

**Full Length Research****AMMI and GGE bipolt analysis of Genotype x Environment Interaction and Yield Stability of Pearl Millet Genotypes [*Pennisetum glaucum* (L.) R. Br.] in Moisture Stressed Areas of Ethiopia****Amare Seyoum, Zigale Semahegn and Adane Gebreyohannes**Ethiopian Institute of Agricultural Research, Melkassa Agricultural Research Center, National Sorghum and Millet research program. \*Corresponding Author: [seyoumamare99@gmail.com](mailto:seyoumamare99@gmail.com) , P.O. Box 436, Adama

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The yield performance of crop varieties is highly affected by genotype x environment interaction, which is the major concern to plant breeders while developing improved varieties. In Ethiopia, high yielding and stable pearl millet varieties that withstand drought in the dry lowland areas are limited. In view of this, the yield performance of 24 pearl millet genotypes and one standard check were tested at seven environments with the objectives of estimating the magnitude of GxE for grain yield and to identify high yielder and stable genotypes across environments. The experiment was conducted using Randomized Complete Block Design with three replications. The combined analysis of variance across environments showed highly significant ( $P \leq 0.001$ ) difference among environments, genotypes and significant ( $P \leq 0.05$ ) interactions for grain yield studied. The result of the combined AMMI analysis of variance showed that the total variation in grain yield was attributed to environment (73.39 %), genotype (5.47 %) and GxE (21.14 %) effects. Based on AMMI and GGE biplot showed that genotypes, SDMV 95032, ICTP8203 and KAT PM 1 showed high yield and they were stable across environments. Therefore, they will be advanced to variety verification trail for evaluation and verification by variety verification committee in the coming cropping season. Whereas, GGE biplot is also revealed that the ideal genotype and ideal environment are Okoa and Mehoni 2014, respectively. Generally, this study showed the importance of testing pearl millet genotypes for their yield and stability across diverse dry lowland areas of Ethiopia.

**Key words:** Grain yield, Genotypes, Genotype x Environment interaction, Yield stability**Cite this article as:** Amare S, Zigale S, Adane G (2019). AMMI and GGE bipolt analysis of Genotype x Environment Interaction and Yield Stability of Pearl Millet Genotypes [*Pennisetum glaucum* (L.) R. Br.] in Moisture Stressed Areas of Ethiopia.. Acad. Res. J. Agri. Sci. Res. 7(4): 190-201**INTRODUCTION**

Pearl millet (*Pennisetum glaucum* (L.) R. Br.) is a C4 tropical and a highly cross pollinated crop (Jat *et al.*, 2012). It is the most drought-tolerant cereal crop grown in the arid and semi-arid regions of the world (Bhagavatula

*et al.* 2013). It is ranked as the sixth most important cereal in the world. In east and central Africa, it is ranked second among stable foods (Lagat *et al.*, 2018).

Pearl millet is a staple food for the majority of poor far

mers and also a vital fodder crop for livestock in arid and semi-arid regions of world. It is commonly grown as rainfed cereal crop in the arid and semi-arid regions of Africa and southern Asia. In Ethiopia, it is also a crop of hot and dry climates and can be grown in areas where rainfall is limited. Even with minimal rainfall pearl millet can typically produce a yield. In addition, it is providing food for human, pearl millet stems are used for the construction of hut walls, fences and thatches, and the production of brooms, mats, baskets, sunshades, etc. (Wedajo, 2014). The crop is also a useful foodstuff since it has neither tannins nor other compounds that decrease digestibility found in sorghum. Besides, among all cereals (maize, sorghum, finger millet etc.) pearl millet is the most nutritious with high levels of protein (up to 12%) and energy (3600 K cal/kg). It has a rich source of protein, grain iron (Fe) and zinc (Zn) (Lagat *et al.*, 2018).

In spite of several advantages, Production and productivity of pearl millet in some parts of Ethiopia is low partly due to the effect of many abiotic (drought, low soil fertility) and biotic (diseases, insects etc.) factors. The major option to control these constraints is through breeding and selecting genotypes adapted to drought prone environments (Lagat *et al.*, 2018). However, the potential performance of improved genotypes under marginal conditions is always influenced by the effect of genotype by environment interaction (GxE). These lead to selection of genotypes not suitable for particular environments and finally leading to low yield. It is thus important to assess GxE effect before releasing varieties.

The concepts of GxE and yield stability have been the impediments to the breeders for a long period of time. A significant GxE for a quantitative trait is known to reduce the usefulness of the genotype means over all environments for screening out and proceeding superior genotypes to the next stage of selection (Pham and Kang, 1988). If there were no GxE, selection would be greatly simplified because the 'best' genotype in one environment would also be the 'best' genotype for all target environments (Basford and Cooper, 1998).

The main reason for change in rank order in the performance of genotypes over environments is the existence of GxE. To solve GxE problem, trials are usually evaluated over several environments to ensure that the selected genotypes have a high and stable performance over diverse range of environments. The data generated in these trials are analyzed for GxE by several methods. The different statistical procedures are in fact accessible to analyze and determine the results of multi-environment trials and GxE data. However, two multivariate analysis such as AMMI and GGE biplot analysis has been made in this study. Crossa (1990) reported that the Additive Main effect and Multiplicative Interaction (AMMI) model proved to be a powerful tool in analyzing GxE patterns. AMMI model can also be used to determine stability of the genotypes across environments using the IPCAs (Interaction Principal Component Analysis). Moreover, the

GGE biplot model is a very significant model to analyze MET data and to interpret complex GxE interaction (Yan 2001; Yan and Tinker 2006). It can effectively detect the interaction pattern graphically besides identifying 'which won- where' and delineation of mega-environments among the testing locations (Yan *et al.* 2007). GGE (genotype plus genotype by environment interaction) analysis partitions G + GxE into principal components through singular value decomposition of environmentally centered yield data (Yan, 2001).

Various studies have been conducted to analyze the effect of GxE interaction in pearl millet varieties (Gupta *et al.*, 2013; Wedajo, 2014; Lubadd *et al.*, 2017; Lagat *et al.*, 2018).

Yield stability is one of the challenges facing plant breeders in developing widely adapted varieties with superior yield (Asfaw, 2007). The national sorghum and millet program have been working and able to identify single pearl millet variety for yield that resist or tolerate harsh environmental conditions and produce consistently better grain yield (Wedajo, 2014). Information on nature and extent of genotype by environment interaction of pearl millet genotypes is important to identify superior and stable variety that can adapt to a wide range of environments and specifically adapted genotypes in drought areas of Ethiopia (Wedajo, 2014). However, there is no information on genotype by environment interaction of pearl millet genotypes developed by the ICRISAT. Therefore, this study was conducted with the objective of estimating the magnitude of GxE for grain yield and to identify high yielder and stable genotypes across environments.

## MATERIAL AND METHODS

### Description of the test environments

Field experiments were conducted in seven environments; in Mieso during 2013 and 2014; in Maitseberi and Babile during 2013; in Humera, Mehoni and Sheraro during 2014 main cropping seasons. The detailed agro-ecological features of the environments are presented in Table 1.

### Genetic materials

Planting materials (Table 2) used for the experiment comprised of twenty four pearl millet genotypes, which were introduced from International Crops Research Institute for the Semi-Arid Tropics (ICRISAT) and one pearl millet variety Kola-1 (released from Melkassa Agricultural Research Center for low moisture stress areas of the Ethiopia) as a standard check, adapted to the dry lowland areas of Ethiopia.

**Table 1:** Agro-ecological features of the experimental environments.

Location	Longitude	Latitude	Altitude in m.a.s.l	Soil type	Rainfall in mm	Minimum T°	Maximum T°
Mieso	39°21'E	8°30'N	1470	vertisol	571.9	16.0	31.5
Maitseberi	-	-	1444	sandy loam	789.3	-	-
Babile	-	-	-	-	-	-	-
Mehoni	39° 42' E	12° 41' N	1578	vertisol	605.4	22	32
Sheraro	38°9' E	14°6' N	1179	vertisol	615.0	20.4	33.7
Humera	36°37'E	14°1'N	609	Chronic vertisol	576.4	18.8	37.6

Source: National Metrology data of 2013 and 2014 main cropping season, m.a.s.l = meters above sea level, To = Temperature.

**Table 2:** Description of pearl millet genotypes tested at seven environments during 2013 and 2014 main cropping season.

Genotype code	Genotype	Source	Status
1	SDMV90031	13ICRISAT RPMVT1	Advanced through selection
2	ICMV 88908	13ICRISAT RPMVT3	Advanced through selection
3	ICMV 91450	13ICRISAT RPMVT4	Advanced through selection
4	ICMV 93771	13ICRISAT RPMVT5	Advanced through selection
5	ICMV 94133	13ICRISAT RPMVT6	Advanced through selection
6	ICMV 94136	13ICRISAT RPMVT7	Advanced through selection
7	ICMV 94151	13ICRISAT RPMVT8	Advanced through selection
8	ICMV 96603	13ICRISAT RPMVT9	Advanced through selection
9	KAT PM 1	13ICRISAT RPMVT10	Advanced through selection
10	Kat PM 2	13ICRISAT RPMVT11	Advanced through selection
11	ICTP8203	13ICRISAT RPMVT12	Advanced through selection
12	Okashana 2	13ICRISAT RPMVT 13	Advanced through selection
13	Okoa	13ICRISAT RPMVT14	Advanced through selection
14	PMV 3	13ICRISAT RPMVT15	Advanced through selection
15	SDMV 92038	13ICRISAT RPMVT16	Advanced through selection
16	SDMV 93032	13ICRISAT RPMVT17	Advanced through selection
17	ICMV 94001	13ICRISAT RPMVT18	Advanced through selection
18	SDMV 94005	13ICRISAT RPMVT19	Advanced through selection
19	SDMV 94014	13ICRISAT RPMVT20	Advanced through selection
20	SDMV 95009	13ICRISAT RPMVT 21	Advanced through selection
21	SDMV 95032	13ICRISAT RPMVT22	Advanced through selection
22	SDMV 96053	13ICRISAT RPMVT23	Advanced through selection
23	SDMV 96063	13ICRISAT RPMVT24	Advanced through selection
24	Shibe	13ICRISAT RPMVT25	Advanced through selection
25	Kola-1 (check)	kola-1	Recently released

## Experimental design and trial management

The experiment was conducted using Randomized Complete Block Design with three replications. The experimental plot consisted of three rows, each 5m in length with 0.75m between row spacing and 0.15m between plants. The total area of each plot had a size of 11.5m<sup>2</sup>.

As per the recommendation for pearl millet production in the lowland areas of Ethiopia, seeds of each genotype were drilled at a rate of 10 kg /ha in a plot consisting of three rows, Di-ammonium phosphate (DAP) and urea were applied in the rate of 50 kg/ha and 50 kg/ha, respectively. Di-ammonium phosphate was applied during planting and urea was applied twice (at the time of planting and tillering stage). Crop agronomic management practices were applied following the recommended practices. Data were recorded for grain yield plot<sup>-1</sup>, which was later converted to ha<sup>-1</sup>.

## Analysis of Variance (ANOVA)

Analysis of variances (ANOVA) was conducted using R software of 3.4.1 version and Gensat17th ed. Data for grain yield were pooled to perform the analysis of variance across environments. Least significance difference was used to determine the significance of differences among the genotype means for grain yield. The treatment was broken down into three components: G, E and GxE effects in the following equation (Ding *et al.*, 2007)  $Y_{ijr} = \mu + \alpha_i + \beta_j + \alpha\beta_{ij} + b_j + \varepsilon_{ijr}$  (1) where  $y_{ijr}$ , is the average value of the dependent variable of genotype  $i$  in environment  $j$  and block  $r$ ,  $\mu$  is a grand mean,  $\alpha_i$  is the effect of the  $i$ th genotype.  $\beta_j$ , is the effect of the  $j$ th environment,  $\alpha\beta_{ij}$  is the effect of the  $i$ th genotype by the  $j$ th environment,  $b_j$  is the block effect at the  $j$ th environment and  $\varepsilon_{ijr}$ , is the residual error term.

## Stability analysis

### AMMI Method

Additive main effects and multiplicative interaction (AMMI) model was performed for the mean data of grain yield (kg/ha) from each location using R software. The AMMI model equation is given as:

$$Y_{ij} = \mu + \alpha_i + \beta_j + \sum_{n=0}^N \lambda_n \gamma_{in} \delta_{jn} + \theta_{ij} + \varepsilon_{ij}$$

Where:  $Y_{ij}$  = the mean yield of genotype  $i$  in environment  $j$ ,  $\mu$  = the grand mean,  $\alpha_i$  = the deviation of the genotype mean from the grand mean,  $\beta_j$  = the deviation of the environment mean from the grand mean,  $\lambda_n$  = the singular value for the IPCA  $n$ ,  $N$  = the number of PCA axis retained in the model,  $\gamma_{in}$  = the PCA score of a genotype for PCA axis  $n$ ,  $\delta_{jn}$  = the environmental PCA score for PCA

axis  $n$ ,  $\theta_{ij}$  = the AMMI residual and  $\varepsilon_{ij}$  = the residuals. The degrees of freedom (DF) for the IPCA axis were calculated based on the following method (Zobel *et al.*, 1988).  $DF = G + E - 1 - 2n$ ; Where:  $G$  = the number of genotypes,  $E$  = the number of environments and  $n$  = the  $n^{\text{th}}$  axis of IPCA.

## GGE Method

Genotype by environment interaction analysis was performed by GGE biplot, which uses singular value decomposition (SVD) to partition GGE into two or more principal components. Each principal component comprised a set of genotype scores multiplied by a set of environment scores, to produce a two-dimensional biplot (Ding *et al.*, 2007). In GGE biplots, genotype plus genotype  $\times$  environment ( $G + G \times E$ ) interaction was studied together and to accomplish this  $G + GE$  effect is separated out from the observed mean from Equation (1) (by omitting random error and block effect) and finally the model becomes as  $ij - \mu - \beta_j = \alpha_i + \alpha\beta_{ij}$  (2). The GGE ( $G + G \times E$ ) effect was decomposed into multiplicative terms using SVD. The model based on singular value decomposition (SVD) of first two principal components (Ding *et al.*, 2007) is:

$$Y_{ij} - \mu - \beta_j = \lambda_1 \xi_{i1} \eta_{1j} + \lambda_2 \xi_{i2} \eta_{2j} + \xi_{ij}$$

Where  $\lambda_1$  and  $\lambda_2$  are the singular values of the first and second largest principal components, PC1 and PC2, respectively;  $\xi_1$  and  $\xi_2$  are the eigenvectors of genotype  $i$  for PC1 and PC2, respectively, and  $\eta_1$  and  $\eta_2$  are the eigenvectors of environment  $j$  for PC1 and PC2, respectively.

## RESULTS AND DISCUSSION

### Combined analysis of variance

The combined analysis of variance for grain yield of twenty five pearl millet genotypes is presented in Table 3. Before data analysis, homogeneity of error variance was determined by Bartlett's test (Steel and Torrie, 1980) and the data collected was homogenous. In addition, normality test was also computed, and the data had confirmed that it came from normal distribution. The result revealed that there were highly significant ( $P \leq 0.001$ ) differences among genotypes, environments and interactions (Table 3). The significant effect of locations is due to their variation in rainfall amount and seasonal distribution, temperature and soil type (Table 3). This indicated that the environments contribution for displayed performance of genotypes accounted greater proportion. Therefore, this shows that the varieties need to be evaluated for their specific adaptation and commercial release. The current finding expressed significant GxE, this revealed that the performance of the genotypes varies across each testing

**Table 3:** Analysis of variance for grain yield (kg/ha) of twenty five pearl millet genotypes tested at seven environments during 2013 and 2014 main cropping season.

Sources of variation	Degree of freedom	Mean square
Genotype	24	602203**
Environment	6	32073600**
GenotypexEnvironment	144	359921*
Replicate/Environment	14	157055**
Error	350	62322
Total	899	537904

environments. Similarly, there was highest variation in grain yield (GY kg/ha) across tested environments this is due to the performance of the genotypes coupled with variation in rain fall amount, pattern, distribution of rain fall. In line with the current research study Gupta and Ndoy (1991); Wedajo (2014); Lubadde *et al.* (2017) and Lagat *et al.* (2018) reported that significant variation in the performance of genotype, environment and GxE in their finding.

This research finding gives an information to the field crop researcher who are working on pearl millet improvement in their variety development in Ethiopia. The ANOVA adequately identified GxE as a significant source of variation but it is not able to explore the nature of the GxE which may mask the true performance of genotypes in certain environments (Crossa, 1990) and thus the need to explore more methods; for which case AMMI and GGE biplot were adopted

### Mean Performance of Genotypes

The overall mean performance of the twenty four pearl millet genotypes along with the one standard check for grain yield evaluated at Babile, Maitseberi, Mieso, Humera, Mehoni and Shiraro is presented in Table 4. The current research findings of seven environment combined analysis of data (Table 4) showed significant effect of most of genotypes for grain yield (kg/ha). Genotype 13 (2261 kg/ha), Genotype 4 (2057.33 kg/ha), Genotype 14 (1981.33 kg/ha), Genotype 18 (1912.33 kg/ha), Genotype 24 (1905.17 kg/ha), Genotype 11 (1897.83 kg/ha), Genotype 2 (1892 kg/ha), Genotype 21 (1885.83 kg/ha), Genotype 16 (1878 kg/ha), Genotype 9 (1861 kg/ha), Genotype 6 (1843 kg/ha), Genotype 3 (1823.83 kg/ha) and Genotype 23 (1814.33 kg/ha), respectively, were higher yielders, while Genotype 5 (1584.5 kg/ha), Genotype 7 (1521.5 kg/ha), Genotype 17 (1517.33 kg/ha), Genotype 12 (1516.83 kg/ha) and Genotype 22 (1495.33 kg/ha) showed similar grain yield. This finding is similar with many researchers (Wedajo, 2014; Lagat *et al.*, 2018 and Habte Nida *et al.*, 2016) reported that experimental varieties showed better

performance than the best check for yield.

The mean performance of tested genotypes across testing environments ranged from 1495.33 kg/ha to 2261 kg/ha. Genotype 13 had superior grain yield at Mehoni 2014, while lower at Humera 2014 and Sheraro 2014. This indicated the presence of cross over interaction across environments. In general, ranking of genotypes changed from one environment to another, indicates that, a remarkable GxE and require further investigation to understand the patterns of interactions.

Mean grain yield (kg/ha) of testing environments varied from 977.32 kg/ha for Humera 2014 to 2855.76 kg/ha for Mehoni 2014. This result showed that the impact of year after year variation of rainfall pattern, distribution, temperature, soil type on grain yield. The highest yield difference of grain yield due to environments, which is inappropriate to genotypes evaluation and mega environment investigation (Yan *et al.*, 2000) explains selection of site regression as the appropriate model for analyzing the multi-environment trials' data. Therefore, the grain yield (kg/ha) data of pearl millet genotypes was subjected to AMMI and GGE biplot analysis.

### Stability Analysis

#### AMMI Model

The combined AMMI model ANOVA of the twenty five pearl millet genotypes over seven environments for grain yield (kg/ha) is presented in Table 5. The ANOVA showed highly significant differences ( $p \leq 0.001$ ) for treatments (environments, genotypes and GxE). The total variation explained (%) was 93.03 % for treatment and 6.97 % for error. The larger contribution of the treatment than the error reveals the reliability of this multi-environment experiment (Table 5). The treatment variation was largely due to among environments variation, genotype and GxE accounted 73.39 %, 5.47 % and 21.14 % for the treatment variation, respectively. As mentioned earlier, the large percentage of the environment is an indication that the major factor that affect yield performance of pearl millet in drought areas of Ethiopia is the environ

**Table 4:** Genotype mean and environment mean for 25 pearl millet genotypes for grain yield performance evaluated across 7 environments.

Genotype code	Genotype name	13Babile	13Maitseberi	13Mieso	14Humera	14Mehoni	14Mieso	14Shiraro	Mean
1	SDMV90031	1748	1544	2233	1216	2369	1725	1087	1695.67
2	ICMV 88908	1340	1598	2529	945	3257	1907	1116	1892.00
3	ICMV 91450	1959	1541	2418	838	2624	2162	1360	1823.83
4	ICMV 93771	1669	1573	2477	887	4376	1823	1208	2057.33
5	ICMV 94133	1771	1427	2090	1105	2089	1695	1101	1584.50
6	ICMV 94136	1327	1597	2490	999	3400	1324	1248	1843.00
7	ICMV 94151	2102	1486	2591	793	1975	1077	1207	1521.50
8	ICMV 96603	1290	1406	2286	862	2692	1745	1050	1673.50
9	KAT PM 1	1750	1383	2772	1158	2642	1824	1387	1861.00
10	Kat PM 2	1858	1460	2533	1163	2381	1117	1450	1684.00
11	ICTP8203	1816	1783	2590	951	3100	1801	1162	1897.83
12	Okashana 2	1629	1368	2486	1034	1946	1119	1148	1516.83
13	Okoa	1912	1673	2679	869	5163	1868	1314	2261.00
14	PMV 3	1533	1750	2344	990	3748	1630	1426	1981.33
15	SDMV 92038	1849	1541	2599	883	2362	1304	1147	1639.33
16	SDMV 93032	1596	1614	2462	1078	2701	2333	1080	1878.00
17	ICMV 94001	1581	1512	1919	892	1964	1721	1096	1517.33
18	SDMV 94005	1723	1502	2450	977	3352	1726	1467	1912.33
19	SDMV 94014	1821	1543	2126	856	3354	1064	1441	1730.67
20	SDMV 95009	1303	1358	2348	941	2397	1646	1437	1687.83
21	SDMV 95032	2173	1759	2581	889	3257	1695	1134	1885.83
22	SDMV 96053	1676	1325	2073	1038	2376	1157	1003	1495.33
23	SDMV 96063	2172	1839	2567	1121	2394	1831	1134	1814.33
24	Shibe	1769	1567	2234	994	3549	1810	1277	1905.17
25	Kola-1 (check)	1431	1736	2181	954	1926	1469	1356	1603.67
LSD (0.05)		222.3	96.07	196.6	110	90.65	79.23	131.0	132.26
CV (0.05)		22.84	10.86	14.39	19.79	5.58	8.58	18.68	14.39
Mean		1711.92	1555.4	2402.32	977.32	2855.76	1622.92	1233.44	1765.6

**Table 5:** Genotype x environment interaction analysis of variance by AMMI for grain yield(kg/ha) of pearl millet genotypes tested at seven environments during 2013 and 2014 main cropping season.

Source	DF	SS	MS	%Total	%Treatment	%GXE	%Cumulative
Total	524	281861907	537904				
Treatments	174	262230744	1507073**	93.03			
Genotypes	24	14352312	598013**		5.47		
Environments	6	192441603	32073600**		73.39		
Block	14	2198765	157055**				
Interactions	144	55436829	384978**		21.14		
IPCA 1	29	38316273	1321251**			69.12	69.12
IPCA 2	27	7976613	295430**			14.39	83.51
Residuals	88	9143943	103908**			16.49	100
Pooled Error	336	17432399	51882	6.97			

DF = degree of freedom, SS =sum of squares, MS = mean of squares, \*\* = highly significant (P<0.001).

ment. Several authors also showed similar results for pearl millet and other cereal crops of different genotypes tested at different environments (Asfaw (2007); Hagos and Fetien (2011); Mahnaz *et al.* (2013); Sewagegne *et al.* (2013); Wedajo (2014); Abiy and Firew (2016); Kinde (2016); Lagat *et al.* (2018). In the AMMI ANOVA, the GxE was further partitioned by IPCA. The Gollob F-test used to estimate significant of the GXE components. The number of IPCA axis to be taken is determined by testing the mean square of each axis with the estimate of error through the F-statistics. The result of ANOVA showed that the first two IPCA are significant at 0.001 probability level, this result suggests the addition of the first two interactions IPCA axes in the model. Therefore, the best fit AMMI model for this multi-environment yield trial data was AMMI-2 (Table 5).

In specific, the first IPCA captured 69.12 % of the total interaction sum of squares, while the second IPCA explained 14.39 % of the interaction sum of squares. Yan *et al.* (2002) also recommended that the most accurate model for AMMI can be predicted by using the first two IPCAs. In the present study the first two IPCAs accounted for a total of 83.51 % of the interaction with 56 of the corresponding degrees of freedoms. This reveals that the GxE of the twenty five pearl millet genotypes with seven environments was adequately predicted by the first two principal components axes and therefore, most evidence may well to graphically display in AMMI1 and AMMI2 biplot.

The AMMI 1 biplot, showing main effects means of grain yield on the abscissa and IPCA 1 values as the ordinates, genotypes or environments that appear on a vertical line have similar means and those that appear on a horizontal line have similar interaction patterns (Crossa *et al.*, 1990). The biplot (Figure 1) shows five of the seven environments (Mieso 2014, Maitseberi 2013, Babile 2013, Shiraro 2014, Humera 2014) had below average

main effects and were unfavorable to the performance of some of the total genotypes as compared to the rest two environments. The remaining two environments i.e., Mehoni 2014 and Mieso 2013 had the highest main effects and were suitable to the performance of almost most of the genotypes. Similar results have been reported by Sintayehu and Kassahun, 2017.

AMMI 2 biplot presents the pattern of the first two IPCA of the interaction effects and aids in visual interpretation of the G x E interaction patterns and identify genotypes or environments that show small and large interaction effects. In AMMI 2 biplot, environments fell into three sections (Figure 2). Among the environments Maitseberi 2013, Mieso 2013 and Humera 2014 had very short spoke and Babile 2013 and Shiraro 2014 had short spokes. They do not exert strong interaction but the environments Mehoni 2014 and Mieso 2014 had long spokes and hence show the most influencing environments. In AMMI 2 biplot, the genotypes, 19, 7, 25, 17, 16 and 13 are the best or poorest genotypes in some or all environments because they are farthest from the origin where as the best genotype is 13 with respect to the best enhancing environment Mehoni 2014 and the poor genotype is 17 due to its value below average value. On the other hand, the genotypes 21, 11, 15 and 9 were close to the origin and therefore were less/non-sensitive to environmental interaction. However, genotype 15 was low yielding due to below average grain yield (Figure 2). Hence, entries 21, 11 and 9 were the highest yielding and stable due to very close to the origin. Similar results were reported by Crossa, (1990); Dagnachew *et al.* (2014 ); Wedajo, 2014; Sintayehu (2017).

### GGE biplot model

Stability analysis of the evaluated genotypes based on their IPCA scores using the GGE biplot of analysis is pre

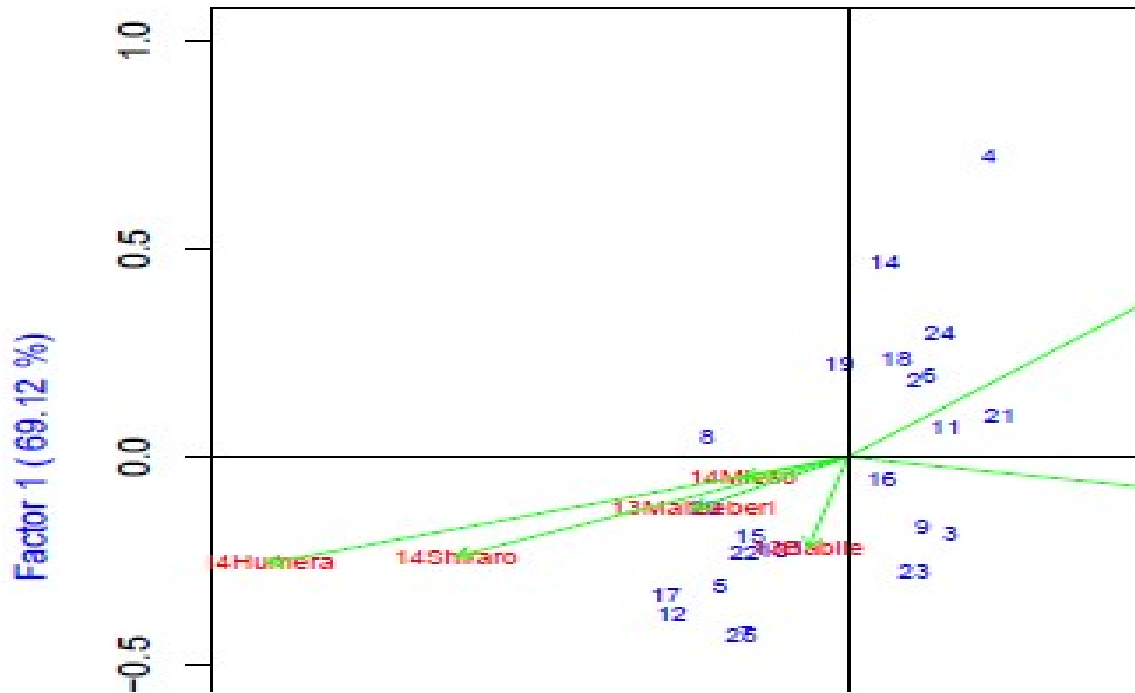


Figure 1: AMMI 1 biplot for grain yield of pearl millet genotypes evaluated across seven environments.

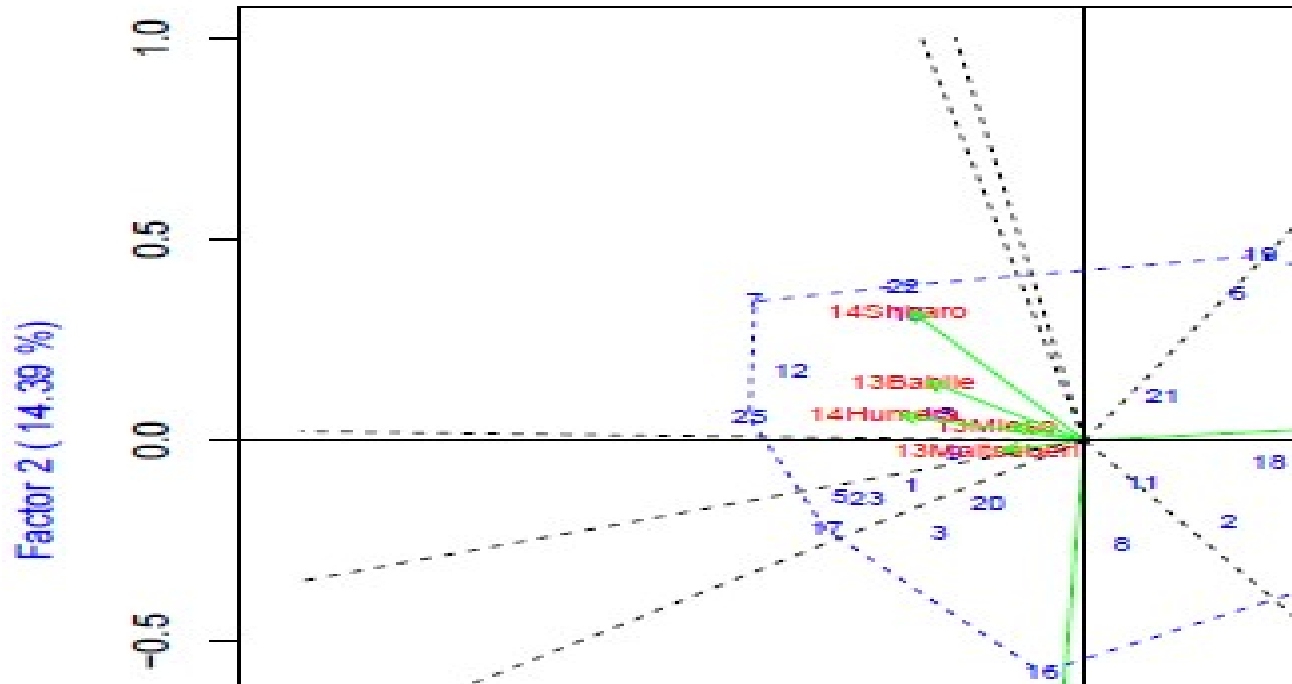
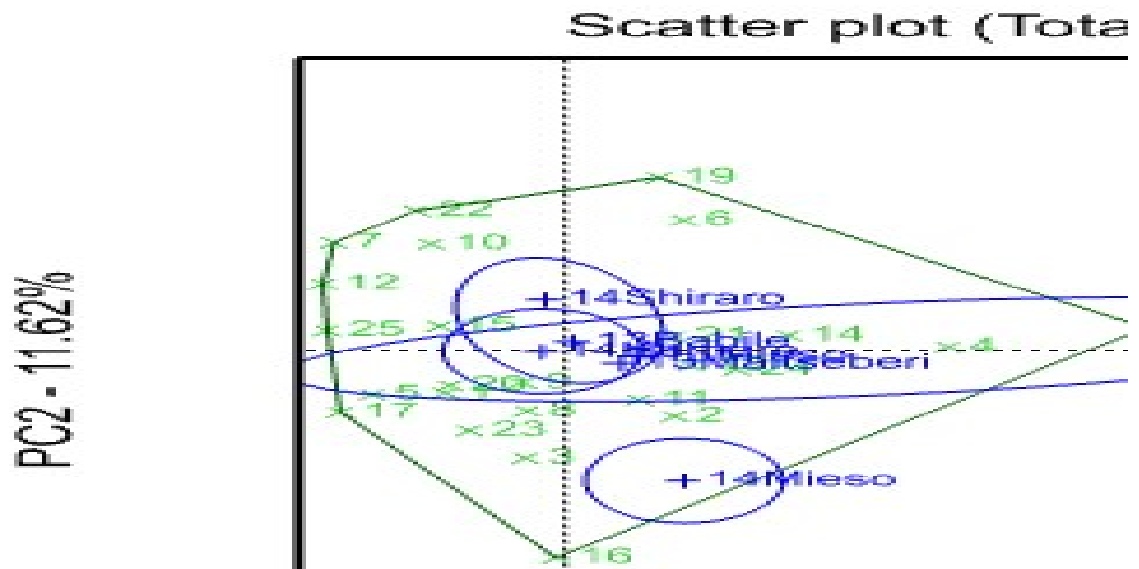


Figure 2: AMMI 2 biplot for grain yield (kg/ha) of pearl millets genotypes in five environments.

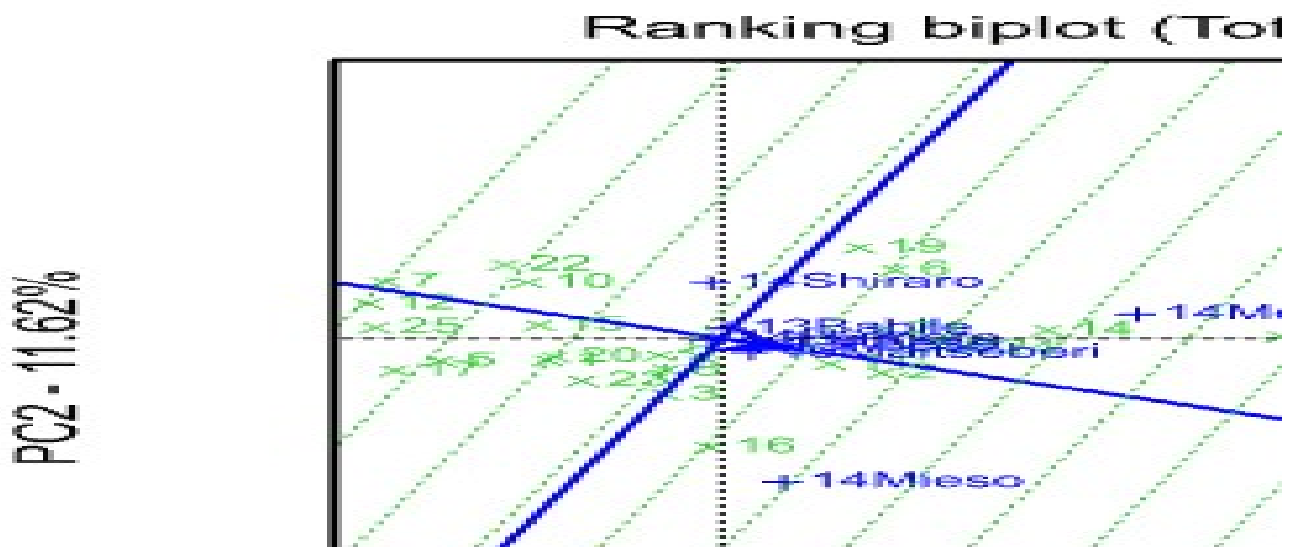
sented in Figure 3 and Figure 4. The polygon of lines in Figure 3 is made by connecting vertex genotypes, by connecting straight lines and rest of genotypes fall inside the polygon. The vertex genotypes were 12, 25, 7, 22,

19, 13, 16 and 17 (Figure 3). These genotypes are either the best or poorest genotypes in some or all environments because they are farthest from the origin (Yan and Kang, 2003).





**Figure 3:** The which-won-where view of the GGE biplot to show which pearl millet genotypes performed best in which environments (mega-environment identification).

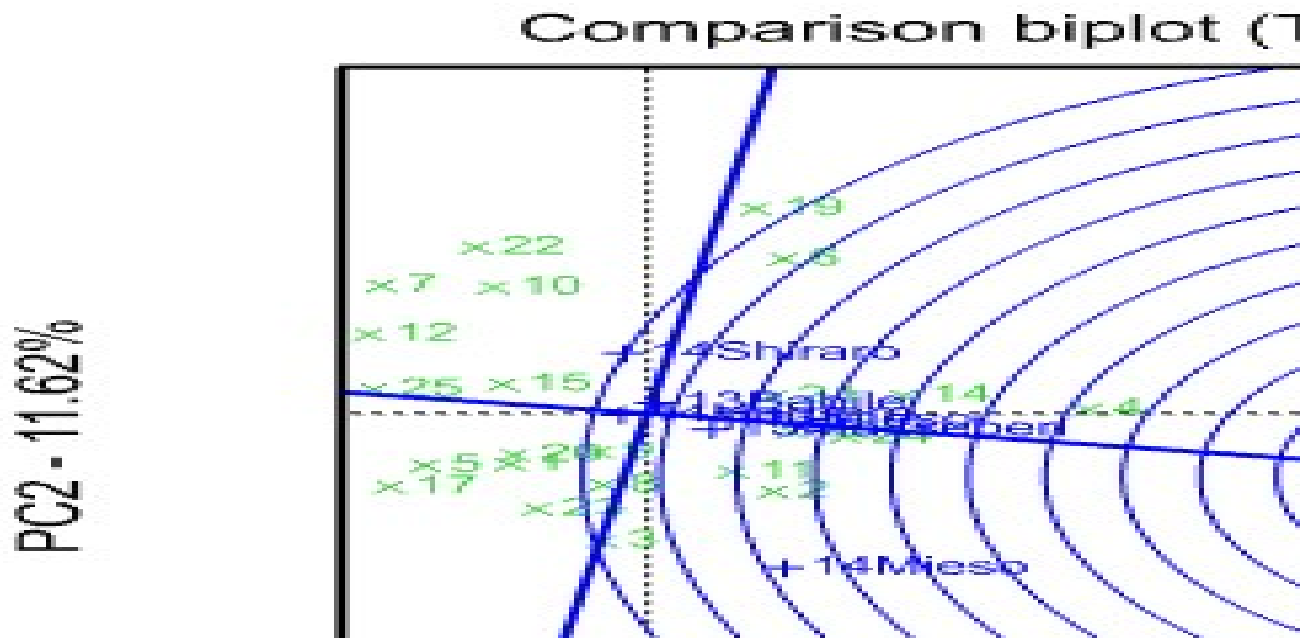


**Figure 4:** GGE ranking biplot indicates the mean grain yield and stability performance of 25 tested pearl millet genotypes.

In the current study, the GGE biplot analysis of the twenty five pearl millet genotypes evaluated at seven environments revealed that the first two principal components explained 80.11 % of the total variance (Figure 3). Genotypes close to the origin are not sensitive to the environments and those distant from the origin are sensitive to environments and have large interactions. Accordingly, statistically stable genotypes and locations were located

near to the biplot origin, with scores practically zero for the two interaction axis (IPCA1 and IPCA2).

Identification of mega-environments (Figure 3) was also studied and very important information on which won-where was revealed in the results found. The mega-environment identification involved a situation whereby one or more environments with similar characteristics were grouped into one large environment. Yan *et al.*



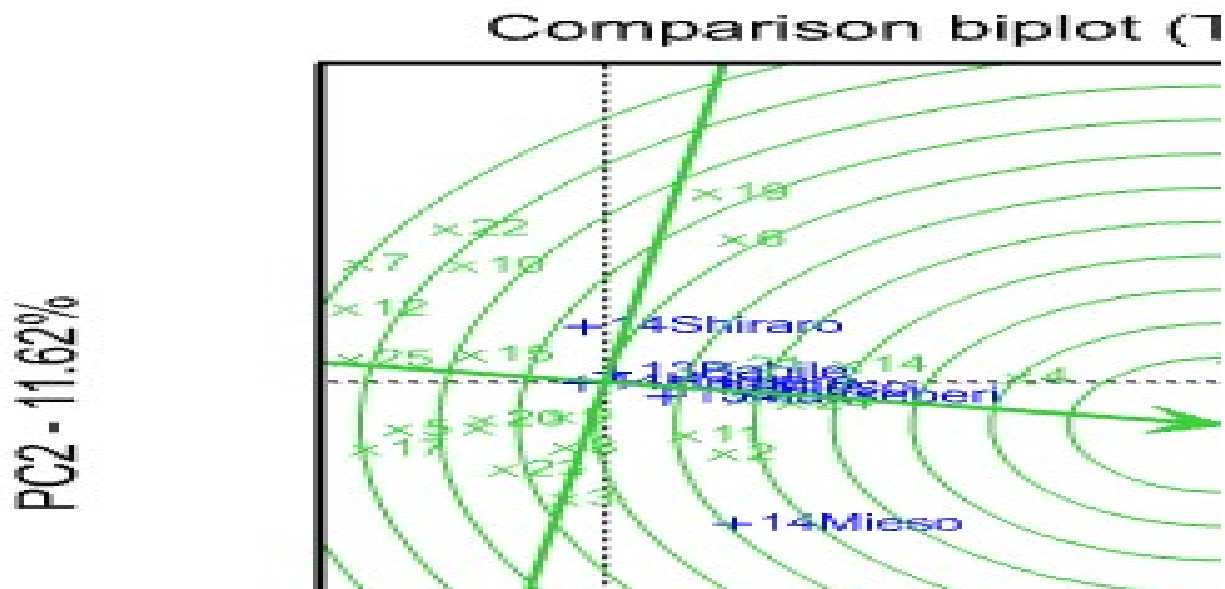
**Figure 5:** GGE-biplot showing a comparison of 7 testing environments with in ideal environment for grain yield (kg/ha)

(2000) defined mega environments as a group of locations or environments that constantly share the same best variety. This allows the breeder to have specific and valid explanation to recommend the promising genotypes which are good for that specific environment (Lubadd *et al.*, 2017). Which-won-where (Yan *et al.*, 2007) identified best winner genotypes for the mega environment. This also means the genotypes can be tested in those few mega-environments and still good yield data results can be obtained. The first mega environment contained environments of Shiraro 2014, Babile 2013, Maitseberi 2013, Mieso 2014, Mieso 2013, Mehoni 2014 with winning genotype 13, were bunched into one environment and the second Mega-environment on the other hand, contained only single environment of Mieso 2014 with winning genotype 16 meaning in the future, costs of multi-environment trials will be reduced by placing that effect into consideration (Gupta *et al.*, 2013). The GGE biplot also gave information which is important if a breeder has to make decisions and conclusions about specific correlations among environments and genotypes. The study results offered a better understanding of how biased a breeder can be if there is GxE and fails to do further GxE biplot analysis. The GGE have a lot of information which validates suitable environment for evaluating and suitable genotypes for identification and recommendation, there was effective evaluation of environments and genotypes based on the mean performance and stability across environments which is important required information for a breeder.

**Mean Performance and Stability of genotypes using GGE biplot:** The Biplot analysis revealed that the AEC view of the GGE biplot. The average tester coordinate (ATC) splits genotypes with above average mean from below average means. Therefore, genotypes with above average means were 13, 4, 21, 14, 11, 24, 18, 23, 9, 3, 16, 2 and 6, while 19, 10, 1, 15, 20, 8, 5, 7, 25, 12, 17 and 22 were genotypes which had below average mean performance (Figure 5). The shorter the genotype vector is more stable it is than others. Hence, among tested genotypes 21, 11, 15 and 9 were identified as high yielder and stable genotype while 15 was identified as low yielding with stable. In agreement with this finding Lubadd *et al.* (2017) in their finding reported high yielder and stable genotype as well as low yielding.

Comparison Biplot of seven test environments: The average environments coordinate (AEC) is a line that pass through the average environment (represented by small circle) and biplot origin. A test environment that has a small angle with the AEC is more representative of other test environments (Yan *et al.*, 2000 and Yan *et al.*, 2006). Hence, Mehoni 2014 was more representative testing environment (Figure 5). In agreement with this finding Lubadd *et al.* (2017) reported the existence of a good testing environment for high yielding variety.

An ideal genotype should have high mean grain yield performance across environments. It is one which is near or at the centre of the concentric circle, and is also a genotype to be on average environmental coordinate (AEC) on positive direction and has vector length equal to the longest vector of the genotype and indicated by an arrow



**Figure 6:** GGE-biplot showing a comparison of all genotypes with in ideal genotypes for grain yield (kg/ha).

pointed to it (Yan *et al.*, 2006 and Kaya *et al.*, 2006). The biplot indicated that genotype 13 is the most ideal genotype, whereas 4 and 14 genotypes were closest to the ideal genotype (Figure 6). Therefore, these genotypes are more desired and ideal genotypes than other tested genotypes. In line with this finding Lubadd *et al.* (2017) found the presence of ideal genotype.

## CONCLUSION

The present study showed that the grain yield performance of the 25 pearl millet genotypes was significantly affected by environment, genotype and their interaction. The total variation explained (%) was 93.03 % for treatment and 6.97 % for error. The larger contribution of the treatment than the error reveals the reliability of this multi-environment experiment. The mean performance of tested genotypes across testing environments ranged from 1495.33 kg/ha to 2261 kg/ha. Genotype 13 had superior grain yield at Mehoni 2014, while lower at Humera 2014 and Sheraro 2014. This indicated the presence of cross over interaction across environments. In general, ranking of genotypes changed from one environment to another, indicates that, a remarkable GxE and a further investigation on the adaptability and stability of genotypes across the seven environments was done. Additive Main effects and Multiplicative Interaction and Genotype Plus Genotype by Environment Interaction biplot were used to identify high yielder and stable genotypes across environments. Genotype 21, 11 and 9 showed both high yielder and stability, and therefore, are the promising ones, while the low yielder and stable genotype was ge-

notype 15 across the test environments. The Genotype Plus Genotype by Environment Interaction biplot revealed that genotype 13 is the ideal genotype, whereas genotypes 4 and 14 were nearest to the ideal genotype (the center of concentric circles) so these genotypes are more desirable and ideal genotypes than other tested genotypes. Test environment Mehoni 2014 showed good discriminating ability and representativeness, making it the most ideal environment.

In general this information could be used as input for further evaluation and also identify promising genotypes to be advanced to variety verification trial and then releasing out standing variety for the moisture stressed areas of Ethiopia.

## REFERENCES

- Abiy Legesse and Firew Mekbib (2016). Genotype X Environment Interaction and Stability of Early Maturing Sorghum [Sorghum bicolor (L.) Moench] Genotypes in Ethiopia. M.Sc. Thesis, Alemaya University of Agriculture, Ethiopia:2016-01-04T05:19:25Z.
- Asfaw Adugna (2007). Assessment of Yield Stability in Sorghum, African Crop Science Journal, vol.15, No, 2 pp 83-92.
- Basford, K. E. and Cooper, M. 1998. Genotype x environment interactions and some considerations of their implications for wheat breeding in Australia. Australian Journal of Agricultural Research 49:153-174.
- Bhagavatula S, P Parthasarathy Rao, G Basavaraj and N Nagaraj (2013). Sorghum and Millet Economies in Asia – Facts, Trends and Outlook. Patancheru 502 324, Te

- langana, India: International Crops Research Institute for the Semi-Arid Tropics. 80 pp. ISBN: 978-92-9066-557-1.
- Crossa, J., Gauch, H.G. and Zobel, R.W (1990). Additive main effects and multiplicative interaction analysis of two international maize cultivar trials. *Crop Science*, 30: 493-500.
- Dagnachew Lule, Masresha Fetene, Santie de Villiers and Kassahun Tesfaye (2014). Additive Main Effects and Multiplicative Interactions (AMMI) and genotype by environment interaction (GGE) biplot analyses aid selection of high yielding and adapted finger millet varieties. *J. Appl. Biosci.*, 76:6291–6303.
- Ding, M., Tier, B. and Yan, W. (2007) Application of GGE Biplot Analysis to Evaluate Genotype, Environment and GxE Interaction on *P. radiata*: A Case Study. [http://proceedings.com.au/afgc/slides%20\(PDF\)/thurs%201600%20ding.pdf](http://proceedings.com.au/afgc/slides%20(PDF)/thurs%201600%20ding.pdf).
- Gasura, E., Setimela, P. S. and Souta, C. M. (2015). Evaluation of the performance of sorghum genotypes using GGE biplot. *Canadian Journal of Plant Sci.* 95(6): 1205–1214.
- Gupta SK, Rathore A, Yadav OP, Rai KN, Khairwal IS, Rajpurohit BS, Das RR (2013). Identifying mega-environments and essential test locations for pearl millet cultivar selection in India. *Crop Science*. 2013;53(6):2444-2453.
- Habte Nida, Amare Seyoum and Adane Gebreyohannes (2016). Evaluation of Yield Performance of Intermediate Altitude Sorghum (*Sorghum bicolor* (L.) Moench) Genotypes Using Genotype x Environment Interaction Analysis and GGE Biplot in Ethiopia. *International Journal of Trend in Research and Development*, Volume 3(2), ISSN: 2394-9333.
- Hagos T. and Fetien A. (2011). Additive Main Effects and Multiplicative Interactions analysis of yield performance of sesame genotypes across environments in Northern Ethiopia. *Journal of the drylands*, 4(1): 259-266.
- Kaya, Y., Akcura, M. and Taner, S. (2006) GGE-Biplot Analysis of Multi-Environment Yield Trials in Breed Wheat. *Turkish Journal of Agriculture and Forestry*, 30, 325-337.
- G. Lubadde, P. Tongoona, J. Derera & J. Sibiya (2017). Analysis of Genotype by Environment Interaction of Improved Pearl Millet for Grain Yield and Rust Resistance. *Journal of Agricultural Science*; Vol. 9, No. 2; 2017.
- Mahnaz, R., Ezatollah, F. and Mohammad, M. J. (2013). Additive Main Effect and Multiplicative Interaction Analysis of phenotypic stability in chickpea genotypes over stress and non-stress environments. *International Journal of Agriculture and Crop Sciences*, 5(36):253-260.
- N. Lagat, P. Kimurto, O. Kiplagat, B. K. Towett, L. Jeptanui, I. Gatongi, N. Njogu, H. Ojulung, E. Manyasa and Siambi (2018). Evaluation of Genotype x Environment Interaction and Stability of Grain Yield and Related Yield Components in Pearl Millet (*Pennisetum glaucum* (L.) R.Br.). *Journal of Experimental Agriculture International*: DOI: 10.9734/JEAI/2018/24311.
- Pham, H. N. and Kang, M.S. (1988). Interrelationships among and repeatability of several stability statistics estimated from international maize trials. *Crop Science* 28: 925-928.
- Sintayehu Admas and Kassahun Tesfaye (2017). Genotype-by-environment interaction and yield stability analysis in sorghum [*Sorghum bicolor* (L.) Moench] genotypes in North Shewa, Ethiopia. *Ethiopian Biodiversity Institute*, P.O. Box 30726, Addis Ababa, Ethiopia: DOI: 10.1515/ausae-2017-0008.
- Sewagegne Tariku, Tadesse Lakew, Mulugeta Bitew and Mitiku Asfaw (2013). Genotype by environment interaction and grain yield stability analysis of rice (*Oryza sativa* L.) genotypes evaluated in north western Ethiopia. *Net Journal of Agricultural Science*, 1(1): 10-16.
- Wedajo Gebre (2014). Evaluation of pearl millet (*Pennisetum glaucum* L.) Genotypes for Yield and Yield Stability in South Omo and West Hararghe. *Journal of Biology, Agriculture and Healthcare*: Vol.4, No.8, 2014.
- Yan, W., Hant, L.A., Qinglai, S. and Szalvics, Z. (2000). Cultivar Evaluation and Megaenvironment Investigation Based on the GGE Biplot. *Crop Science*, 40, 597-605: <http://dx.doi.org/10.2135/cropsci2000.403597x>.
- Yan, W. (2001). GGE biplot: a windows application for graphical analysis of Multi-Environment trial data and other types of two way data. *Agronomy Journal* 93: 1111-1118.
- Yan, W. (2002). Singular-value partitioning in biplot analysis of multi-environment trial data. *Agron. J.*, 94: 990-996.
- Yan, W. and M.S. Kang, 2003. *GGE Biplot Analysis: A Graphical Tool for Breeders, Geneticists and Agronomists*. 1st Edn., CRC Press, Boca Raton, FL., USA., ISBN-13: 9781420040371, Pages: 288.
- Yan, W. and Tinker, N.A (2006). *Biplot Analysis of Multi-Environment Trial Data: Principles and Applications*. *Canadian Journal of Plant Science*, 86, 623-645. <http://dx.doi.org/10.4141/P05-169>. W.
- Yan, M.S. Kang, M. Baoluo, S. Woods, P.L. Cornelius (2007). GGE Biplot vs. AMMI analysis of genotype-by-environment data. *Crop Sci.*, 47 (2007), pp. 643-655.
- W.R. Zobel, W.J. Wright, H.G. Gauch (1988). Statistical analysis of a yield trial *Agron. J.*, 80 (1988), pp. 388-393.