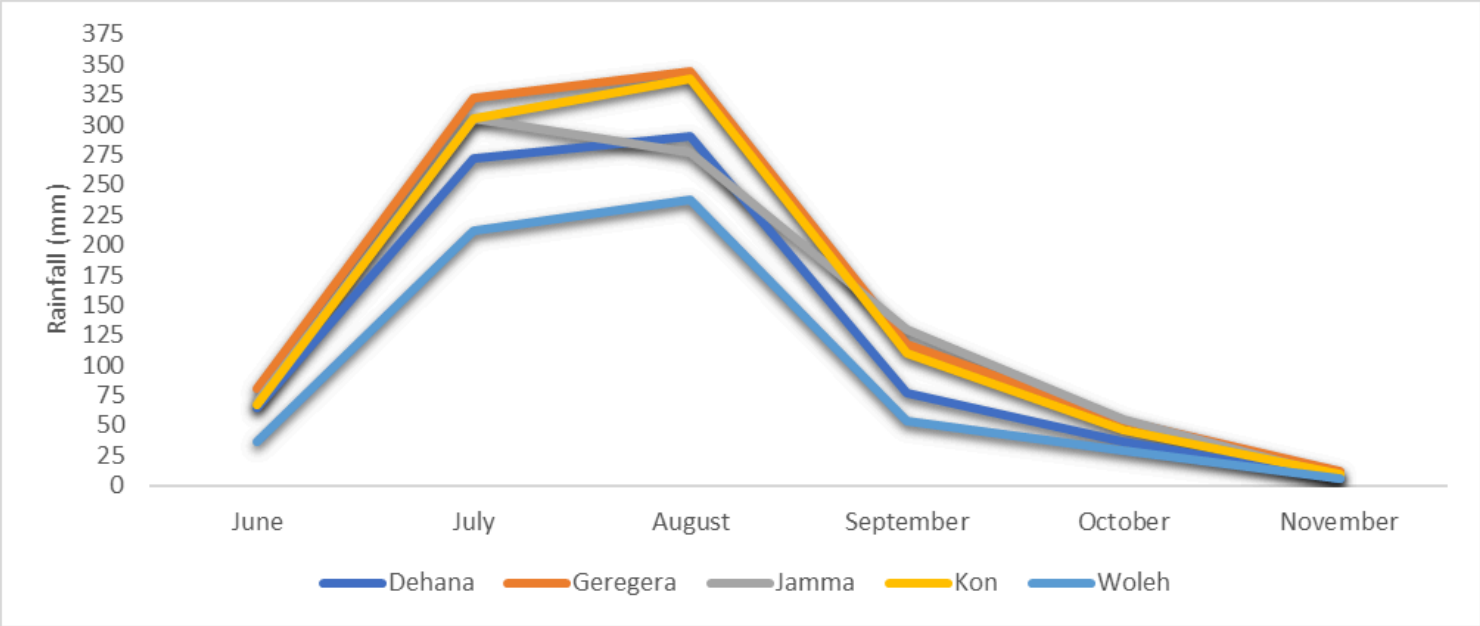


Figure 1

Monthly rainfall from June to November (2016-2017 cropping seasons)(Source: National Meteorological Agency, Kombolcha, Ethiopia

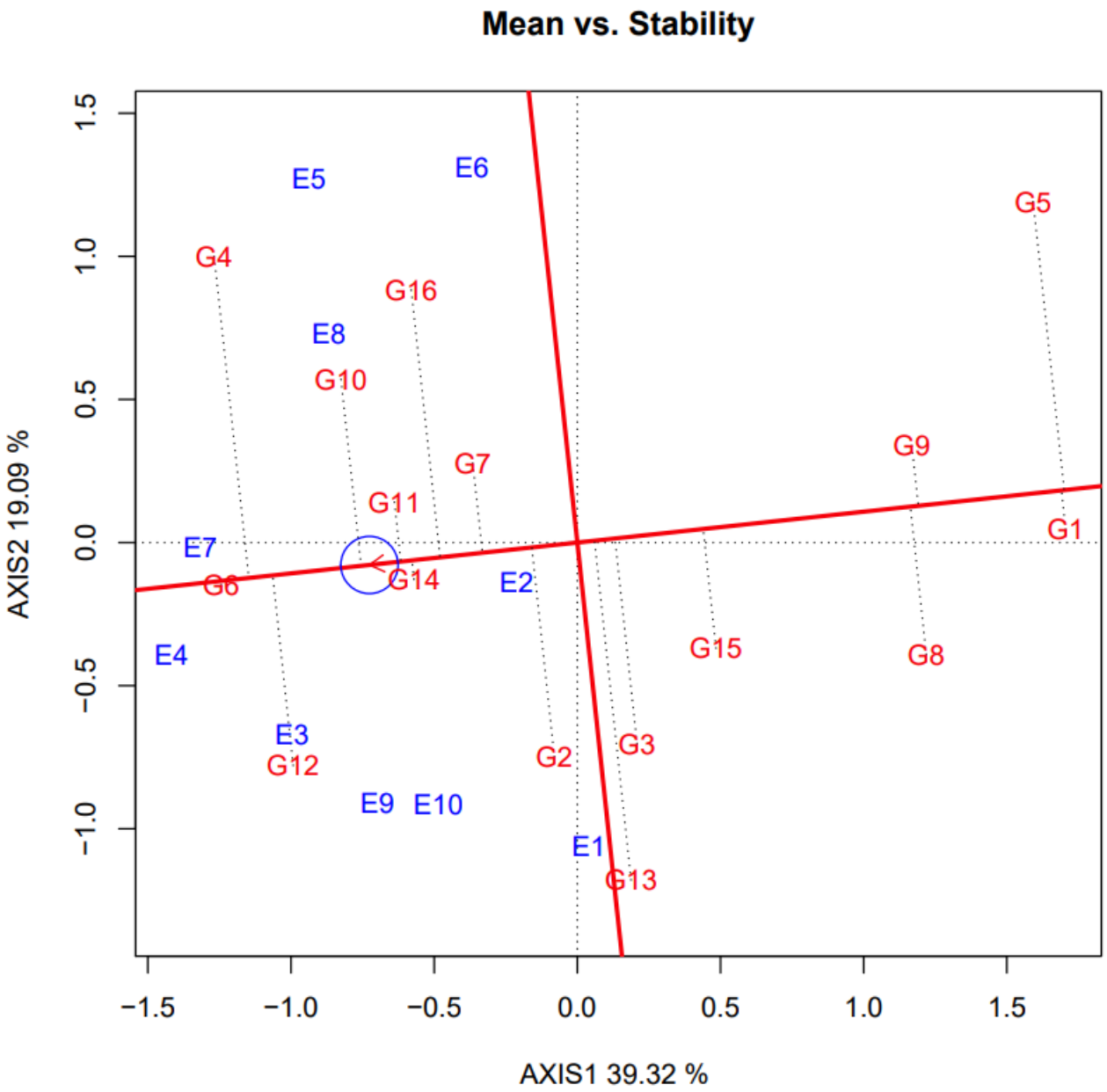


Figure 2

The GGE biplot shows the ranking of varieties for both yield and stability performance over environments. The varieties (G1 to G16) and environments are E1 to E10

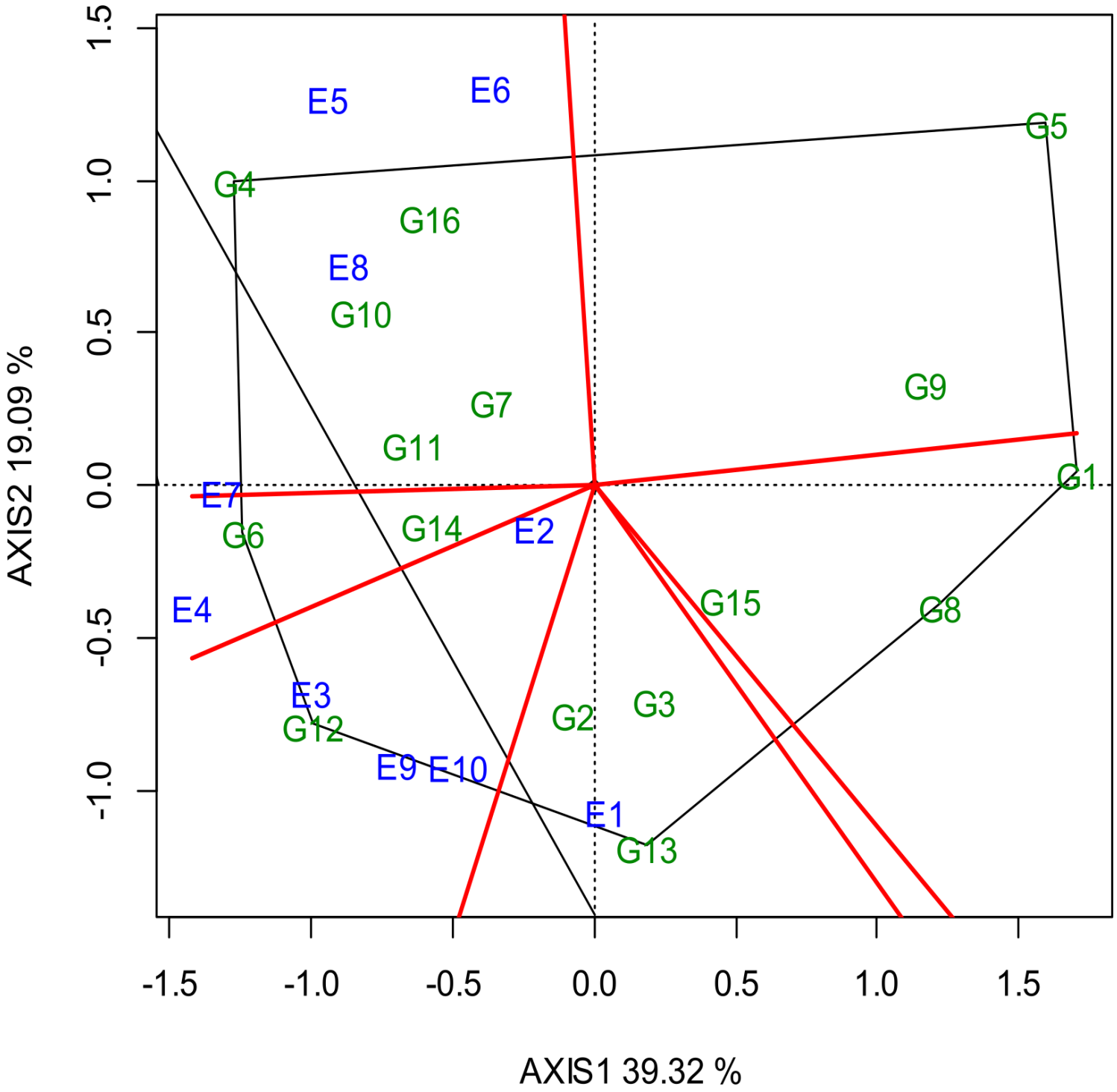


Figure 3

Polygon view of the GGE-biplot for the which-won-where pattern for genotypes(G) and environments(E)

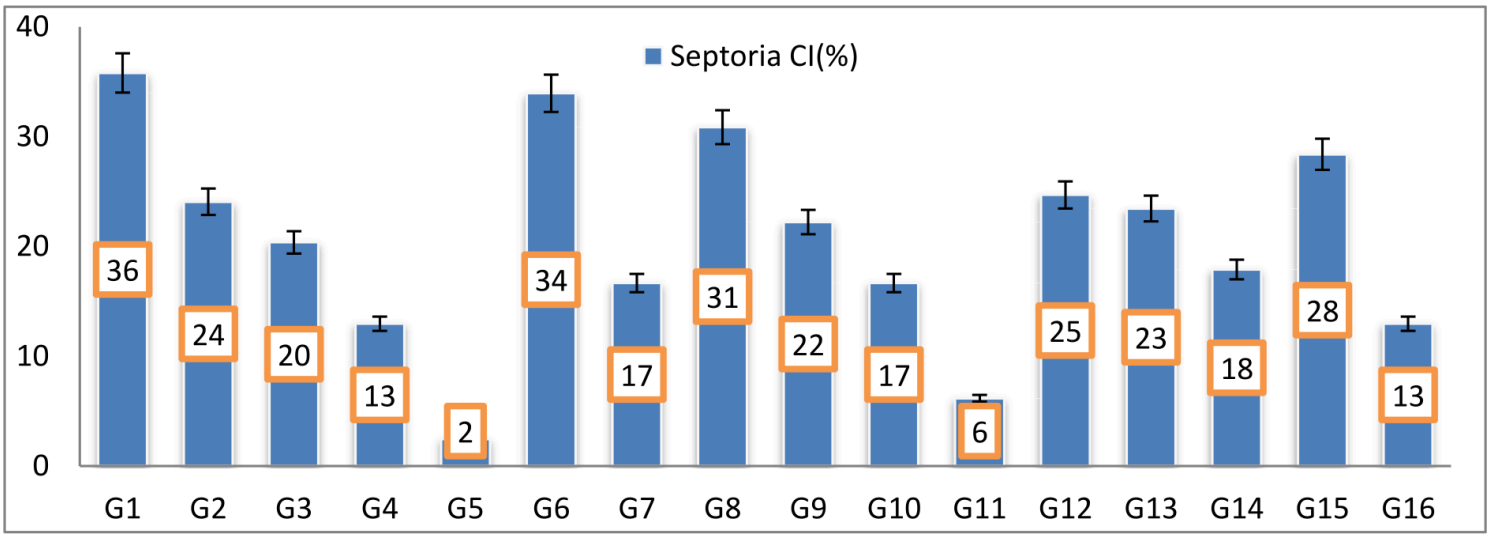


Figure 4

Infections of Septoria tritici blotch on sixteen bread wheat genotypes. Genotype names (G1 to G16) are depicted in Table 2