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Grain Yield Stability and Phenotypic Correlation Analysis of Bread Wheat (Triticum aestivum L.) Genotypes in North Western Ethiopia

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Abstract
An experiment was conducted at Adet, Simada and Debretabor experimental sites of Adet Agricultural Research Center in 2014 and 2015 cropping season under rain-fed condition to study stability and traits correlation of bread wheat genotypes. Twelve bread wheat genotypes were used as experimental treatments. The genotypes were laid out in randomized complete block design with three replications per site. The results of AMMI analysis depicted significant differences among genotypes across environments (locations and years) ($P \leq 0.001$). According to the study, the performances of genotypes grain yield were highly affected by environments (locations and years) and the genetic composition of genotypes. The highest variation was accounted for by location (29 %) followed by genotype (18%) and location by year (18 %) and genotype by year (12%) effects. Based on AMMI, GGE biplot and stability coefficient analyses, G4, G2, G11 and G9 were wide adaptable and relatively stable genotypes all over the test environments (locations and years) than the checks, G7 (TAY) and G12 (Kubsa). Therefore, based on the adaptability and stability and overall mean grain yield of genotypes, recently released genotypes Gambo (G4), Ogolcho (G2) and Tsehay (G9) and relatively older genotypes Shorima(G11) and TAY (G7) could be recommended for production at test environments in the Western Amhara Region. However, there is a need to study the effect of environmental variation on the occurrence of rust disease.
Keywords: AMMI, Correlation, GGE, Yield stability

1. INTRODUCTION

Ethiopia is frequently exposed to food shortage due to environmental variability, degradation of soil fertility, ever increasing of the population (Ashenafi, 2008) and inappropriate use of improved technologies (Zerihun, 2014). Even though the production and productivity of wheat crop in Ethiopia has increased in the last decades, the national average yield has not exceeded 2.54 tones/ha (CSA, 2014). It is lower than the world's average yield/ha which is about 3.3 tones/ha (FAO, 2014). This is due to factors such as use of unimproved low yielding varieties, uneven distribution of rainfall, poor agronomic practices and serious diseases like stem rusts (Dereje *et al*., 2000).

Among the factors limiting wheat production and productivity, diseases are the foremost critical constraints all over the world. Particularly rust diseases cause highest yield loss of wheat production. A number of studies illustrated that wheat rusts could cause yield losses of 20-100 % on susceptible wheat genotypes (CIMMYT, 1989; Temesgen *et al*., 1995; Emebet *et al*., 2005; Stubbs, 1998; Marshall, 1988). Now that Ethiopia's wheat production covers only 75% of the national demand, the remaining 25% of the wheat is fortified through imported (Eyob *et al.*, 2014). Hence to overcome wheat yield losses and to cut down wheat national demand deficiency conducting considerable research works that contribute positive impact on wheat productivity and production are mandatory.

The process of variety development in the country is continuing year after year through various research institutes and universities. However, once released for production, the varieties are used for a long period of time continuously without considering their adaptation domain, grain yield stability and testing whether they are losing their potential or not. Now a day high yielding and rust disease resistant bread wheat varieties have recently been released in Ethiopia. However, farmers in Western Amhara Region commonly use relatively older bread wheat varieties such as Kubsa and TAY which were released in 1995 and 2005, respectively. Therefore, evaluation of recently released bread wheat varieties across environments and over years through different statistical methods enables to identify genotypes with better performance.

Hence, it is vital to evaluate grain yield stability and correlation of parameters of bread wheat genotypes used in the region with the following objectives: to evaluate the extent of grain yield stability, to assess the grain yield advantage of recently released varieties over farmers commonly used varieties and to investigate the relation of parameters to grain yield for future breeding program.

2. MATERIALS AND METHODS

2.1. Study Areas Description and Experimental Treatments

The experiment was conducted during 2014 and 2015 cropping season under rain-fed conditions at experimental sites of Adet Agricultural Research Center namely Adet, Simada and Debretabor. Twelve improved bread wheat genotypes were used as treatments for the study. The detail agro-ecological data of environments and the description of genotypes are listed in Table 1 and 2, respectively.

Table 1. Altitude, geographical location, soil type and climate data of the research sites

Locations	Code	Cropping season	Code	Environments	Altitude (masl)	Geographical location		Soil type	Climate data	
						Latitude	Longitude		RF(mm)	Temp(C^0)
Adet	Loc1	2014	Yr1	E1	2240m	11^{0}16'N	37^{0}29'E	Nitosol	658.6	17.53
Simada	Loc2	2014	Yr1	E2	2460m	11^{0}03N	37^{0}30'E	Luvisol	736.1	13.27
Debretabor	Loc3	2014	Yr1	E3	2591m	11^{0}51'N	38^{0}01'E	Luvisol	1102.7	15.48
Adet	Loc1	2015	Yr2	E4	2240m	11^{0}16'N	37^{0}29'E	Nitosol	948.9	19.4
Simada	Loc2	2015	Yr2	E5	2460m	11^{0}03N	37^{0}30'E	Luvisol	770.6	15.07
Debretabor	Loc3	2015	Yr2	E6	2591m	11^{0}51'N	38^{0}01'E	Luvisol	958.1	15.94

Source: AARC (2014) and ANRSMA (2014 and 2015)

Note : Total amount of rainfall and average temperature from July to November

Table 2. Description of bread wheat genotypes used for the study

Genotypes name	Code	Released by	Year of release	Grain yield (t/ha) during releasing time		Adaptation Zone	
				On station	On farm	Altitude(masl)	RF(mm)
Hidase(ETBW 5795)	G1	KARC	2012	4.4-7	3.5-6	2200-2600	>500
Huluka(Flag 5)	G3	KARC	2012	4.4-7	3.8-6	2200-2600	500-800
Ogolcho(ETBW 5520)	G2	KARC	2012	2.8-4	2.2-3.5	1600-2100	400-500
Shorima(ETBW 5483)	G11	KARC	2011	2.9-7	2.3-4.4	2100-2700	700-1100
Gambo(QUIAU#2)	G4	KARC	2011	3.5-5.7	4.5	750	-
Tsehay(HAR 3837)	G9	DBARC	2011	3.8	2.8-3.5	2600-3100	>900
Danda'a(DANPHE#1)	G5	KARC	2010	3.5-5.5	2.5-5	2000-2600	>600
Bolo(HAR 3816)	G8	DBARC	2009	2.8-3.5	2.3-3.3	2580-3100	>904
Menze(HAR 3008)	G10	DBARC	2007	1.9-3.3	1.5-2.7	2800-3100	>904
Gassay(HAR 3730)	G6	ADARC	2007	4.4-5	3.5-4.7	1890-2800	>700
TAY (ET-12 D4/ HAR-604(1) (SC)	G7	ADARC	2005	2.5-6.1	3.4-5.8	1900-2800	>700
Kubsa(HAR 1685) (SC)	G12	KARC	1995	5.8-6.3	4-4.5	1850-2800	500-800

Source: MoA, Crop Variety Register (1995-2012)

ADARC- Adet Agricultural Research Center, DBARC- Debrebirhan Agricultural Research Center, KARC- Kulumsa Agricultural Research Center, SC-Standard Check, SC-Standarad Check

2.2. Experimental Procedures and Method of Statistical Analysis

The treatments were laid out using a randomized complete block design with three replications per site and six rows per plot. Planting was done in the second week of July with seeding rate of 150 kg/ha on the plot area of 1.2 m*2.5 m with net harvested area of 0.8m*2.5m. Urea and DAP fertilizers as source of nitrogen and phosphorous were applied as per their recommendation rate and time of application for bread wheat specified to each experimental site. All other agronomic practices like weeding were applied uniformly for all the treatments at all experimental sites.

Grain yield was analyzed by using GenStat (17th Ed) software to compute analysis of genotypes and environments main and interaction effects, seasonal variation effects and grain yield stability of genotypes. Whenever the analysis results were highly-significant or significant, Fisher's LSD test at 1 % and 5% probability level, respectively, was used to separate the variable means of genotypes, environments and genotypes by environments interaction.

The AMMI analysis of variance summarizes most of the magnitude of genotype by environment interactions into one or few interaction principal component axes (IPCA) (Zobel *et al.* 1988, Crossa, 1990). The following AMMI model equation was used:

$$Y_{ger} - u - \alpha_g - \beta_e = \Sigma_n \lambda_n \tau_{gn} \delta_{en} + p_{ge} + \xi_{ger}$$

where Y_{ger} is the grain yield of genotype (g) in environment (e) for replicate (r), u is the grand mean, α_g are genotype mean, β_e are the environment mean deviations, λ_n is the singular value for IPCA axis n, τ_{gn} are genotype eigenvector values for IPCA axis n, δ_{en} are the environment eigenvector values for (PCA) axisn, p_{ge} are the residuals and ξ_{ger} is the error term.

GGE biplot analysis was carried out to identify high yielding and stable varieties as well as representative and discriminating environments as per Yan (2001):

.Y ger - βe = Σn^ n τgnδen+pge+ξger

where Y_{ger} is the grain yield of genotype (g) in environment (e) for replicate (r), β_e are the environment mean deviations, λ_n is the singular value for IPCA axis n, τ_{gn} are genotype eigenvector values for IPCA axis n, δ_{en} are the environment eigenvector values for (PCA) axisn, p_{ge} are the residuals and ξ_{ger} is the error term.

AMMI Stability Value (ASV) is the distance from the coordinate point to the origin in a two-dimensional plot of IPCA1 scores against IPCA2 scores in the AMMI model (Crossa, 1990). ASV was calculated for each genotype and each environment according to the relative contribution of IPCA1 to IPCA2 to the interaction sum of squares as follows:

$$ASV = \sqrt{[(SS_{IPCA1} \div SS_{IPCA2})(IPCA1score)]^2 + (IPCA2score)^2}$$

Lin and Binns (1988) defined the superiority measure (Pi) of the i^{th} test cultivar as the MS of distance between the i^{th} test cultivar and the maximum response as:

$$P_i = [n(\overline{X_i} - \overline{M})^2 + (\sum_{j=1}^{n}(X_{ij} - \overline{X_{i.}} - M_{j.} + \overline{M})^2]/2n$$

Where Xij=is the average response of the i^{th} genotype in the j^{th} environment, Xi=is the mean deviation of genotype i, Mj=is the genotype with maximum response among all genotypes in the j^{th} location, and n is the number of locations. The first term of the equation represents the genotype sum of squares and the second part represents the GE sum of squares.

Becker and Leon (1988) defined the concept of ecovalence(Wi)as the contribution of each genotype to the GEI sum of squares. The Wi or stability of the i^{th} genotype is its interaction with the environments, squared and summed across environments, and expressed as:

$Wi = [Yij - Yi. - Y.j - Y..]^2$

Where, Yijis the mean performance of genotype i in the j^{th}environment,Yi. andY.jare the genotype and the environment mean deviations, respectively, and Y.. is the overall mean.

According to Lin *et al*. (1986) the variance of genotype yields recorded across the test environments can be used as a measure of stability. For the genotype greatest stability is $S_i^2=0$. The formula is:

$$S_i^2=\sum(R_{ij}- m_{i.})^2/ (e-1)$$

Where; S_i^2= environmental variance, R_{ij}= observed genotype yield across environments, $m_{i.}$= marginal means of genotypes, e=number of environments

3. RESULTS AND DISCUSION

3.1. Impact of Genotypes, Locations and Years on grain yield

The analyses of variances depicted highly significant ($P \leq 0.001$) differences among genotypes, locations, years and their interactions for grain yield (Table 3). The highest variation was accounted for by location (29 %) followed by genotype (18%) and location by year (18 %) and genotype by year (12%) effects (Table 3). The grain yield of genotypes was highest at Adet in 2014 cropping season, and at Debretabor in 2015 cropping season. Similarly, grain yield of genotypes was lowest at Simada in 2015 (Table 4). Genotype 4 (Gambo) was the highest yielder both at the highest (Adet in 2014) and the lowest (Simada in 2015) yielding environments. Genotypes G4, G2, G11 and G9 showed 12.41, 10.22, 4 and 3.45 qt/ha grain yield advantage over standard check (G7) respectively, and 17.16, 14.97, 8.75 and 8.2 qt/ha grain yield advantage over standard check (G12), respectively (Table 4). Based on this study, grain yield response of genotypes was highly affected by location, environments (location by seasonal variation) and seasonal variation in line with Frey (1983) and Falconer (1990). As a result, screening and development of wide adaptable and relatively stable genotypes are determinant factor to increase bread wheat productivity and production.

Table 3. The analysis of variance of genotypes, locations, years and their interactions

SV	DF	SS	MS	% SS (gen+loc+yr+gen*loc+gen*yr+ loc*yr+gen+loc+yr+ residual)
Gen	11	9187.87	835.26**	18
Loc	2	14393.4	7196.7**	29
Yr	1	2764.46	2764.46**	5.6
Gen*Loc	22	3798.1	172.64**	7.6
Gen*Yr	11	5809.92	528.17**	12
Loc*Yr	2	8998.73	4499.37**	18
Gen*Loc*Yr	22	2591.46	117.79**	5.2
Residual	142	2247.1	15.82	4.5
Total	213	49791.04		

Gen-genotype, Loc- Location, Yr- Year, SV- Source of variation

Table 4. Genotypes mean grain yield (qt/ha) across locations and over years

	Loc1		Loc2		Loc3		
Genotypes	Yr1	Yr2	Yr1	Yr2	Yr1	Yr2	Mean
G1	46.68	42.59	42.94	18.52	18.4	54.45	37.26^{cde}
G2	64.67	58.19	51.96	25.91	48.03	49.13	49.65^{a}
G3	57	53.17	24.55	21.21	28	43.42	37.89^{cd}
G4	70.85	60.62	56.86	26.37	49.35	47	51.84 ^{a}
G5	52.98	30.86	44.86	16.73	37.01	36.47	36.48^{de}
G6	44.95	38.06	42.73	20.56	32.54	39.12	36.33^{de}
G7	59.15	52.24	27.98	17.84	30.96	48.74	39.49^{c}
G8	50.64	13.88	34.93	14.67	35.91	33.66	30.61^{f}
G9	66.78	45.48	45.85	17.74	35.31	46.11	42.88^{b}
G10	52.73	11.98	36.6	14.04	27.68	33.78	29.47^{f}
G11	56.13	51.55	46.12	23.52	38.22	45.06	43.43^{b}
G12	49.68	55.73	12.75	22.01	17.07	50.85	34.68^{e}
YrMean	**56.02**	**42.86**	**39.01**	**19.93**	**33.21**	**43.98**	
Loc mean	**49.44**		**29.47**		**38.59**		**39.17**
LSD	**7.62**		**4.38**		**6.95**		**6.42**
CV	**9.4**		**9**		**11**		**10.2**
P level	**<0.001**		**<0.001**		**<0.001**		

G1=Hidase, G2= Ogolocho, G3=Hulluka, G4= Ga'ambo, G5= Danad'a, G6= Gassay, G7=Tay, G8= Bolo, G9= Tsehay, G10=Menze, G11=Shorima, G12=Kubsa, Loc1=Adet, Loc2= Simada, Loc3= Debretabour, Yr=Year, Loc=Location, Yr1=2014, Yr2=2015

3.2. The Main and Interaction Effects of Genotypes and Environments

The AMMI analysis of grain yield showed highly significant differences among genotypes, environments and their interactions (Table 5). Environments depicted the highest variation on grain yield performance of genotypes which accounted for 41.9% followed by genotypes (14.7%), and genotype by environments interaction (19.5%) which was in agreement with the findings of Misganaw *et al*. (2015) (Table 5).

The partitioning of the genotype-environment interaction by employing AMMI model analysis showed that four of the Interaction Principal Component Axes (IPCAs) were highly significant (P<0.001).The four IPCAs accounted for 99.2% of the interaction sum of squares (SS), with 87.27% of the corresponding degrees of freedom (Table 5). Out of the four, the first interaction PCA captured 66.54% of the interaction SS with 27.27% of the corresponding degrees of freedom. Similarly, the second interaction PCA captured 15.72% of the interaction SS with 23.4% of the corresponding degrees of freedom. The two interaction PCAs explained 82.26% of the total variation in grain yield of the bread wheat genotypes. The AMMI1biplot captured 43462 of the treatment SS of 60462. Therefore, it revealed 71.88% of the treatment SS. Approximately as much variation in grain yield was explained by the interaction term captured by IPCA1 as by the genotypic main effect. This showed that interaction is as important as genotypic main effect; implying that both specific and wide adaptations are important. In the biplot axes system, either main effects and IPCA1, or IPCA1 and IPCA2 are commonly used as abscissa and ordinates (Zobel *et al*., 1988; Gauch, 1992).

The AMMI biplot showing the main and IPCA1 effects of both genotypes and environments on bread wheat grain yield is depicted in Figure 1. In such a system, distances along the abscissa (horizontal line) shows main effect differences, whereas the ordinate (vertical line) shows differences in interaction. In the present study,

G1, G3, G5 and G6 had more or less similar genotypic main effect, differing in interaction. However; G2 and G11, and G4 and G9had nearly similar interaction effects, only differing in genotypic main effects. In the same manner, E4 and E2 had higher interaction effect; whereas E5 and E1 had minimum interaction effect, but they had higher differences in environmental main effect. According to Gauch and Zobel (1996)and Gauch and Furnas (1991), when a genotype and an environment have the same sign on the IPCA1 axis, their interaction is positive i. e., that particular genotype is adaptable and the environment is conducive for the genotype; if different, their interaction is negative. Accordingly G2, G4, G5, G6, G8, G9 and 10 were adapted to E1, E2 and E3. In contrast, G1, G3, G7, G11 and G12 were adapted to E4, E5 and E6.

Figure 2, in addition to delineating mega-environments, showed the interaction pattern of the 12 bread wheat genotypes with the six environments. The distances from the origin indicate the magnitude of interaction exerted by environments on genotypes, or vice versa (Voltas *et al*., 2002). In other words, genotypes near the origin are not sensitive to environmental interaction, whereas genotypes distant from the origin are sensitive and have large interaction effects. Hence from this study, genotypes G11, G9, G6, G7 and G3 were weakly influenced by environmental factors while G10, G8, G12 and G4 were strongly affected by environmental factors. Therefore, genotypes which buffer variable environmental factors are more or less stable. Inversely, genotypes performance which varies due to environmental factors is specific adaptable.

Table 5. AMMI analysis of variance for genotypes, environments and their interactions based on Grain Yield Response

SV	DF	SS	MS	% of SS (Gen+Env+ Gen*Env+IPCA1+2+3+4)
Genotypes	11	9188	835.3**	14.7
Environments	5	26157	5231.3**	41.9
Block	12	718	59.8**	1.15
Interactions	55	12199	221.8**	19.5
IPCA 1	15	8117	541.1**	13
IPCA 2	13	1918	147.5**	3.07
IPCA 3	11	1476	134.2**	2.37
IPCA 4	9	592	65.8**	0.95
Residuals	7	97	13.8	0.16
Error	132	1943	14.7	3.11
Total	270	62405	7265.3	

SV-Source of variation, Gen-Genotypes, Env- Environments, IPCA-Interaction principal component axes

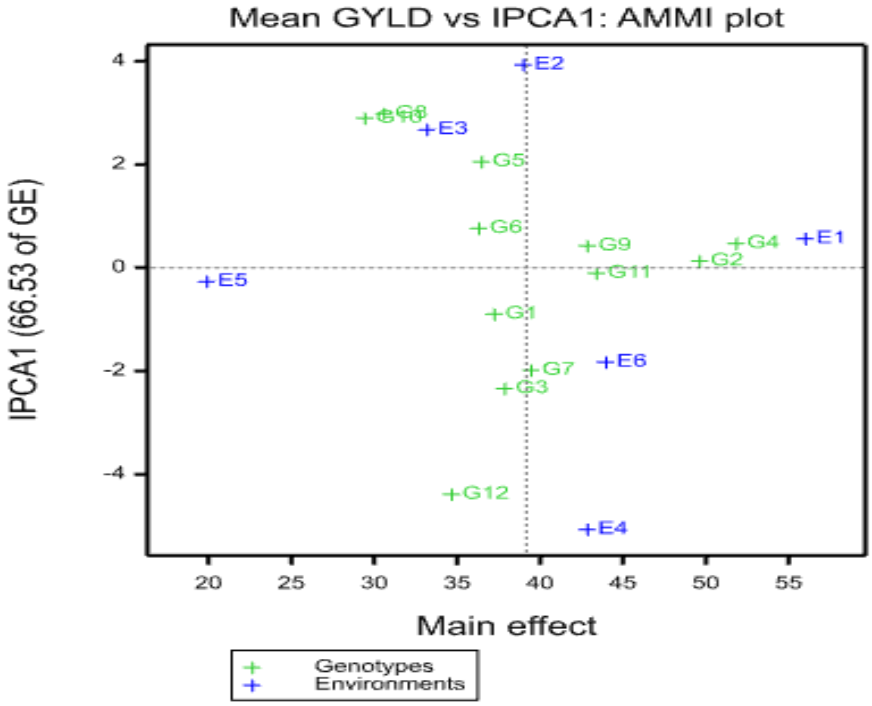

Figure 1. AMMI biplotof main effects of genotypes and environments using symmetrical scaling

G1=Hidase, G2= Ogolocho, G3=Hulluka, G4= Gaambo, G5= Danda'a, G6= Gassay, G7=Tay, G8= Bolo, G9= Tsehay, G10=Menze, G11=Shorima, G12=Kubsa, E1 and E4= Adet E2 and E5=Simada and E3 and E6= Debretabor, IPCA= Interaction Principal Component Axes

3.3. Clustering of Environments based on Genotypes Grain Yield Response

The GGE biplot is useful for identification of mega-environments, ideal genotype and test environments, among other things. Based on GGE biplot, environments were grouped into two mega environments. Mega environment one includes E1, E2, E3, E4 and E5 and mega environment two had singleton environment E6. Genotype G2 was the winning one across environments E1, E2, E3, E4 and E5 (Figure 2).

According to Yan *et al*. (2000) and Yan and Rajcan (2002), ideal genotypes are those having large PC1 scores (high grain yield) and small absolute PC2 scores (high stability). Accordingly G11 G6, G2 and G9 were better stable genotypes. Genotypes G4, G2, G11 and G9 were high-yielder in that order of importance. Though G6 was relatively stable genotype, it not preferable for production due its low-yielding capacity.

Ideal environments should be more representative of the entire set of environments and should have more genotype discriminating power, such environments should have small PC2 scores (absolute) and large PC1 scores (Yan *et al*., 2000; Yan and Rajcan, 2002). Thus E5 and E1 are more representative, whereas E5, E4 and E1 are more discriminating environments.

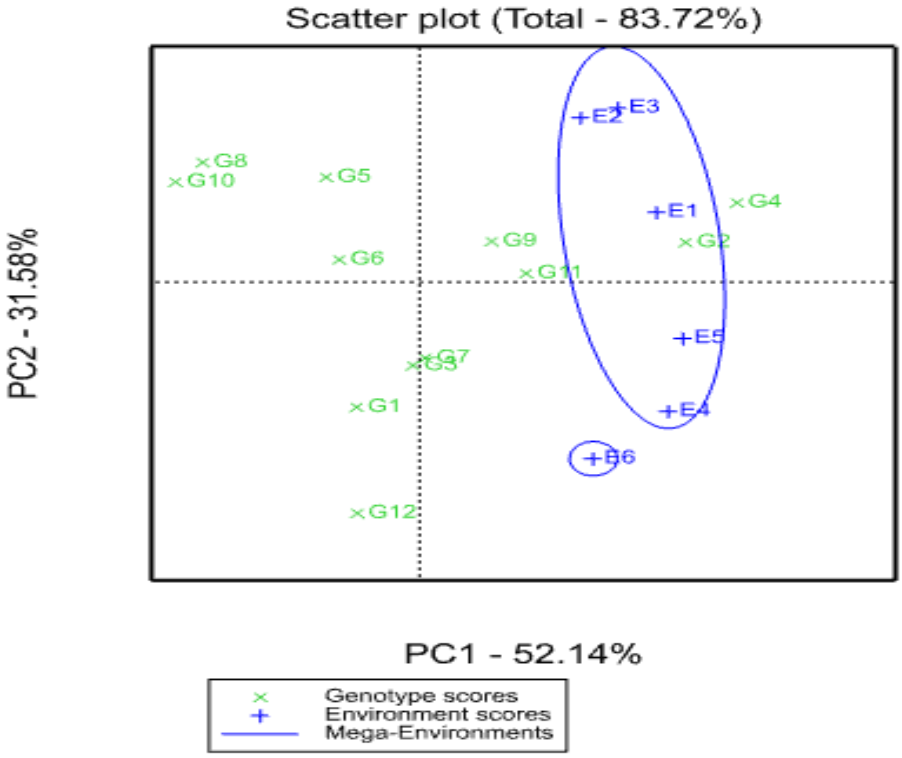

Figure 2. GGE biplot analysis of genotypes and environments using environment scaling

G1=Hidase, G2= Ogolocho, G3=Hulluka, G4= Gaambo, G5= Danda'a, G6= Gassay, G7=Tay, G8= Bolo, G9= Tsehay, G10=Menze, G11=Shorima, G12=Kubsa, E1 and E4= Adet E2 and E5=Simada and E3 and E6= Debretabor, PC= Principal Component

3.4. Grain Yield Stability of Genotypes over Environments

AMMI and GGE biplot analyses show adaptable and stable genotypes in graphical forms. As a matter of fact, to know the stability of genotypes in numerical values further stability analysis works are pertinent to explore stable genotypes using different stability analyses methods. According to this study, grain yield stability of genotypes rank varies with the methods used. Based on statements of Becker and Leon (1988) and Crossa (1990) genotypes with a low Wi value have smaller deviations from the mean across environments and are thus more stable and the larger the ASV value, either negative or positive, the more specifically adapted a genotype is to certain environments while smaller ASV values indicate more stable genotypes across environments. Therefore G4, G2, G11 and G9 were relatively stable genotypes based on AMMI stability, cultivar superiority and static stability analyses values (Table 6).

Static stability analysis had a drawback which implies both higher and lower grain yielding genotypes as stable. AMMI stability value shows consistency of genotypes contribution to genotype by environment interactions. While cultivar superiority analysis only showed mean performance of genotypes across environments, nonetheless it is difficult to know consistency of genotypes yield response across environments. This shows the necessity of combined use of different stability analysis methods to properly identify stable genotypes both in potential and consistency of grain yield over environments.

Table 6. Grain yield stability of bread wheat genotypes based on different methods of analyses

Genotypes	Mean	AMMI stability		Stability coefficient analysis methods			
		ASV	**R**	Cultivar Superiority	**R**	Static stability	**R**
G1	37.26	4.28	6	176.9	9	230.4	7
G2	**49.65**	**1.99**	**3**	**8.2**	**2**	**174**	**4**
G3	37.89	9.91	9	157.9	6	236.7	9
G4	**51.84**	**3.34**	**5**	**4.6**	**1**	**228.3**	**6**
G5	36.48	8.7	8	159.8	7	152.8	3
G6	**36.33**	**3.23**	**4**	**160.9**	**8**	**77.8**	**1**
G7	39.49	8.4	7	123.7	5	261.7	11
G8	30.61	12.7	11	318.6	11	198.3	5
G9	**42.88**	**1.89**	**2**	**59**	**4**	**257.3**	**10**
G10	29.47	12.4	10	346.1	12	231.5	8
G11	**43.43**	**1.17**	**1**	**52.9**	**3**	**132.1**	**2**
G12	34.68	18.9	12	291	10	376.2	12

G1=Hidase, G2= Ogolocho, G3=Hulluka, G4= Gaambo, G5= Danda'a, G6= Gassay, G7=TAY, G8= Bolo, G9= Tsehay, G10=Menze, G11=Shorima, G12=Kubsa, ASV=AMMI stability value, R=Rank

3.5. Phenotypic Correlation Analysis of Parameters

Correlation study helps to identify important traits in a breeding program and practice effective selection method. In this study, plant height, dry biomass, harvest index, thousand-seed weight and hectoliter weight depicted highly significant positive correlation(r= 0.54, 0.9, 0.61, 0.73 and 0.66) respectively to grain yield; whereas days to maturity, spike length, numbers of spikelet per spike and numbers of seeds per spike showed positive non significant correlation to grain yield ($P \leq 0.05$) (Table 6). Therefore, selecting genotypes with tall plant types, heavier above ground mass, larger seed size, effective assimilate partitioning capacity and higher flour return rate is important in attaining higher yield in bread wheat. Tkachur *et al*. (1978), Tayyar (2010), Mohibullah *et al*. (2011) and Beheshtizadeh *et al*. (2013) stated that plant height, spike length, number of spikelet per spike, number of seeds per spike, biomass yield and 1000-grain weight had positive correlation with grain yield. Grain yield is the result of comprehensive effects of traits. Hence, for bread wheat breeding works to be successful, breeders should consider the traits which have strong positive relation to grain yield.

Table 7. Phenotypic correlation of bread wheat genotypes for 10 traits across test environments in 2014 and 2015

	DM	PHT	SL	NSLPS	NSPS	DB	HI	TSW	HLW	**GYLD**
DM	1	0.39**	-0.25**	0.19**	0.34**	-0.03^{ns}	0.12 ^{ns}	-0.07	0.09^{ns}	**0.01^{ns}**
PHT		1	-0.11^{ns}	0.43**	0.39**	0.65**	0.08 ^{ns}	0.3**	0.39**	**0.54****
SL			1	0.17 *	0.11^{ns}	0.04^{ns}	0.17**	0.06^{ns}	0.08 ^{ns}	**0.12^{ns}**
NSLPS				1	0.62**	0.18**	-0.14	0.01^{ns}	0.09^{ns}	**0.07^{ns}**
NSPS					1	0.11^{ns}	0.09^{ns}	0.06^{ns}	0.09^{ns}	**0.11^{ns}**
DB						1	0.24**	0.54**	0.45**	**0.9****
HI							1	0.71**	0.65**	**0.61****
TSW								1	0.66**	**0.73****
HLW									1	**0.66****
GYLD										**1**

**** = Highly significant at P≤0.01, * = Significant at P≤ 0.05 and ns= nonsignificant**

DM= Days to Maturity, PHT= Plant Height, SL= Spike Length, NSLPS= Number of Spikelets per Spike, NSPS= Number of Seeds per Spike, DB= Dry Biomass, HI= Harvest Index,TSW= Thousand Seed Weight, HLW=Hectoliter Weight, and GYLD=GrainYield

4. CONCLUSION AND RECOMMENDATIONS

According to the study, genotypes' grain yield was highly affected by environments (locations and years) and the genetic composition of genotypes. The highest variation was accounted for by location (29 %) followed by genotype (18%) and location by year (18 %) and genotype by year (12%) effects. Genotypes' grain yield response was highest at Adet in 2014 cropping season, and at Debretabor in 2015 cropping season. Genotypes G4, G2, G11 and G9 were showed 12.41, 10.22, 4 and 3.45 qt/ha grain yield advantage over standard check (G7) respectively and 17.16, 14.97, 8.75 and 8.2 qt/ha grain yield advantage over local check (G12) respectively. Depending on AMMI, GGE biplot and different coefficients of stability, G4, G2, G11 and G9 were wide adaptable and relatively stable genotypes all over the test environments (locations and years) than the two checks. Therefore, these genotypes that had a higher mean grain yield in a wide range of environments are important to improve production

and productivity and crossing purpose due to their buffering capacity of the variability of environmental factors. In this study, plant height, dry biomass, harvest index, thousand seed weight and hectoliter weight were depicted highly significant positive correlation to grain yield. These traits should, therefore, be considered to improve grain yield in bread wheat breeding programs.

Therefore, based on the adaptability and stability of overall mean grain yield, recently released genotypes Gambo (G4), Ogolcho (G2) and Tsehay (G9) and relatively older genotypes Shorima (G11) and TAY (G7) could be recommended for production at the test environments in the Western Amhara Region. However, there is a need to study the effect of environmental/seasonal variation on rust disease occurrence.

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