Performance and Stability of Finger millet [*Eleusine coracana* (L.) Gaertn] Genotypes in Northwestern Ethiopia

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Abstract

Background: Finger millet is one of the neglected (orphan) crops which thrive even on marginal lands where other crops cannot perform well. To boost the productivity and production of the crop, improved varieties are a key input. However, effect of genotype by environment interaction hampers variety development process. This causes instability of genotypes across environments. Hence, information on performance and stability is of prime importance for breeders before releasing a certain variety of the crop.

Objective: This study was conducted to evaluate the performance and stability of finger millet genotypes for grain yield and other agronomic traits.

Materials and Methods: Sixteen finger millet genotypes were evaluated during the 2017, 2018 and 2019 main cropping seasons at Adet, Merawi and Finoteselam district in the Amhara Regional State using a randomized complete block design with three replications. Data were collected both on plot and plant basis, and then subjected to analysis of variance and Pearson correlation.

Results: The combined analysis of variance revealed significant variations due to genotype, environment and their interaction. A significant positive correlation was observed between yield related traits with grain yield, which is important for selection. Mean grain yields of the genotypes were ranged between 1.48 t ha^{-1} and 2.34 t ha^{-1}, which could be to genetic variability among genotypes and the environments. Variances due to environment and genotype by environment interaction were found to be greater than that of genotype, and there was a crossover effect. In such cases, stability analysis is a possible procedure to examine genotypes for stability. Thus, GGE bi-plot analysis showed variance among genotypes. Hence, G-6, G-7 and G-1 were found to be stable genotypes. Among them, G-7 was found to be superior to all other genotypes in terms of yield advantage and stability.

Conclusion: Genotypes exhibited variances in stability due to the effect of genotype by environment interaction (about 8.9%). Among all the genotypes, G-7 was found to be an ideal genotype with higher yield, stability, and moderate resistance to blast disease. Having such merits, the Ethiopian Variety Release Standing Committee has officially approved G-7 (AD14-SEL045) as a new variety with breeder name "*Adet-05*" for wider cultivation and use.

Keywords: Environment; Genotype x Interaction; Stability; Yield

1. Introduction

The world has faced challenges to produce more food to feed the growing population. Predictions indicate that agricultural production needs to increase by 60% to 110% by 2050 (Tilman *et al*., 2011). Rice, wheat and maize are currently feeding the world dominantly, providing the daily energy intake of more than 60% of the world population. With these few mega crops, it will be challenging to bridge the gap. Thus, working on neglected crops such as finger millet could have a significant contribution on future food production in the world. Finger millet belongs to a group of secondary crops that provide another 25% of the world's food energy (Opole, 2019). The crop occupies about 12% of global millet area and is cultivated in more than 25 African and Asian countries (Vetriventhan *et al*., 2015). In Ethiopia, the crop is mainly grown in the northern, northwestern and western parts of the country, especially during the main rainy season (Asfaw Adugna *et al*., 2011). It covers 0.48 million ha of land, ranking 6th among cereals in Ethiopia, of which, 54% (0.26 million ha) was cultivated in the Amhara Region, and from such 36.17% (0.094 million ha) was cultivated in West Gojjam zone alone (CSA, 2021).

Finger millet can grow in diverse agro-ecological conditions with minimal inputs, and generally thrives on marginal land where other crops cannot perform

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well (Hittalmani *et al.*, 2017). It serves as a dietary staple food crop in various regions of India and Africa especially for peoples living on marginal lands and with limited economic resources (Dagnachew Lule *et al.*, 2012). In addition, finger millet has high nutritional value and excellent storage qualities. It contains rich amounts of nutrients especially calcium as compared to other major cereals like wheat, rice and sorghum (Gupta *et al.*, 2017; Sharma *et al.*, 2017). Moreover, finger millet has various health benefits as it is linked to its high calcium, iron and dietary fiber content and is gluten-free (Adane Gebreyohannes *et al.*, 2021). Finger millet is grown mainly for its grain, which is utilized to make traditional food and drinks, while the stalks are used for livestock feed, construction and fuel (Adane Gebreyohannes *et al.*, 2021). Likewise, finger millet has various uses in the study area, mainly for food (*Injera* and local beverages) and feed.

Ethiopia is the center of origin and diversity for finger millet (de Wet *et al.*, 1984); however, the genetic potential of the crop is not fully exploited (Zigale Semahegn *et al*, 2021). Accordingly, the average productivity of the crop is estimated to be 2.5 t ha^{-1}, 2.54 t ha^{-1}, 2.58 t ha^{-1} in Ethiopia, in Amhara Regional State and in West Gojjam Zone, respectively (CSA, 2021), which is low as compared to its potential of 4–5 t ha^{-1} (Kebede Dessalegn *et al.*, 2019). This can be due to numerous obstacles including lack of commitment and little research attention, poor agronomic managements, high lodging, disease (mainly blast) and weed (Molla Fentie, 2012; Tafere Mulualem and Adane Melak, 2013). What is more, there has been lack of sustained efforts for the improvement of the crop and slow progress in development of new improved varieties (Erenso Degu *et al.*, 2009). Clearly, research effort particularly a strong breeding program has to be established in the country, and such efforts must be made in finger millet potential areas of the country and particularly in Amhara Region. The aforementioned production constraints and strategic drivers need to be incorporated in to Ethiopia's finger millet breeding and technology development so as to enhance finger millet productivity (Adane Gebreyohannes *et al.*, 2021).

In Ethiopia, formal research on finger millet improvement started in the early 1986s. Much of the early efforts focused on collection, conservation and characterization of finger millet germplasms for pure line selections. Since then, efforts have been underway to develop high yielding finger millet varieties (Erenso Degu *et al.*, 2009) by pure line selection and crossing. As a result, 29 finger millet varieties have been registered and released for wider production (EAA, 2022). However, most varieties are late maturing, susceptible to diseases, and have relatively low human nutrition value (Adane Gebreyohannes *et al.*, 2021). Thus, genetic variation is a prerequisite for a successful breeding program because it provides opportunities to breeders to select high yielding genotypes, or to combine or transfer genes. Yield potential and phenotypic expression of a given genotype depend on its genetics, environment and genotype by environment interaction. Selection of genotypes for wider adaptability is often limited by the existence of genotype by environment interaction, making the variety development process more complex and expensive (Yan *et al.*, 2001). So, the process needs due attention about the impact of genotype by environment interaction in genetic exploitation for efficient selection of superior genotypes (Kebede Dessalegn *et al.*, 2019).

Prior to release a certain variety of the crop plant breeders need to identify stable and high yielding genotypes under varying environmental conditions (Flores *et al.*, 1998). Thus, multi-environment trials are among the basic procedure to identify and recommend superior and stable genotypes with wide adaptation (Yan *et al.*, 2001). Performance of a given genotype is not necessarily the same under diverse agro-ecological conditions; some genotypes may perform well in certain environments but fail in several others. In such cases, researchers have to identify widely adapted and stable genotypes. Then, to identify stable genotypes, genotype by environment interaction must be partitioned in to stability statistics that are assigned to each genotype evaluated across a range of environments (Yayeh Zewudie and Bosland, 2000). Accordingly, Adet Agricultural Research Center has conducted a multi-environment experiment using different finger millet landraces collected from the Northwestern part of Ethiopia. The objective was to evaluate the performance and stability of the collected finger millet genotypes for yield and other agronomic traits, and identify stable, high yielding and disease resistant/tolerant finger millet genotypes for production.

2. Materials and Methods

2.1. Description of Study Areas

The experiment was conducted at Yilmana Densa (Adet), Mecha (Merawi) and Jabitehenan (Finoteselam) districts for three consecutive cropping years (2017–2019) under rain-fed condition. The brief descriptions of the testing sites are e presented in Table 1 and Figure 1.

Table 1. Description of the study areas.

Location	Altitude (m a.s.l)	Latitude	Longitude	Soil type	Average RF (mm)	Mean Temperature(C)
Adet	2200	11°17' N	37°28' E	Nitosol	110.02	18.58
Merawi	1890	11°39' N	37°05' E	Nitosol	140.12	20.10
Finoteselam	1940	10°41' N	37°15' E	Nitosol	87.58	21.90

Note: *m a.s.l. = Meters above sea level and RF = Rainfall. The weather variables were sourced from the National Meteorological Agency of Ethiopia (2017–2019).*

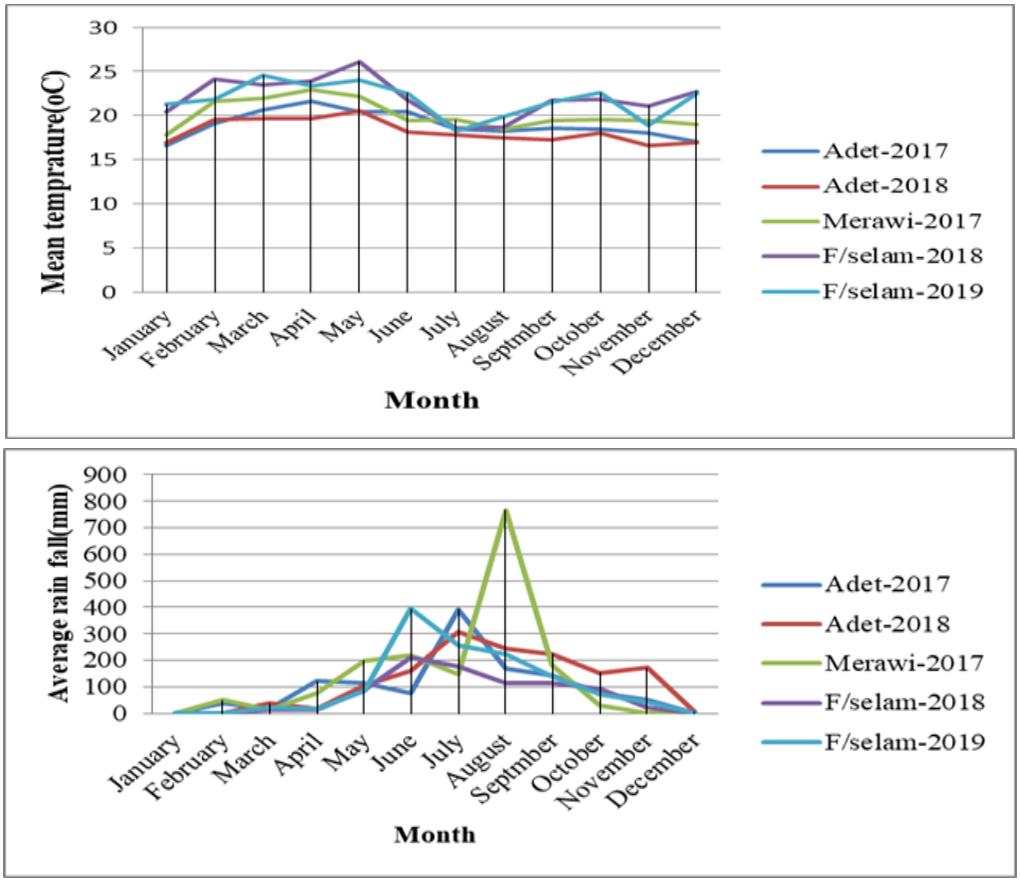

Figure 1. Monthly mean temperature and average rainfall of study areas.

2.2. Experimental Materials and Field Management

Sixteen finger millet genotypes, including local and standard checks were tested in randomized complete block design with three replications. Each plot consisted of four rows with row spacing of 0.4 m; and the size of the plot was 5 m x 1.6 m. P_2O_5 (46%), N (46%) and S (8.5%) nutrients were applied in the form of NPS and Urea fertilizers at the rate of 121 kg ha^{-1} and 50 kg ha^{-1}, respectively. Total amount of NPS was applied during sowing, whereas total amount of urea was applied at tillering stage of the crop. Other agronomic practices like weeding and hoeing were carried out as required.

2.3. Data Collection and Analysis

Data were collected both on plot and plant basis. Among plot basis, days to heading, days to maturity, head blast severity, and grain yield were recorded. However, fingers per ear, plant height, and finger length were recorded on plant basis. Then, the collected data were subjected to analysis of variance using SAS software. Treatments, environments, and blocks were class variables, whereas measured traits were response variables. Prior to analysis, the collected data were evaluated for homogeneity of error variance using Bartlett's test and followed by combined analysis of variance. Due to heterogeneity of error variances, the data of head blast score were transformed using Square-Root transformation procedure. Differences between treatment means were determined using LSD at 5% probability level and employed depending on significance of analysis of variance.

The collected data for individual environment was computed as follows:

$$Yij = \mu + Gi + Rj + eij$$

Where, Yij = observed value of genotype i in block j; μ = grand mean of the experiment; Gi = effect of variety i; Rj = effect of block; and j and eij = random error effect of variety i in block j. Whereas, the following statistical model was used for combined analysis across environments:

$$Yijk = \mu + Gi + Ej + GEij + Bkj + \varepsilon ijk$$

Where, Yijk = observed value of genotype i in block k of environment (location) j, μ = grand mean, Gi = effect of genotype i, Ej= environment or location effect, GEij = the interaction effect of genotype i with environment j, Bkj = the effect of block k in location (environment) j, and εijk = error (residual) effect of genotype i in block k of environment j.

Phenotypic and genotypic correlations were estimated by the standard procedure suggested by Kashiani and Saleh (2010) from the corresponding variance and covariance components. Thus, correlation

between traits using means of each variety was calculated as:

Phenotypic correlation coefficient = rpxy= $\frac{\text{COV pxy}}{\sqrt{\sigma^2\text{px}.\sigma^2\text{py}}}$

Genotypic correlation coefficient = rgxy = $\frac{\text{COV}gxy}{\sqrt{\sigma^2\text{gx}.\sigma^2\text{gy}}}$

Where, rp(xy) = phenotypic correlation coefficient between trait x and y, rg(xy) = genotypic correlation coefficient between trait x and y, COVp(xy) = phenotypic covariance between trait x and y, COVg(xy) = genotypic covariance between trait x and y, Vp(x) and Vp(y) = phenotypic variance for trait x and y, and Vg(x) and Vg(y) = genotypic variance for trait x and y.

Combined analysis of variance was carried out using a mixed model, genotype as a fixed and location and replication as a random. Then, effects of environment, genotype and their interactions were examined; finally grain yield data were graphically visualized for interpreting genotype by environment interaction. Thus, additive main effects of environment, genotype and their interaction were estimated by using GenStat software through GGE bi-plot analytical procedure as suggested by Yan *et al.* (2000). Then, all genotypes had evaluated for its stability using the following model as suggested by Yan *et al.* (2000):

$Yij = yij + l_1xi_1hj_1 + l_2xi_2hj_2 + \varepsilon ij$

Where, Yij = productivity mean of cultivar i in environment j, yij = general mean of the cultivars in environment j, $l_1xi_1hj_1$ = first principal component (PC1), $l_2xi_2hj_2$ = second principal component (PC2), l_1 and l_2 = eigenvalues associated with PC1 and PC2, respectively, xi_1 and xi_2 = values of the first and second principal components, respectively, for cultivar i, hj_1 and hj_2 = values of the first and second principal components, respectively, for environment j, and εij = error ij associated with the model.

3. Results and Discussion

3.1. Analysis of Variance

The analysis of variance revealed significant differences were observed for agro-morphological traits except number of fingers per ear among the tested finger millet genotypes. The result revealed that, genotypes performed differently for the assessed agronomic traits across the target environments, implying the presence of genetic variability among genotypes and environmental difference. Genotypes were found to be variable in phenological and agronomic traits, exhibited broad spectrum of ranges between the maximum and minimum mean values. In line with this result, Wossen Tarekegne *et al.* (2019) reported that such broad spectrum of variability in phenological and yield related traits across environments could be due to the inherent genetic differences among the varieties; while among locations, environment plays a significant role in influencing the expression and variability of these traits. In addition, Hailegebrial Kinfe *et al.* (2017) also revealed that, yield variability among environments can be due to variation in rainfall amount and distribution, temperature and soil type.

In this study, most of genotypes relatively took intermediate to high number of days for heading and maturity (Table 2). Despite finger millet can resist terminal moisture stress, earliness is an important parameter to escape and make adequate use of available soil moisture during the growing period. In addition, yield related traits like plant height, and finger length showed significant ($P < 0.01$) differences. However, there was a non-significant difference for number of fingers per ear (Table 2). This is in agreement with the findings of Chemeda Daba and Gemechu Keneni (2010) who found significant ($P < 0.05$) differences in all traits of finger millet except number of fingers per main ear which was non-significant.

Table 2. Phenological and agronomic mean performance genotypes across environments.

Genotype code	DH	DM	PH (cm)	FPE	FL (cm)	HBS (%)
G-1	104.50	175.10	87.30	7.50	10.00	7.00 (2.58)
G-2	101.70	174.00	84.30	6.40	8.90	7.53 (2.68)
G-3	97.00	173.20	83.50	5.30	10.20	9.53 (2.92)
G-4	103.40	173.00	75.50	5.80	8.00	7.67 (2.57)
G-5	99.80	174.30	61.90	5.80	8.40	6.67 (2.40)
G-6	109.10	175.80	86.70	6.60	9.50	5.33 (2.01)
G-7	99.50	175.30	85.90	7.20	8.90	7.33 (2.52)
G-8	104.30	177.40	76.90	5.80	9.50	6.00 (2.12)
G-9	106.70	176.40	88.00	6.80	10.70	8.33 (2.78)
G-10	105.40	175.40	81.70	7.50	9.60	5.00 (2.15)
G-11	105.20	175.90	82.50	6.70	9.20	6.00 (2.31)
G-12	102.50	175.60	85.60	5.20	11.20	6.13 (2.44)
G-13	97.80	172.60	74.70	6.80	10.60	24.47(4.62)
G-14	101.00	173.90	77.80	4.90	7.90	6.00 (2.42)
G-15	87.40	180.50	68.00	5.50	6.70	24.33(4.40)
G-16	101.00	172.70	80.40	6.40	13.60	16.33(3.84)
Mean	101.60	175.10	80.00	6.30	9.60	2.80
G	***	***	***	ns	***	***
E	***	***	***	ns	***	***
G*E	***	***	***	ns	***	***
LSD	1.34	11.17	4.05	–	3.27	0.56
CV (%)	2.20	10.50	8.30	15.10	5.10	27.93

Note: *G-1 = AD14-SEL015; G-2 = AD14-SEL034; G-3 = AD14-SEL035; G-4 = AD14-SEL036; G-5 = AD14-SEL039; G-6 = AD14-SEL042; G-7 = AD14-SEL045; G-8 = MR14-SEL054; G-9 = MR14-SEL064; G-10 = MR14-SEL073; G-11 = MR14-SEL087; G-12 = FS14-SEL089; G-13 = Standard check-1 (Necho); G-14 = Standard check-2 (Mecha); G-15 = Standard check-3 (U-15); and G-16 = Local check. DH = Days to heading; DM = Days to maturity; PH = Plant height; FPE = Fingers ear^{-1}; FL = Finger length; and HBS = Head blast score. G = Genotype; E = Environment; and G*E = Genotype by environment interaction. *** = very highly significant at P ≤ 0.001; ns = non-significant at P < 0.05; LSD = Least significant difference; and CV = Coefficient of variations.*

Table 3. Grain yield mean performance of genotypes across years and locations.

Genotype code	2017			2018		2019	Mean GY (t ha^{-1})
	Adet	Merawi	Finoteselam	Adet	Finoteselam	Finoteselam	
G-1	2.25	1.76	3.64	3.28	1.09	1.07	2.18
G-2	2.08	1.44	2.78	2.72	1.28	0.82	1.85
G-3	2.07	2.08	3.21	2.63	1.80	1.21	2.17
G-4	1.77	1.41	2.58	2.95	1.24	1.45	1.90
G-5	2.09	2.26	2.25	2.84	1.21	1.04	1.95
G-6	2.03	1.89	3.66	3.29	1.44	1.25	2.26
G-7	2.33	1.93	3.51	3.27	1.52	1.50	2.34
G-8	2.04	2.20	3.11	3.53	1.16	1.66	2.28
G-9	1.92	1.62	3.24	3.17	0.97	0.91	1.97
G-10	1.89	1.86	3.12	3.66	1.40	1.10	2.17
G-11	1.74	1.98	3.86	2.75	1.28	0.97	2.10
G-12	1.64	1.46	3.16	2.99	1.33	1.40	2.00
G-13	2.08	1.48	2.72	2.81	1.29	1.23	1.93
G-14	2.17	1.82	2.85	3.10	1.50	1.23	2.11
G-15	1.22	1.42	2.34	0.88	1.86	1.15	1.48
G-16	2.59	1.21	2.63	3.06	1.63	1.00	2.02
Mean	2.00	1.74	3.04	2.95	1.39	1.19	1.94
Sign. (G)	*	ns	*	*	**	ns	***
LSD	0.56	–	0.74	1.05	0.40	–	0.27
CV (%)	16.90	25.00	14.60	21.30	17.40	19.50	22.90

Note: *G-1 = AD14-SEL015; G-2 = AD14-SEL034; G-3 = AD14-SEL035; G-4 = AD14-SEL036; G-5 = AD14-SEL039; G-6 = AD14-SEL042; G-7 = AD14-SEL045; G-8 = MR14-SEL054; G-9 = MR14-SEL064; G-10 = MR14-SEL073; G-11 = MR14-SEL087; G-12 = FS14-SEL089; G-13 = Standard check-1 (Necho); G-14 = Standard check-2 (Mecha); G-15 = Standard check-3 (U-15); and G-16 = Local check. G = Genotype and GY = Grain yield. *** = very highly significant at P ≤ 0.001; ** = highly significant at P ≤ 0.01; * = significant at P ≤ 0.05; ns = non-significant at P > 0.05; LSD = Least significant difference; and CV = Coefficient of variations.*

Besides, the tested genotypes showed differences in head blast reaction, implying considerable genetic variability for disease resistance. Among the tested genotypes, standard check varieties (*Necho* and *U-15*) were highly susceptible to blast, followed by local check, while the rest of genotypes exhibited medium to low susceptibility reaction. However, the degree of head blast severity was significant among environments. This might have occurred due to dissimilarity in weather conditions of the testing districts (Figure 1). In accordance with this, Wossen Tarkegne *et al.* (2019) found susceptibility difference for head blast disease among the tested finger millet varieties at Merawi and Adet, and concluded that, the variation might have occurred due to genetic variation among finger millet varieties and dissimilarity in weather conditions and altitudes of the research areas.

Analysis of variance for grain yield also revealed significant differences among genotypes, environments and their interactions (Table 3). Mean grain yield of genotypes were ranged between 1.48 t ha^{-1} and 2.34 t ha^{-1} with a grand mean of 1.98 t ha^{-1} (Table 3). This can be attributed to the variability among the tested finger millet genotypes and the test environments. Similarly, Kebede Desalegn *et al.* (2019) found a significant variation on grain yield among black-seeded finger millet genotypes. Genetic variations in finger millet have been also conveyed in previous studies (Ganapathy *et al.*, 2011; Hailegebrial Kinfe *et al.*, 2017; Ashok *et al.*, 2018; Yaregal Damtie *et al.*, 2019; Manoj *et al.*, 2019). They all reported that, the variation among traits of finger millet genotypes is very important for every breeding program as they can either affect yield positively or negatively depending on the variation in question. High variability brings much needed information for genetic improvement program of finger millet (Manoj *et al.*, 2019). Thus, measurement and evaluation of variability are essential steps in drawing meaningful conclusions from a given set of phenotypic observations (Joshi *et al.*, 2007).

3.2. Stability Analysis

Analysis of variance for grain yield across environments revealed significant ($P < 0.01$) variations due to genotypes, environments and their interaction (Table 3). Thus, the variations that occurred were estimated to be due to genotypic difference (4.63%), environmental variability (71.47%) and their interactions (8.9%) (Table 4). In line with the present result, Dagnchew Lule *et al.* (2014) also reported significant genotype by environment interaction for finger millet varieties tested across environments in Ethiopia. In the present study, the variation explained by environment and genotype by environment interaction was greater than that of the genotype (Table 4), suggesting the importance of stability analysis to identify a widely adapted or stable genotype. Similarly, Asfaw Adugna *et al.* (2011) found 2.5%, 79.1% and 18.3% of the total sum of squares was attributed to genotypes, environments and genotype by environment interaction effects. In addition, Molla Fentie *et al.* (2013) reported that, the magnitude of the genotype by environment interaction sum of squares was more than three times than for genotypes, indicating that there were substantial genotypic responses across environments. A significant genotype by environment interaction is an indication of unstable performance of genotypes across environments. In such cases, stability analysis is a possible procedure to examine the performance of genotypes across environments. Based on this, one of the analytical procedures called GGE bi-plot was used for the present study to estimate genotypic stability. The bi-plot for grain yield explained 76.04% of the total variation (57.62% and 18.42% by PC1 and PC2, respectively) (Figure 2).

Table 4. Combined analysis of variance for grain yield of finger millet genotypes.

Source of variation	df	SS	MS	Pr > F	Explained variation
Environment	5	165.34	33.07	<.0001	71.47%
Blocks (Environment)	12	6.28	0.52	0.0002	2.72%
Genotype	15	10.70	0.71	<.0001	4.63%
Genotype*Environment	75	20.59	0.27	0.0015	8.9%
Error	180	28.44	0.16		
Total	287	231.35			

Note: *SS = Sum square; MS = Mean square; and df = degrees of freedom.*

Among GGE bi-plot procedures, ranking of genotypes relative to ideal genotype is a common tool. An ideal genotype should have a high mean yield combined with a low degree of fluctuation under different environments (Yan and Tinker, 2005). In the present study, the bi-plot for grain yield explained 76.04% of the total variation (57.62% and 18.42% by PC1 and PC2, respectively). Thus, G-7 and G-1 being at the center of the concentric circle can be considered as ideal genotypes because they have low genotype by environment interaction, better yield and consistency across environments. Genotypes like G-6, G-8, G-10 and G-9 are good genotypes as they are close to the center of concentric circle and average environmental axis, and are less responsive to the genotypic by environment interaction. However, G-15 and G-16 were found to be less stable as they are far apart from the average environmental axis and average environments coordinate (Figure 2). Various other studies have also found stable genotypes by GGE bi-plot analysis through ranking plot relative to ideal genotype (Dagnchew Lule *et al.*, 2015; Chemeda Birhanu *et al.*, 2020; Dagnchew Lule *et al.*, 2020).

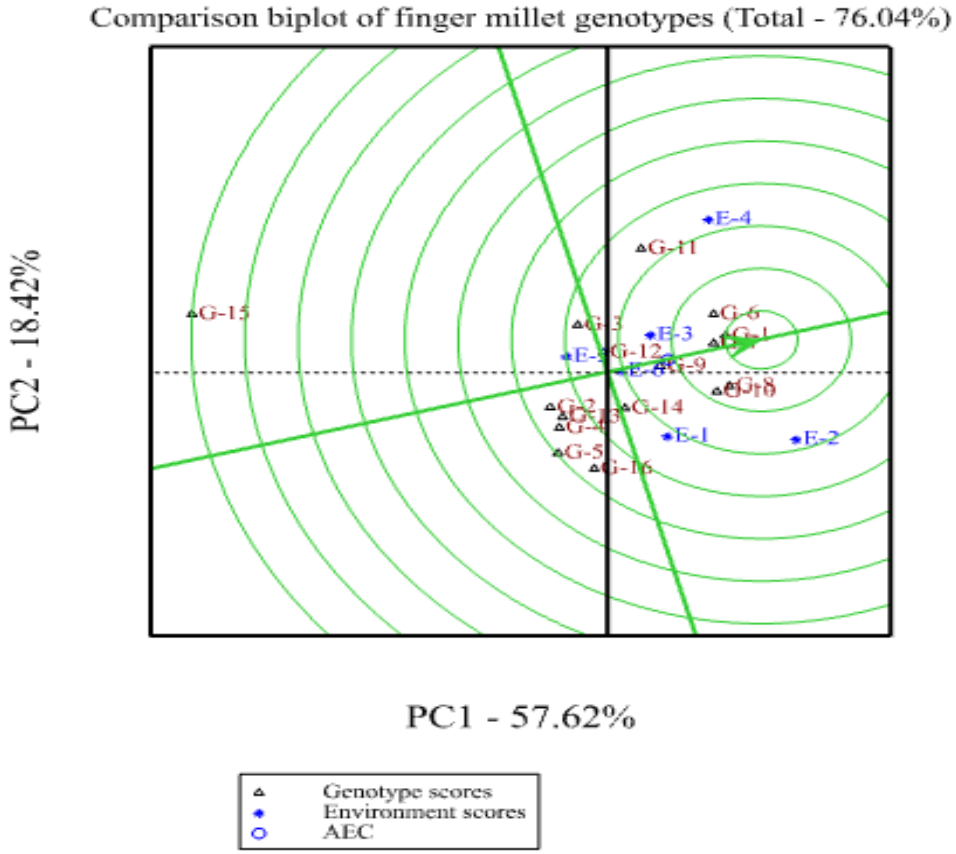

Figure 2. Comparison plot for ranking genotypes relative to ideal genotype [Note: *E-1 = Adet-2017; E-2 = Adet-2018; E-3 = Merawi-2017; E-4 = Finoteselam-2017; E-5 = Finoteselam-2018; E-6 = Finoteselam-2019; G-1 = AD14-SEL015; G-2 = AD14-SEL034; G-3 = AD14-SEL035; G-4 = AD14-SEL036; G-5 = AD14-SEL039; G-6 = AD14-SEL042; G-7 = AD14-SEL045; G-8 = MR14-SEL054; G-9 = MR14-SEL064; G-10 = MR14-SEL073; G-11 = MR14-SEL087; G-12 = FS14-SEL089; G-13 = Standard check-1 (Necho); G-14 = Standard check-2 (Mecha); G-15 = Standard check-3 (U-15); and G-16: Local check*].

The second employed GGE bi-plot analytical procedure was ranking genotypes according to mean performance versus stability. In such method, lines perpendicular to the average environmental axis measures the stability of genotypes in either direction (Kaya *et al.,* 2006). Genotypes with smallest perpendicular line and close to the average environmental coordinate are called stable genotype. Thus, genotypes that had PC1 score > 0 were identified to be high yielder, while genotypes that had PC1 < 0 identified to be as low yielders. In the present ranking plot, it is possible to say that almost all genotypes except G-5, G-15 and G-16 have very short to medium perpendicular line to the average environmental axis, indicating their relative stability. Those genotypes having long perpendicular lines indicate their responsiveness to the varying environmental variation, and they are unstable. More precisely, G-9, G-7 and G-1 has very short perpendicular lines to average environmental axis and are close to average environmental coordinate (Figure 3). In accordance with the present result, various investigators also found stable finger millet genotypes (Dagnachew Lule *et al.*, 2015; Amare Seyoum *et al.*, 2019; Chemeda Birhanu *et al.*, 2020; Dagnachew Lule *et al.*, 2020).

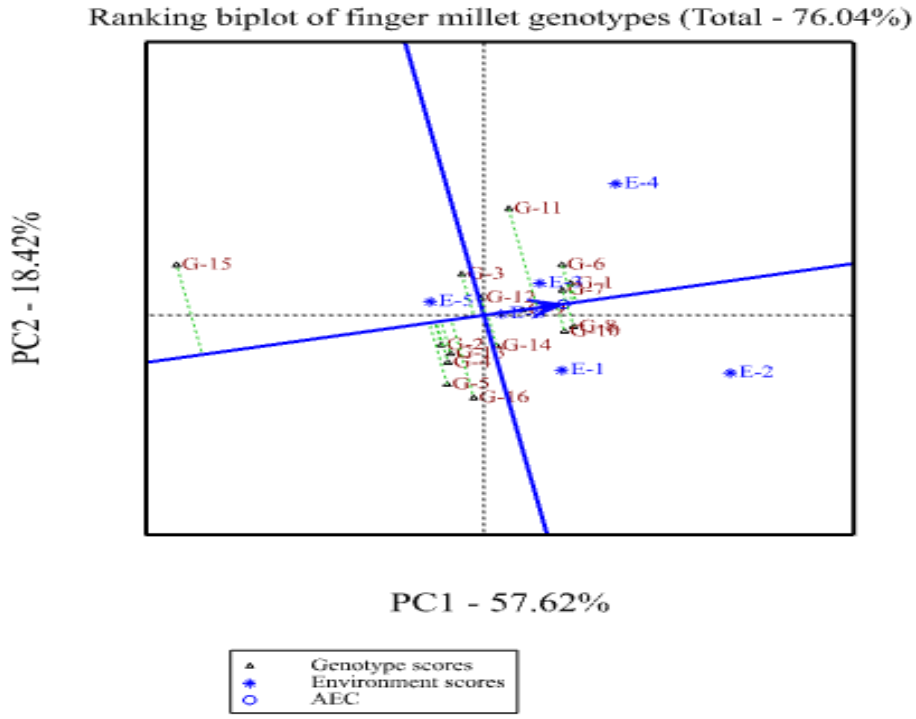

Figure 3. Ranking plot for ranking genotypes based on mean performance and stability [Note: *E-1 = Adet-2017; E-2 = Adet-2018; E-3 = Merawi-2017; E-4 = Finoteselam-2017; E-5 = Finoteselam-2018; E-6 = Finoteselam-2019; G-1 = AD14-SEL015; G-2 = AD14-SEL034; G-3 = AD14-SEL035; G-4 = AD14-SEL036; G-5 = AD14-SEL039; G-6 = AD14-SEL042; G-7 = AD14-SEL045; G-8 = MR14-SEL054; G-9 = MR14-SEL064; G-10 = MR14-SEL073; G-11 = MR14-SEL087; G-12 = FS14-SEL089; G-13 = Standard check-1 (Necho); G-14 = Standard check-2 (Mecha); G-15 = Standard check-3 (U-15); and G-16: Local check*].

The other GGE bi-plot analytical procedure used was the "which won where" pattern analysis. Among the GGE bi-plot parameters, this parameter has most attractive features as it enables to show which genotypes won where and more importantly, it enables to classify mega environments. Off course, classifying environments by considering locations and years as a separate environment is not a common procedure. Because effect of seasonal variations which take different environments of the same location will fell on different clusters, and bring difficulties in environmental classification and exploiting genotype by environment interaction. In the current scatter polygon, genotypes fell in to five sections and the test environments fell in to five mega environments. Environments grouped inside the same polygon had similar influence on the genotypes. Thus, E-3 and E-4 were grouped in one mega environment whereas the remaining testing environments were grouped individually (Figure 4).

Varieties and environments found inside the polygon were less responsive to environment stimuli. Genotypes from the polygon vertex that were grouped in any one of the environments are non-fitted genotypes for the tested environment. In the present study, the vertex genotypes, G-15, G-16 and G-11 had no corresponding environment and hence, have the lowest mean grain yield across environments (Figure 4). These genotypes were the best or the poorest in some or all of the environments because they were far apart from the origin of the bi-plot. On the other side, genotypes found within one environmental polygon were found to be more adaptable for that environment. For example, genotypes like G-7, G-1 and G-6 were found to be on one environmental polygon (Figure 4), and are best adaptable and performed well in that environment. Likewise, Wedajo Gebre *et al.* (2018) and Amare Seyoum *et al.* (2019) found similar results from finger millet genotypes tested in Ethiopia.

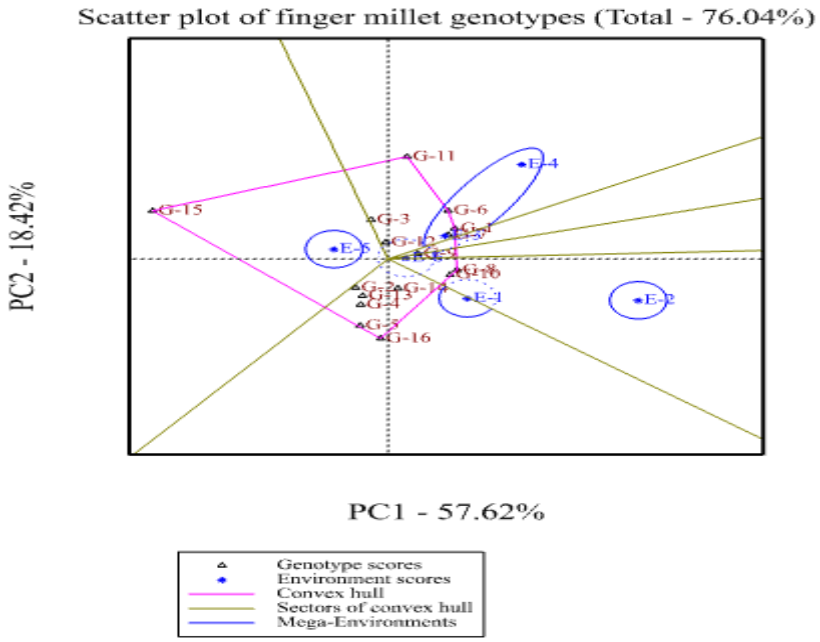

Figure 4. Scatter plot for which-won-where pattern analysis [Note: *E-1 = Adet-2017; E-2 = Adet-2018; E-3 = Merawi-2017; E-4 = Finoteselam-2017; E-5 = Finoteselam-2018; E-6 = Finoteselam-2019; G-1 = AD14-SEL015; G-2 = AD14-SEL034; G-3 = AD14-SEL035; G-4 = AD14-SEL036; G-5 = AD14-SEL039; G-6 = AD14-SEL042; G-7 = AD14-SEL045; G-8 = MR14-SEL054; G-9 = MR14-SEL064; G-10 = MR14-SEL073; G-11 = MR14-SEL087; G-12 = FS14-SEL089; G-13 = Standard check-1 (Necho); G-14 = Standard check-2 (Mecha); G-15 = Standard check-3 (U-15); and G-16: Local check].*

3.3. Correlation of Traits

Estimates of genetic and phenotypic correlation coefficients were done among all traits (Table 5). All measured traits showed positive phenotypic and genotypic correlation with each other and with grain yield; however, the magnitude of correlation varied from very highly significant to non-significant level of difference. Phenotypically grain yield showed positive significant phenotypic correlation with days to heading ($r = 0.38^{***}$), days to maturity ($r = 0.43^{***}$), plant height ($r = 0.55^{***}$) and number of fingers per ear ($r = 0.25^{***}$) but showed non-significant correlation with finger length ($r = 0.005^{ns}$). Likewise, traits like number of fingers per ear and finger length had significant correlation whereas plant height and pheonological traits showed positive but non-significant association with grain yield (Table 5). In accordance with this, Manoj *et al.* (2019) reported a significant positive phenotypic association of most of the agronomic traits with grain yield. Similarly, Devaliya *et al.* (2017) found a positive but non-significant correlation among finger millet traits. Sao *et al.* (2016) also found a positive phenotypic and genotypic correlation between days to maturity and grain yield. However, Abunu Marefia *et al.* (2022) and Kebere Bezaweletaw *et al.* (2006) found significant negative correlation between grain yield and days to maturity for the tested finger millet genotypes. Likewise, Devaliya *et al.* (2017) found a non-significant negative correlation among phenological traits and grain yield. Positive association of trait suggests selecting for the trait with high positive correlation would improve the grain yield of respective crop. Positive association between phenological traits with grain yield implies that the tested late maturing genotypes can give better yield than the early maturing ones. But this occasion may be true if the rainfall can be extended, unless terminal moisture stress may force the crop to be mature forcedly. In line with this, Falconer (1989) stated selection for one trait can indirectly introduce changes in the other trait in positive or negative direction due to either genetic linkage or presence of pleiotropic gene effect or both.

In the current study, the magnitude of genotypic correlation coefficients for most of the traits was higher than their corresponding phenotypic correlation coefficients (Table 5). This indicates that, even though there is a strong inherent association between characters, its expression is lessened due to influence of environment and considering the importance of phenotypic correlation. In line with the results of this study, Andualem Wolie and Tadesse Dessalegn (2011) reported that the magnitudes of genotypic correlation coefficients for most of the characters were higher than their corresponding phenotypic correlation coefficients, except a few cases, which indicate the presence of inherent association among various traits. Thus, information on the phenotypic and genotypic interrelationships of grain yield with its component characters and among the component characters themselves would be useful for the breeder in developing an appropriate selection strategy. Since, yield is a complex character and is influenced by several traits and selection based on yield is usually not much effective, indirect selection on the basis of desirable

component characters could be of great use (Mahanthesha *et al.*, 2018).

Table 5. Phenotypic (upper diagonal) and genotypic (lower diagonal) correlation coefficients of measured parameters.

Parameters	DH	DM	PH	FL	FPE	GY
DH	–	0.48^{***}	0.52^{***}	0.02^{ns}	0.19^{***}	0.38^{***}
DM	0.89^{***}	–	0.22^{***}	0.01^{ns}	0.29^{***}	0.43^{***}
PH	0.58^{*}	0.56^{*}	–	0.10^{ns}	0.39^{***}	0.55^{***}
FL	0.20^{ns}	0.38^{ns}	0.48^{ns}	–	0.11^{ns}	0.05^{ns}
FPE	0.42^{ns}	0.34^{ns}	0.41^{ns}	0.37^{ns}	–	0.25^{***}
GY	0.32^{ns}	0.39^{ns}	0.48^{ns}	0.53^{*}	0.43^{*}	–

Note: *DH = Days to heading; DM = Days to maturity; PH = Plant height; FPE = Fingers ear^{-1}; and FL = Finger length. *** = very highly significant at P ≤ 0.001); highly significant at P ≤ 0.01; and ns = non-significant at P ≤ 0.05.*

4. Conclusion and Recommendation

The results of this study have demonstrated a highly significant ($P < 0.01$) effect of genotypes, environments and genotype by environment interaction on agronomic and yield traits. Genotype by environment interaction was found to be greater than that of the genotype. There was a crossover in which genotypes change their ranks from one environment to another. This clearly indicates multi-environment trials would be useful for breeders to identify stabile genotypes. Even though the genotype by environment interaction is greater, performances of genotypes were differed significantly. This could be an indicative of the necessity of testing finger millet genotypes at multiple locations so as to identify promising ones for wider and specific adaptation. Moreover, there was a positive correlation among yield related traits and grain yield, which would be useful for breeders in developing an appropriate selection strategy. The existing high environmental and genotype by environment interaction variance allowed us to further partition it using stability measures. Accordingly, the GGE bi-plot analytical procedure was used and showed the tested genotypes are variable in stability for the environments in which they were tested. As a result, G-7 (AD14-SEL045) was found to be a superior genotype, and officially released as a commercial variety with breeder name '*Adet-05*' for the Northwestern part of Ethiopia as well as for areas with similar agro-ecologies. Therefore, the variety has to be delivered for beneficiaries.

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