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Research Article

Genotype x Environmental Interplay and Yield Stability Evaluation on Bread Wheat Genotypes in North Shewa Zone, Oromia, Ethiopia

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Abstract

Wheat is one of Ethiopia's most imperative food safety plants. Demand for wheat in Ethiopia has been growing over the years. But, wheat imports improved during the last five years. The know-how of the interaction between genotypes and the environments with yield and its components is a number one aspect of effective selection in crop improvement. Therefore, this looks at aimed to perceive bread wheat genotypes with high grain yield ranges, yield stability and disease tolerance across locations. The study used 20 bread wheat genotypes inclusive of one local and one standard check (Sanate) at fitche agricultural research center (FiARC) within the 2022-2023 essential cropping seasons. 8 agronomic traits and 4 economically essential disease reaction data were evaluated. Analysis of variance detected significant differences among genotypes in both separated and combined evaluation of variance (ANOVA). The mixed ANOVA and the additive main effects and multiplicative interactions (AMMI) evaluation for grain yield across check environments exhibited, vast outcomes via environments, explained 12.5% of the entire variation. The genotype and genotype environmental interplay (GEI) had been great and accounted for 36.5% and 35.5%, respectively. Essential additives (PCA1 and PCA2) accounted for 16.9% and 11.6% of the GEI respectively, with 28.5% of the whole version. Normally, G124 and G127 had been recognized as ideal genotypes in-terms of yield, stability, and tolerance to the respective disease reactions and can be encouraged for use as parental line within the future breeding packages.

Keywords

Triticum Aestivum, AMMI, GGEI, Overall Performance, Stability

1. Introduction

Wheat (Triticum spp) is widely cultivated global, an everyday staple food for 40% of the sector's population, and affords 20% of its daily dietary calories and protein [15, 19]. Wheat and its produce sourced 14% of general calories, making wheat the crucial food in the back of maize (19%) and a head of tef (10%), sorghum (11%), and enset (12%) in Ethiopia [2] though Ethiopia is the top wheat producer in sub-Saharan Africa [12], abiotic stresses (drought and heat) are commonplace challenges, resulting in intensive yield loss and decreased grain quality [21].

Wheat production and productivity tiers have no longer met the demand, triggering fee instability and hunger unrest. With the exponential increasing world population, the call for wheat

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is expected to growth in double rate. To fulfill this excessive call for, growth in annual wheat yield production and productivity ought to upward push in folds. For this, research plays great role and stocks the largest component in growing the grain yield through developing variety that tolerate abiotic stresses, pathogens and pests and enhancing input use efficiency for greater sustainable wheat production. Improved agronomic practices and improvement of modern cropping systems also are a priority [10]. The continuous weather alternate immediately or circuitously affect Ethiopian agriculture and needs to broaden site-specific with progressed management practices (water logging stresses, low pH, etc.) for wheat in wheat growing areas.

In Ethiopia, the variation in wheat productivity most of the small holder farmers for the duration of the main season is quite giant due to the variations in use of advocated control applications, stepped forward variety and weather variation [14]. So, multi-environment yield trials are critical in estimating genotype by environmental interplay (GEI) and identifying superior and stable genotypes within the final selection cycles [13, 16]. Enormous of GEI end result from variation in the volume of variations amongst genotypes in diverse environments, known as qualitative or rank modifications, or versions in the comparative rating of the genotypes, called quantitative or absolute variations between genotypes [4, 7]. The study of GEI is important in numerous agro-ecologies and allows identifying genotypes adapted to those numerous environments. The additive main effects and multiplicative interaction (AMMI) model also helped us better know-how the complex styles of genotypic responses to the environment [8].

Therefore, the objective of this study turned into to evaluate and pick out bread wheat genotypes with better grain yield, yield stability and disease tolerance throughout the test locations.

2. Materials and Methods

2.1. Description of the Location

The study carried out at three locations in north shewa zones in Oromia, Ethiopia: at Fitche agricultural research center subsites vs. Kuyu (altitude 2540 masl), Debre-libanos (altitude 2630 masl) and Jidda (altitude 2730 masl) at some stage in the 2022-2023 main cropping season.

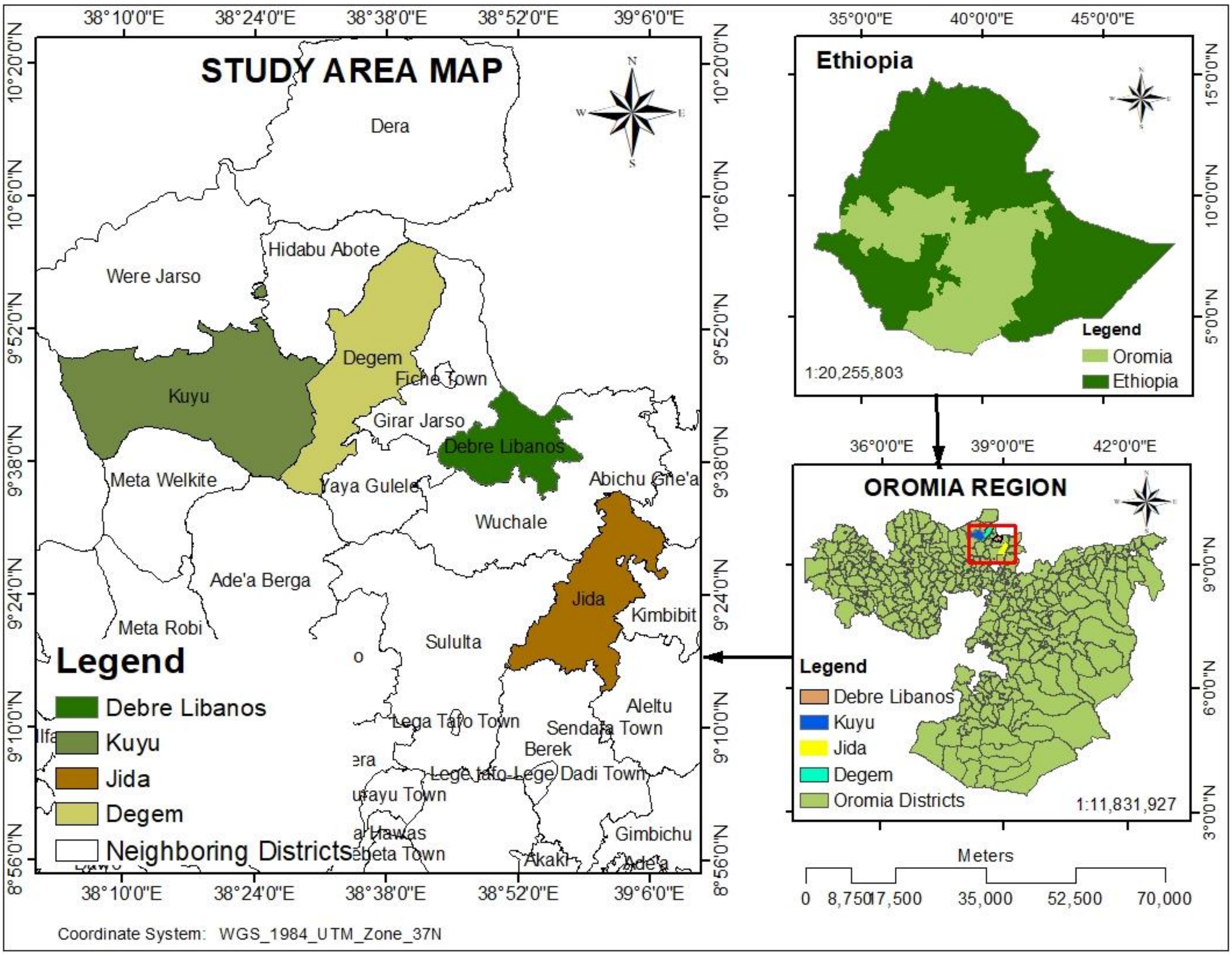

Figure 1. Map of the study experimental districts.

2.2. Experimental Material

Twenty bread wheat genotypes from the Ethiopia Biodiversity Institute (EBI), including one check, (senate) and a local check (Table 1) were evaluated.

Table 1. Passport information and outlines of bread wheat landraces used in the study.

Acc. Code	Accession Number	Genus name	Species name	Region	Zone	District	Latitude	Longitude	Altitude	Source
G179	6873	Triticum	aestivum	Oromiya	BALE	AGARFA	07-19-00-N	39-49-00-E	2480	EBI
G176	7112	Triticum	aestivum	Oromiya	SEMEN SHEWA	KEMBIBIT	09-27-00-N	39-15-00-E	2850	EBI
G021	7310	Triticum	aestivum	Oromiya	MISRAK SHEWA	SHASHE-MENE	07-17-00-N	38-36-00-E	2030	EBI
G121	7407	Triticum	aestivum	Amhara	DEBUB GON-DAR	TACH GAYINT	11-38-00-N	38-34-00-E	2500	EBI
G018	35253	Triticum	aestivum	Amhara	Debube Gonder	Farat	11-44-45-N	38-05-33-E	2845	EBI
G008	204453	Triticum	aestivum	Oromiya	ARSSI	JEJU	08-05-00-N	39-38-00-E	2660	EBI
G020	204454	Triticum	aestivum	Oromiya	ARSSI	JEJU	08-05-00-N	39-38-00-E	2620	EBI
G154	204506	Triticum	aestivum	Oromiya	SEMEN SHEWA	KEMBIBIT	09-27-00-N	39-15-00-E	2850	EBI
G017	222556	Triticum	aestivum	Oromiya	ARSSI	SHERKA	07-42-00-N	39-33-00-E	2400	EBI
G171	222559	Triticum	aestivum	Oromiya	ARSSI	BEKOJI	07-38-00-N	39-14-00-E	2530	EBI
G023	226858	Triticum	aestivum	Oromiya	ARSSI	JEJU	08-03-00-N	39-38-00-E	2710	EBI
G001	226860	Triticum	aestivum	Oromiya	ARSSI	CHOLE	08-10-00-N	39-54-00-E	2920	EBI
G119	228760	Triticum	aestivum	Oromiya	MIRAB SHEWA	AMBO			2000	EBI
G042	231605	Triticum	aestivum	Oromiya	MISRAK HARERGE	KOMBOLCHA	09-29-00-N	42-14-00-E	2420	EBI
G174	242427	Triticum	aestivum	Oromiya	MIRAB HARERGE	CHIRO	09-06-00-N	40-58-00-E	2220	EBI
G127	243702	Triticum	aestivum	Amhara	SEMEN WELLO	DAWUNTNA DELANT	11-34-00-N	39-14-00-E	2950	EBI
G124	243734	Triticum	aestivum	Amhara	DEBUB GON-DAR	KEMEKEM	12-08-00-N	37-50-00-E	2135	EBI
	Local									Farmers
	Senete									SARC
G 189	244971	Triticum	aestivum	Oromiya	MISRAK WELLEGA	GIDA KIREMU			2043	EBI

Key, EBI= Ethiopia biodiversity institute, SARC= Sinana Agricultural Research Center

2.3. Experimental Design and Trial Managements

Randomized completed block design (RCBD) with three replications was used in all experimental locations. Every experimental plot had six rows of 3m in length and 20cm apart with a plot area of 1.2m×3m. Sowing was accomplished by way of hand drilling with the same seed rate of 150kg/ha for every test locations. Fertilizer changed into implemented at a rate of 100kg/ha and 150kg/ha of NPS and UREA respectively. All of the encouraged NPS and half of UREA had been carried out at sowing time, while half of the rest UREA implemented in splitting techniques at 35-45 days after sowing. The data gathered from harvestable four critical rows. After harvesting, each plot pattern becomes sundried earlier than being tested for moisture content material, which 12% turned into the favored common moisture content material using moisture tester system. The dried grain for every plot pattern turned into weighted the usage of a virtual scale to obtain the very last grain yield weight.

3. Data Collection Method

Ten plants were selected randomly before heading from each row (four harvestable rows) and tagged with thread and plant-based data were collected from the sampled plants.

3.1. Plant –Based

Plant height, spike lets per spike and seed per spike. Plant height (cm); was measured and recorded when reached at 90% physiological maturity from the ground level to the base of the spike of plant. Spike lets per spike; is the average number of spike lets of the ten plants randomly selected.

3.2. Plot- Based

Days to heading, days to maturity, thousand seed weight, biomass yield, grain yield and four economically important disease reactions like stem rust, leaf rust, septoria and fusarium head blight. Days to heading; was recorded by counting the number of days from sowing to the time when at least 50% of the heads of the plot fully exerted from the boom or flowered. Days to maturity; was recorded by counting the number of days from sowing to the days when 95% of the heads of the plot were physiologically matured. Thousand seed weight (g); five hundred wheat grains were counted and weighed then multiplied by two to obtain thousand seed weight. Grain yield per plot (g); yield per plot was taken and moisture was adjusted to the standard moisture content of 12% moisture basis after threshing the crop using moisture tester

4. Statistical Analyses

Evaluation of variances became calculated using the model:

$$Yij = \mu + Gi + Ei + GEij \qquad (1)$$

and carried out by R software program (model 4.2.2) where: Yij is the corresponding variable of the ith genotypes in jth environment, μ is the total mean, Gi is the main effect of ith genotype, Ej is the main effect of jth environment, GEij is the impact of genotype via environment interplay.

$$Yij = \mu + gi + ej + \sum N1\, ʎk\, Yik\, \delta jk + Ɛij \qquad (2)$$

4.1. AMMI Analysis

In which: Yij is the grain yield of the i-th genotype inside the j-th environment, μ is the grand mean, gi and ej are the genotype and environment deviation from the grand mean, respectively, ʎk is the eigenvalue of the major thing evaluation (PCA) axis, Yik and δjk are the genotype and environment primary aspect scores for axis, N is the quantity of fundamental components retained inside the variation, and Ɛij is the residual time period.

4.2. AMMI Stability Value (ASV)

ASV is the gap from the coordinate point to the foundation in a -dimensional plot of IPCA1 rankings against IPCA2 scores in the AMMI model [18]. Due to the fact that the IPCA1 score contributes more to the GE interaction sum of squares, a weighted value is needed. This weighted value becomes calculated for each genotypes and every environment consistent with the relative contribution of IPCA1 to IPCA2 to the interplay sum of squares as follows:

$$ASV=\sqrt{[(SSIPCA1 / SSIPCA2) (IPCA1score)]^2 + (IPCA2score)^2} \qquad (3)$$

In which: SSIPCA1/SSIPCA2 is the weight given to the IPCA1- value by way of dividing the IPCA1 sum of squares by way of the IPCA2 sum of squares. The larger the ASV value, either negative or positive, the more specifically adapted a genotype is to a positive environment. Smaller ASV values suggest greater stable genotypes across environments [18].

4.3. Genotype Selection Index (GSI)

Stability isn't always the simplest parameters for selection as most stable genotypes might no longer always give better yield performance. Consequently, based on the rank of mean grain yield of genotypes (RYi) across environments and rank of AMMI stability value (RASVi), genotype selection index (GSI) turned into calculated for every genotype as: GSIi = RASVi +RYi. (4) A genotype with the least GSI is taken into consideration as more stable [5].

5. Results and Discussions

5.1. Analysis of Variances (ANOVA)

Mean square of analysis of variance for all genotypes at different environmental conditions, for grin yield and yield associated trends are presented in Table 2. Significant difference was located amongst years (P < 0.01) for all parameters, except plant height. The mixed analysis of variance revealed that year*location outcomes had been significant for all parameters. Year*genotypes effects were large for the parameters excluding plant height, seed per spike and spikelet per spike. Year*location*genotypes were significant for a few traits like days to maturity, days to heading, thousand seed weight and grain yield. Hence, evaluation of variance also indicates that the life of considerable effect of fluctuating climate circumstance on mean performance of maximum of the traits which an agreement with [3].

Table 2. *Evaluation of variance (ANOVA) for grain yield and yield associated traits of bread wheat genotypes evaluated in 2022-2023 major cropping season.*

SV	DF	DH	DM	PH	SPK	SPSK	TSW	Bmkgha	YLDkgha
rep	2	12.2**	23.5**	562.2**	1051.0ns	219.0^{ns}	5.2^{ns}	10207881**	374566**
Gen	19	916.5**	1454.6**	748.4**	198.6**	81.2**	333.6**	8937129**	3853556**
Year	1	497.0**	6908.1**	144.5^{ns}	119.4*	42.4**	359.5**	28191343**	1333929**
loc	2	1132.7**	782.0**	349.3**	283.1**	575.0**	726.0**	27236946**	2005978**
Gen.Year	19	64.2**	130.9**	0.0^{ns}	0.0^{ns}	0.0^{ns}	95.6**	7350308**	1530431**
Gen.loc	38	17.1**	43.4**	159.7**	32.9^{ns}	13.2**	58.6**	1894133*	675103**
Year.loc	2	1204.2**	317.7**	242.9**	260.3**	125.4**	454.2**	19623697**	9890394**
Gen.Year.loc	38	7.4**	30.0**	0.0^{ns}	0.0^{ns}	0.0^{ns}	36.6**	977797^{ns}	431607**
Residual	238	4.6	11.5	41.6	27.9	2.4	16.2	1222936	126999

ns *,** none significant, at 5% and 1% respectively, SV= source of variation, rep= replication, Gen= genotypes, Loc= Location, Gen x Loc = genotype * Location, Gen x year = genotype * year, Loc*year = location *year, Gen*Loc* year = genotypes*location* year, DF= degree of freedom, DH= days to heading, DM= days to maturity, PH= plant height, SPK= seed per spike, SPSK= spikelete per spike, TSW= thousand seed weight, BMkgha = biomass kilogram per hectare, YLDkgha = yield kilogram per hectare.

5.2. Agronomic Performances

Combined mean grain yield and other agronomic developments are supplied in Table 3. High mean of seed per spike, spikelete per spike, thousand seed weight, biomass yield and grain yield were recorded via G-124. These can provide high-quality flexibility for developing advanced varieties that become suitable for one of a kind agro-ecology with variable duration of developing length and high in grain yield status. This genotype also recorded medium mean plant height, days to heading and days to physiological maturity, indicating that the medium maturing genotypes were suited when moisture become the proscribing elements for bread wheat production and productivity. In assessment to this, G-17, G-20, G-42 and G-121 have been recorded with high plant height, demonstrating that, the varieties more vulnerable to the lodging issues and facilitate situation for disease and insect pest and can case excessive yield reductions. However, G-119 and G-174 genotypes were with medium plant height that plays position to expand resistance types in opposition to lodging problems. Moreover, G-124 and G-127 were recorded more grain yield and had 20.4% and 2.8% of yield benefits over the standard check (senate) respectively.

Table 3. *Combined imply grain yield and different agronomic traits of bread wheat genotypes.*

Genotype	DH	DM	PH	SPK	SPSK	TSW	Bmkgha	YLkgha	YLDA
G-1	80^{f}	131^{d}	64^{ij}	34.8^{efg}	23.9^{b}	26.2 ^{fg}	7961^{h-k}	1883^{ij}	
G-8	92.8 ^{a}	147.3^{ab}	77.4 ^{bcd}	33^{fgh}	23.9b	36ab	8567c-h	2233ef	
G-17	78.2 g	130.7d	83.4a	29 i	22d-g	26.5fg	8987b-e	2171e-h	
G-18	75.2hij	126f	74.9c-f	38a-e	20hi	29.9cde	8003f-k	2644c	

Genotype	DH	DM	PH	SPK	SPSK	TSW	Bmkgha	YLkgha	YLDA
G-20	92.3ab	147ab	80.6ab	34.9efg	21.6efg	35b	8727c-f	2226efg	
G-21	91.4bc	148ab	72.8ef	33.8g	21g	36.6ab	8294e-j	2119fgh	
G-23	79.1fg	130.7d	65.3ij	32ghi	19.6hi	27.5ef	7457k	1996ghi	
G-42	79.9f	130.6d	83.3a	38.9abc	22.8cd	26fg	8091f-k	2014f-i	
G-119	85e	141.1c	65.9hi	35.7c-g	21.9d-g	30cde	7769ijk	1756j	
G-121	74.7 ij	130.1d	79.5ab	30hi	19ij	28.8def	8690c-g	2541cd	
G-124	76.2h	126.6f	67.9ghi	40a	24b	38a	10055a	3860a	20.40%
G-127	75.7hi	129.3de	71.6fg	39.7ab	23.6bc	30.8cd	9270bc	3159b	2.80%
G-154	74.9hij	130.7d	74.4def	36c-f	22def	32c	9515ab	2640c	
G-171	78.2g	129.6d	78.9bc	35d-g	22.6de	24.6g	7997g-k	1944hij	
G-174	73.1k	127.1ef	68.5gh	36b-f	20h	27.5ef	7671jk	2401de	
G-176	90.8cd	148.2ab	76.7b-e	40.8a	26a	35.7ab	8433d-i	2010f-i	
G-179	90.8cd	146.7b	76.9b-e	35efg	21.5fg	34.9b	8686c-h	2020f-i	
G-189	85.8e	141.1c	75c-f	38.5a-d	23.6bc	36ab	9101bcd	2208efg	
local	89.9d	149.2a	78.7bc	40.8a	25.8a	35b	7407k	1814ij	
Senete	74 jk	124.8f	61.6j	35.3d-g	18.4j	28.6def	8006f-k	3072b	
Mean	81.9	135.8	73.9	35.9	22.2	31.4	8434.3	2303.3	
LSD5%	1.4	2.2	4.2	3.5	1.1	2.6	726	234	
CV%	2.6	2.5	8.7	14.7	7	12.8	13.1	15.5	

Key, DH = days to heading, DM = days to maturity, PH= plant height, SPK= seed per spike, SPSK= spikelet per spike, TSW= thousand seed weight, YLD kgha-1=Yield in kilogram per hectare, Bmkgha^{-1}= Biomass in kilogram per hectare, YAD = yield advantage, CV = coefficient of variation, LSD= least of significant differences

5.3. Grain Yield Throughout the Environments

The overall performance of the examined bread wheat genotypes for grain yield throughout locations and years are provided in Table 4. In this examine, some genotypes like G-124 and G-127 are constantly completed satisfactory in a set of environment, whilst different genotypes along with G-21 and G-121 are changed when it comes to grain yield from one environment to the other which become governed by way of environments. Such genotypes are site-specific adaptation. The average grain yield ranged from the lowest of 1978.2kg/ha at kuyu site in 2022 to the very best of 2797.8kg/ha in the same test site in 2023 cropping season with grand mean of 2331.3kgha. The grain yield across environments ranged from the lowest of 1756kgha for G-119 to the very best of 3860kgha for G-124. From the evaluated genotypes, G-124 was the top rating pipeline in all environments. Correspondingly, G-127 ranked first in any respect sites except at Jida in 2022 cropping calendar. Though, G-119 became ranked the least in all environmental sites at some point of the cropping seasons. The distinction in yield rank of genotypes throughout the environments exhibited the high crossover type of genotypes x environmental interplay [22].

5.4. Disease Reactions

Majority of genotypes evaluated had drastically ratings low for their corresponding economically important disease reactions. But few of them have been less resistance to the respective disease reactions. Based totally on the evaluated genotypes, two genotypes along with G-124 and G-127 had been resistances to the respective disease reactions.

Table 4. *Mean grain yield (kgha) of bread wheat genotypes evaluated at three locations for 2 consecutive years.*

Genotype	Year						Mean
	2022			2023			
	Locations						
	Jida	kuyu	D. Libanos	Jida	kuyu	D. Libanos	
G-1	2106de	1919^{cde}	1889 ^{ij}	1474^{ij}	2037^{i}	1871^{fgh}	1883
G-8	1889 ^{de}	2068^{cd}	2123 $^{f-i}$	2574^{bcd}	2798 ^{fg}	2015^{efg}	2244
G-17	2211 $^{b-e}$	1869^{c-f}	2658 ^{cde}	1774^{ij}	2218 ^{hi}	2295^{def}	2171
G-18	3043 ^{b}	1386 ^{gh}	3720 ^{a}	1739^{hij}	2759 ^{gh}	2914^{ab}	2594
G-20	2072de	1590 $^{e-h}$	2217 $^{f-i}$	2415^{b-f}	3056 $^{d-g}$	2003^{efg}	2226
G-21	1538^{e}	1701^{d-g}	2044^{g-j}	2157^{c-h}	2931 $^{d-g}$	1978^{efg}	2058
G-23	2201^{b-e}	1836^{c-f}	1862^{ij}	1983^{d-i}	2091^{i}	2336^{cde}	2052
G-42	2228^{b-e}	1519 ^{fgh}	2517^{c-f}	2028^{d-i}	1984^{i}	2143^{d-g}	2070
G-119	2015de	1365^{gh}	2186^{f-i}	1339^{j}	1732^{i}	1896^{e-h}	1756
G-121	2269^{b-e}	1412^{gh}	2428 $^{d-g}$	2340^{b-g}	4277 ^{a}	2518^{bcd}	2541
G-124	4217^{a}	4517^{a}	4117^{a}	3183^{a}	3988 ^{ab}	3137^{a}	3860
G-127	2606^{bcd}	3728^{b}	2925^{bc}	2800^{ab}	3939 ^{abc}	2956^{ab}	3159
G-154	2511^{bcd}	1669 $^{e-h}$	2766^{cde}	2534^{b-e}	3481 ^{bcd}	2776^{abc}	2623
G-171	2206 $^{b-e}$	1632 $^{e-h}$	2375^{e-h}	1535^{ij}	1664^{i}	1988^{efg}	1900
G-174	2129^{cde}	872 ^{i}	2840^{bcd}	1963^{e-i}	3394 ^{cde}	3108^{a}	2385
G-176	1558^{e}	2104 ^{c}	1661^{j}	2328^{b-h}	2901 ^{efg}	1508^{h}	2010
G-179	1464^{e}	1554 $^{e-h}$	2067^{g-j}	2343^{b-g}	2825 ^{fg}	1866^{fgh}	2020
G-189	1856de	2099 ^{c}	2370 $^{e-h}$	1911^{f-j}	2673 ^{gh}	2243^{def}	2192
local	1936de	1299 ^{h}	1963^{hij}	2036^{c-i}	1872^{i}	1778^{gh}	1814
Senete	3000^{bc}	3422 ^{b}	3200 ^{b}	2624^{abc}	3335 ^{def}	2849^{ab}	3072
LSD5%	875.82	379.31	418.56	593.03	556.65	463.24	376.92
CV%	23.5	11.6	10.1	16.7	12	12.1	24.7
Mean	2252.7	1978.2	2496.3	2154.1	2797.8	2308.9	2331.3

Key G= genotype, CV= coefficient of variation, LSD = least significant differences

Table 5. *Disease severity scale following a modified Cobb's scale using zero-nine scale of bread wheat genotypes examined in 2022-2023.*

Genotype	SEP	FHB	LR	SR
G-1	10r	10r	60ms	10r
G-8	10r	10r	20mr	10r
G-17	20mr	10r	60ms	20mr
G-18	20mr	60ms	20mr	20mr

Genotype	SEP	FHB	LR	SR
G-20	20mr	10r	10r	10r
G-21	10r	10r	10r	10r
G-23	20mr	10r	60ms	10r
G-42	20mr	10r	60ms	10r
G-119	60ms	10r	60ms	60ms
G-121	60ms	20mr	10r	10r
G-124	10r	10r	10r	10r
G-127	10r	10r	10r	10r
G-154	10r	10r	20mr	10r
G-171	20mr	10r	20mr	10r
G-174	60ms	60ms	60ms	20mr
G-176	10r	10r	10r	10r
G-179	10r	10r	10r	10r
G-189	60ms	10r	10r	10r
local	20mr	10r	20mr	10r
senete	20mr	20mr	10r	10r

Key= G= genotypes, SEP = Septoria, FHB= Fusarium head blight, LR= leaf rust, SR= stem rust, r= resistance, mr= moderately resistance, ms= moderately susceptible.

5.5. Additive Main Effects and Multiplicative Interaction (AMMI) Model

The mixed ANOVA and AMMI analysis for grain yield at six environments display on Table 6 changed into drastically affected greater through genotypes instead of by environments. This defined 36.5% of the overall variation, even as the environment and GEI have been widespread and accounted for 12.5% and 35.5% respectively. Similar findings had been suggested in previous studies [6, 13]. Study by [9], pronounced in well-known multi-environment trial (METs), environment impact contributes 80% of the whole sum of remedies and 10% effect of genotypes and interaction. In additive variance, the portioning of genotype environmental sum squares (GEss) records matrix the use of AMMI analysis indicated the primary PCAs have been significant ($P< 0.01$). PCA1 and PCA2 accounted for 16.9% and 11.6% of the GE interaction respectively; representing a complete of 28.5% of the interaction variant. This finding in agreement with the study has been reported in in advance via [17]. Large yield variation defined by means of genotypes certainly indicated that the genotypes had wider genetic base and can contributing maximum of the variation in grain yield.

Table 6. *AMMI evaluation of variances for grain yield of 20 bread wheat genotypes evaluated at six environments.*

Source Variation	D.F	S.S	EX.SS%	M.S
Genotypes	19	73217559	36.5	3853556**
Environments	5	25126672	12.5	5025334**
Block	12	4516235	2.3	376353**
Interactions	95	71133170	35.5	748770**
IPCA 1	23	33803651	16.9	1469724**
IPCA 2	21	23198165	11.6	1104675**

Source Variation	D.F	S.S	EX.SS%	M.S
Residuals	51	14131355	7.0	277085**

Key DF= degree of freedom, SS= sum of squares, MS= mean square, IPCA= interaction principal components axis, EX SS%= explained sum squares ns *, ** non-significant, significant at 5% and 1% level of probability respectively.

The average ordinate environment (AOE) is defined through the line that is perpendicular to the AEA (average environment axis) line and pass through the origin. This line divides the genotypes in to those with better yield than average and in to those decrease yield than average. By projecting the genotypes on AEA axis, the genotypes are ranked via yield; where in the yield increases inside the route of arrows. In this example, the highest yield had G-124 and G-127 (Figure 2). Stability of the genotypes relies upon on their distance from the AE abscissa. Genotypes closer to or across the center of concentric circle indicating these genotypes are stable than others. The finest stability in the high yielding group had G-124 and G-127 (Figure 2). The genotypes ranked became proven on the graph of genotype so-known as" ideal" genotypes (Figure 2) a really perfect genotype is described as one this is the very best yielding throughout the tested environments and it is absolutely stable in performance that ranks inside the highest in all the examined environments; along with G-124 and G-127. [6, 23], even though such a perfect genotype may not exist in reality, it could be used as a references for genotype assessment [16]. A genotype is greater appropriate if it's far placed closer to best genotype (6, 13). So, the right genotype on this examine turned into G-124 (Figure 2).

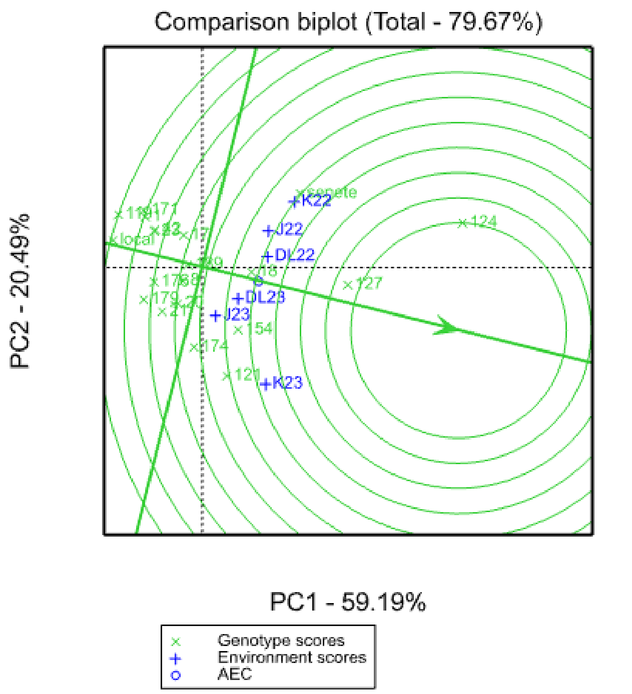

Figure 2. GGE bi-plot based totally on genotype-centered for their yield ability and stability.

The appropriate take a look at environment ought to have large PC1 score (more power to discriminate genotypes in terms of the genotypic important effect) and small (absolute) PC2 score (extra representatives of the general environments). Such an excellent environment becomes represented via an arrow pointing to it (Figure 3). Actually, such an ideal environments may not exist, but it may be used as an illustration for genotype choice within the METs. An environment is extra proper if it is placed toward the proper environments. Therefore, the use of the best environment as the center, concentric circles have been drawn to assist visualize the distance among each environment and the perfect environments [24]. accordingly, K22 (kuyu in 2022), which fell into the center of concentric circles, was a super test environment in terms of being the maximum representative of the overall environments and the most powerful to discriminate genotypes (Figure 3).

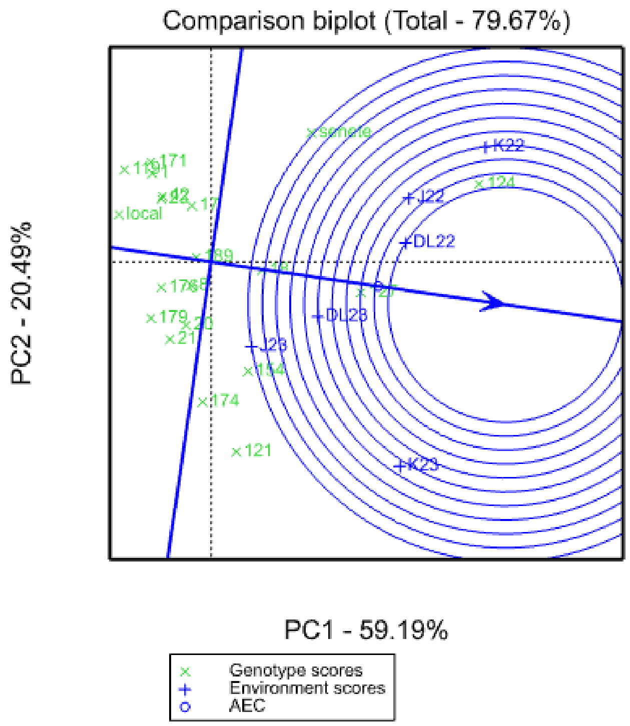

Figure 3. GGE bi-plot base on the test environment relationship.

5.6. AMMI Stability Value (ASV)

Genotypes x environment interaction discovered significant effects and the AMMI effect stability analysis (ASV) implied splitting the interaction impact. In view of the mean grain yield as a first criterion for comparing, G-124 become the very best imply grain yield (3860kgha^{-1}), followed via the G-127 with the mean grain yield of 3159kgha^{-1}. While, genotypes G-119, G-1 and G-171 have been with low imply grain yields throughout the testing locations (Table 7). The IPCA1 and a pair of scores inside the AMMI model are signs of stability [18]. Thinking about IPCA1, G-124 changed into the maximum stable genotype with IPCA1 value (3.087), observed through G-127 with IPCA1 value of (5.914). The two essential components have their very own extremes; however, calculating the AMMI stability value (ASV) is a balanced measure of stability [18]. Genotypes with lower ASV values are taken into consideration more stable and genotypes with better ASV are unstable. In keeping with the ASV ranking within the (Table 7), local check become more stable with an ASV value of 1 observed by using G-189 with ASV value 2. However, G-18 becomes the most unstable considering higher ASV value of 20. The stable genotype changed into accompanied with mean grain yield above the grand mean and this end result changed into an agreement with [11], who has used ASV as one technique of comparing grain yield stability of bread wheat types and similar reports been made by [1, 20] in barley and bread wheat using AMMI stability value. A genotype with the least of genotype selection index (GSI) is considered as the most stable genotype [5]. Hence, G124 changed into the maximum stable genotype when you consider that with the low of genotype selection index (GSI) and the best mean grain yield of all (Table 7).

Table 7. AMMI stability value, AMMI rank, yield, yield rank and genotype selection index and principal component axis.

Genotype	ASV	ASV rank	YLD	YLD rank	GIS	IPCAg1	IPCAg2
G-124	7.3	4	3860	1	5	3.087	6.234
G-127	17.9	14	3159	2	16	5.914	16.924
Senate	29	18	2761	3	21	23.956	1.59
G-18	30.4	20	2644	4	24	-1.71	-30.284
G-154	16.6	13	2640	5	18	-13.542	-2.635
G-121	27.5	17	2541	6	23	-22.222	6.015
G-174	29.8	19	2401	7	26	-21.455	-14.796
G-8	11.8	7	2233	8	15	-3.913	10.839
G-20	13.1	10	2226	9	19	-9.822	5.677
G-189	4.2	2	2208	10	12	0.247	4.203
G-17	10.1	5	2171	11	16	5.234	-7.943
G-21	18.5	15	2119	12	27	-11.591	12.089
G-179	16	12	2020	13	25	-10.732	9.433
G-42	12.4	8	2014	14	22	4.027	-11.44
G-176	21.6	16	2010	15	31	-3.868	21.13
G-23	6.6	3	1996	16	19	4.667	-3.358
G-171	13.3	11	1944	17	28	7.502	-9.761
G-1	10.5	6	1883	18	24	8.732	0.208
local	3.8	1	1814	19	20	-1.15	-3.56
G-119	12.7	9	1756	20	29	5.852	-10.563

6. Conclusion and Recommendation

Considering the 2 analyses of AMMI and GGE-bi-plot fashions, G124 and G127 recorded good grain yield and more stable, as a result, G124 and G127 close to best genotype, so this genotype is adaptable to a wide range of environmental situations. Consequently, those genotypes can be superior for release and use as parents in destiny breeding programs.

Abbreviations

AMMI	Additive Main Effects and Multiplicative Interaction
GGE	Genotype by Genotype Environmental Interaction
PCA	Principal Component Analysis

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Author Contributions

Geleta Negash: Conceptualization, Resources
Alemayehu Birr: Data curation, Methodology

Conflicts of Interest

The authors have not declared any conflict of interests.

References

[1] Abay, F. and Bjørnstad, A. (2009). Specific adaptation of barley varieties in different locations in Ethiopia. Euphotic 167: 181- 195.

[2] Anteneh, A. and Asrat, D., (2020). Wheat production and marketing in Ethiopia: Review study. *Cogent Food & Agriculture*, *6*(1), p. 1778893.

[3] Bedassa Mokonin. (2014). Selection of Barley varieties for their yield potential at low rainfall area based on both quantitative and qualitative characters North West Tigria, Shire, Ethiopia. International Journal of plant breeding and genetics.

[4] Falconer DS. (1952). the problem of environment and selection. The American Naturalist. 86: 293–298.

[5] Farshadfar E (2008). Incorporation of AMMI Stability Value and Grain Yield in a Single Non-Parametric Index (Genotype Selection Index) in Bread Wheat. Pakistan Journal of Biological Sciences, 11, 1791-1796.

[6] Farshadfar, E., Mohammadi, R., Aghae, M. andVaisi, Z. (2012). GGE biplot analysis of genotype × environment interaction in wheat-barley disomic addition lines. Australia Journal of Crop Sciences 6: 1074-1079.

[7] Fernandez GCJ. (1991). Analysis of genotype x environment interaction by stability estimates. Hort Science.; 26: 947–950.

[8] Gauch, H. G. (2006). Statistical analysis of yield trials by AMMI and GGE Crop Sciences 46: 1488-1500.

[9] Gauch, H. G. and Zobel, R. W. (1997). Interpreting megaenvironments and targeting genotypes. Crop Sciences 37: 311- 326.

[10] GCARD. (2012). Second Global Conference on Agricultural Research for Development, 29 Oct. - 01 Nov. 2012, Punta Este, Uruguay.

[11] Hintsa, G. and Abay, F. (2013). Evaluation of bread wheat genotypes for their adaptability in wheat growing areas of Tigray Region, northern Ethiopia. Journal of Biodiversity and Endangered Species.

[12] Hodson, M. E., Brailey-Jones, P., Burn, W. L., Harper, A. L., Hartley, S. E., Helgason, T. and Walker, H. F., (2023). Enhanced plant growth in the presence of earthworms correlates with changes in soil microbiota but not nutrient availability. *Geoderma*, *433*, p. 116426.

[13] Kaya, Y., Akcura, M. andTaner, S. (2006). GGE-bi-plot analysis of multi- environment yield trials in bread wheat Turkish Journal of Agriculture 30: 325-337.

[14] Manna Michael L, and Warner James M. (2017). Ethiopian wheat yield and yield gap estimation: A spatially explicit small area integrated data approach, Field CropsResearch, 60–74. http://dx.doi.org/10.1016/j.fcr.2016.10.014

[15] Marin-Acevedo, J. A., Dholaria, B., Soyano, A. E., Knutson, K. L., Chumsri, S. and Lou, Y., (2018). Next generation of immune checkpoint therapy in cancer: new developments and challenges. *Journal of hematology & oncology*, *11*, pp. 1-20.

[16] Mitrovic, B., Stanisavljevi, D., Treski, S., Stojakovic, M., Ivanovic, M., Bekavac, G. and Rajkovic, M. (2012). Evaluation of experimental Maize hybrids tested in Multi-location trials using AMMI and GGE bi-plot analysis. Turkish Journal of Field Crops 17: 35-40.

[17] Mohammadi, R. and Amri, A. (2009). Analysis of genotype × environment interactions for grain yield in durum wheat Crop Sciences 49: 1177-1186.

[18] Purchase, J. L. (1997). Parametric analysis to describe genotype x environment interaction and yield stability in winter wheat Ph. D. Thesis, Department of Agronomy, Faculty of Agriculture of the University of the Free State, Bloemfontein, South Africa.

[19] Shiferaw, B., Smale, M., Braun, H. J., Duveiller, E., Reynolds, M. and Muricho, G., (2013). Crops that feed the world 10. Past successes and future challenges to the role played by wheat in global food security. *Food security*, *5*, pp. 291-317.

[20] Sivapalan, S., Obrien, L., Ortiz-Ferrara, G., Hollamby, GJ., Barclay, I. and Martin, PJ. (2000). an adaptation analysis of Australian and CIMMYT/ICARDA wheat germplasm in Australian production environments. Crop Science Pastures 51: 903-915.

[21] Tadesse, M. M., Lin, H., Xu, B. and Yang, L., (2019). Detection of depression-related posts in reddit social media forum. *Ieee Access*, *7*, pp. 44883-44893.

[22] Yan, W. and Hunt, LA. (2001). Genetic and environmental causes of genotype by environment interaction for winter wheat yield in Ontario. Crop Science 41: 19-25.

[23] Yan, W. and Kang, MS. (2003). GGE bi-plot analysis: a graphical tool for breeders, In: Kang MS. (Ed). Geneticists, and Agronomist. CRC Press, Boca Raton, FL. pp. 63-88.

[24] Yan, W. and Rajcan, I. (2002). Bi-plot analysis of test sites and trait relations of soybeanin Ontario. Crop Science 42: 11-20.