

*Full Length Research Paper*

# **Genotype by environment interaction and stability analysis of cowpea [*Vigna unguiculata* (L.) Walp] genotypes for yield in Ethiopia**

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Received 3 June, 2018; Accepted 25 July, 2018

Ethiopia is claimed to be a center of diversity for cowpea production. The crop is the most drought tolerant and could help the country overcome the recurrent drought problem; however, the yield is very low due to lack of effort to develop varieties. This research was conducted to evaluate the stability of cowpea genotypes and to estimate the magnitude of genotypes by environment interaction (GEI) effect on grain yield. Sixteen cowpea genotypes were tested at seven environments in an experiment laid out in a 4 × 4 triple lattice design during 2016/17 cropping season. The combined analysis of variance over environments showed significant differences among genotypes and environments, along with significant effect of GEI on grain yield, days to flowering, days to maturity, plant height and pods per plants. Analysis of variance for grain yield from AMMI model indicated the contribution of genotype and environment, with GEI accounting for about 63.3, 5.3 and 29.7% of the total sum of squares, respectively. The result indicated that environments contributed much to the observed variations suggesting the need to test cowpea genotypes in diverse environments. Considering all stability parameters, viz; deviation from regression ( $S^2_{di}$ ), coefficient of regression (bi) from ER's model, IPCA1, IPCA2 and AMMI stability value (ASV) from AMMI model, GGE biplot and variety TVU was identified as the most stable with mean yield above the mean grain yield of genotypes. Two genotypes: IT-99K-1060a (1398.8 kg/ha) and 86D-378 (1377.1 kg/ha) had first and second highest yield, identified as responsive to both environments but more to favorable environments suggesting the need to further test and develop as varieties. The other two genotypes: 95K-1095-4A and 93K-619-1, identified as unstable and highly responsive to environments suggested to consider the genotypes as candidate varieties where they performed best. Melkassa, Sekota and Jinka were identified as more discriminating environments, whereas Arbaminch and Kobo were ideal for selecting superior genotypes; however, Babile and Meisso were non discriminating environments.

**Key words:** Additive main effects and multiplicative interaction (AMMI) stability value, Eberhart and Russell, deviation from regression and triple lattice.

## **INTRODUCTION**

Cowpea [*Vigna unguiculata* (L.) Walp] is an annual herbaceous legume that belongs to Fabaceae family. It is one of the widely cultivated and consumed grain legumes

globally, especially in the arid and semi-arid tropics (Baidoo and Mochiah, 2014; Noubissietchiagam et al., 2010). Generally, cowpea production and utilization in

Ethiopia is very low as compared to other African countries though the country is claimed to be the center of diversity and/or origin. The country has high potential for the production of the crop as more than 66.5% of the arable land is very suitable for cowpea production (Collaborative Crop Research Program (CCRP), 2015). It plays a critical role in the lives of millions of people in the developing world, providing them a major source of dietary protein that nutritionally complements low protein staple cereal and tuber crops. Its grain is the most important part of the plant for human consumption (Agbogidi and Egho, 2012). Drought is the most important abiotic stress limiting production of all crops worldwide, even the most drought tolerant cowpea (Hall, 2004). More importantly, Ethiopia is known as a victim with recurrent droughts that causes partial or total crop failure, and subsequently, famine in the country. In such situations, cowpea can be a potential crop to reduce the consequences of drought because of its drought tolerant nature more than other staple crops. The relative magnitude of environment, genetic and their interaction effects are a challenge that makes production difficult (Hall et al., 2003). Therefore, in the process of developing cowpea varieties for desirable traits, it is necessary to evaluate genotypes in contrasting environments in the country. However, information on the effect of genotype, environment, and their interaction on cowpea grain yield under diversified agro-climatic conditions of Ethiopia is limited. The present study was initiated to estimate the magnitude of genotype, environment and genotype by environment interaction for grain yield of cowpea and characterize yield stability of cowpea genotypes across different environments.

## MATERIALS AND METHODS

The experiment was conducted in seven environments during 2016/17 cropping season in Ethiopia (Table 1). Sixteen cowpea genotypes (14 advanced lines and two standard checks) were used for this study (Table 2). The experiment was laid out in 4 × 4 triple lattice experimental design with three replications. The seeds of the experimental genotypes were planted on 4 m × 3.6 m plots (14.4 m<sup>2</sup>) having six rows, with inter-row spacing of 60 cm and 20 cm within rows. Fertilizer (DAP 100 kg/ha) was applied for the experiment along with other agronomic managements based on the recommendation. Data were collected on the basis of five sample plants randomly taken from the four central rows, viz. plant height at maturity, number of pods per plant, and number of seeds per pod, and on the basis of entire plot, such as days to 50% emergence, days to 50% flowering, days to 75% maturity, grain yield per net plot and 100-seeds weight. All data were subjected to analysis of variance (ANOVA) separately for individual environment and other environments. ANOVA is important in revealing the presence of GEI, but it does not indicate genotypes contribution to the

interaction and which genotype was stable across environments. Stability was computed for grain yield by SPAR 2.0 software for Eberhart and Russell's stability parameters along with Genstat statistical software (16<sup>th</sup> edition) for AMMI stability parameters and GGE biplot. Mean that differ significantly were separated by Duncan Multiple Range Test. The regression coefficient ( $b_i$ ) (Eberhart and Russell's stability parameters) measures the response of genotypes to environments. When the regression coefficient of the genotype is nonsignificant from unity/one ( $b_i = 1$ ), the genotype is said to be averagely responsive and suitable for both poor and good environments; when the  $b_i$  value of genotypes is significantly different from one/unity ( $b_i > 1$ ), the genotype is said to be highly responsive above the average and suitable only in good environment; whereas, when the genotype  $b_i$  value is significantly different from one/unity ( $b_i < 1$ ), it indicates the genotype is low responsive and suitable for poor environment (Wachira et al., 2002). No significant  $S^2_{di}$  (deviation from regression) value from zero indicates stable genotypes across environments and with significant  $S^2_{di}$  value from zero considered as unstable genotypes across environments. AMMI stability value (ASV) is used to judge stable genotypes (the smaller the value, the more stable the genotype is).

## RESULTS AND DISCUSSION

The combined analysis of variance over environments showed significant ( $p < 0.01$ ) mean squares of genotypes, environments and interaction of genotypes × environments (GEI) for grain yield (Table 3). The results indicated the presence of significant variations among genotypes and environments and the genotypes had inconsistent performance across the test environments for the mentioned traits. This in turn, suggested the need to conduct further GEI and thereby stability analyses to understand the nature of GEI and stability of the performance of genotypes across environments. Akande (2009) in cowpea, Kaya et al. (2002) in wheat, Solomon et al. (2008), Wende (2013) and Workie et al. (2013) in maize and Yayis et al. (2014) in field pea also reported the significant effect of genotype, environment and GEI on yield and some other yield related traits and suggested the importance of further stability analysis.

### Mean performance of genotypes for grain yield

The first three genotypes (Table 4) with highest mean grain yield were IT-99K-1060a (1398.8 kg/ha) and 86D-378 (1377.1 kg/ha) without significant differences between the two followed by 95K-1095-4A (1321.8 kg/ha). The three genotypes with lowest mean grain yield were IT-96D-610 (1112.5 kg/ha), Kenketi (1128.5 kg/ha) without significant difference among the two and IT-97K-568-18 (1007.0 kg/ha).

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**Table 1.** Description of test environments.

Environments	Soil type	Altitude (masl)	Average rainfall (mm)	Temperature(°C)		Geographical location	
				Minimum	Maximum	Latitude (N)	Longitude (E)
Arbaminch	Vertisols	1216	1000.0	16.0	37.0	06° 06' 41"	37° 35'
Babile	*	1650	671.0	15.5	28.1	9° 13' 09"	42° 19'
Sekota	*	*	1043.0	12.9	32.9	38° 56' 00"	12° 14'
Kobo	Vertisol	1450	673.4	13.0	34.0	12° 8' 21"	39° 18'
Melkassa	Andosol	1500	763.0	14.0	24.8	8° 30' 00"	39° 21'
Jinka	Vertisol	1383	1274.7	16.6	27.6	5° 52' 00"	36° 38'
Meisso	Vertisol	1332	787.0	14.9	28.2	9° 28' 00"	38° 08'

Source: Arba Minch University and Melkassa Agricultural Research Center, \*= Data not available.

**Table 2.** List of experimental materials.

Code	Genotype	Status
G1	KENKETI	Standard check
G2	86D-378	Advanced line
G3	IT-89KD	Advanced line
G4	MEL-NURL-96-3	Advanced line
G5	IT-96D-610	Advanced line
G6	IT-93K-556-4	Advanced line
G7	IT-97K-568-18	Advanced line
G8	IT-99K-1060a	Advanced line
G9	95K-1095-4A	Advanced line
G10	IT-87D-1137	Advanced line
G11	IT-96D-604	Advanced line
G12	93K-619-1	Advanced line
G13	IT-93K-293-2-2	Advanced line
G14	IT-99K-1060	Advanced line
G15	IT-960-604	Advanced line
G16	TVU	Standard check

Source: Melkassa Agricultural Research Center.

The AMMI for grain yield showed the significant ( $p < 0.01$ ) effect of environment, genotype, and genotype by environment interaction. Environment, genotype, and genotype by environment interaction accounted for about 63.3, 5.3, and 29.7% of the total sum of squares, respectively. Most of the total sum of squares of the model was attributed to the environment and the interaction effect. This result is in agreement with the results reported by Akande (2009), Sarvamangala et al. (2010) and Nunes et al. (2014) in cowpea along with Taye et al. (2000) in fieldpea which revealed that the contribution of environment to the observed variation of yield was large. The larger sum of squares of GEI compared to the genotype indicated larger differences in genotypic response across environments. In cowpea (Stanley Omar et al., 2005) and chickpea (Solomon et al., 2008), larger contribution of GEI than genotype effect for

the observed yield variation was also reported. The greater contribution of the treatment (98.3%) than the error (1.53) indicated the reliability of the multi-environment experiment. The AMMI model further partitioned the genotype by environment interaction sum of square into interaction principal component axes (IPCA) and residual term. The mean squares of the first three IPCAs were significant and all together contributed 79.33% of the total sum of squares of GEI. The IPCA 1, IPCA 2 and IPCA 3 accounted for 37.93, 24.67 and 16.73%, respectively, for the observed variation due to GEI. For the validation of the variation explained by GEI, the first three multiplicative component axes are adequate (Gauch, 2006). This is because of notable reduction of dimensionality and graphical visualization for the stability patterns of genotypes (Annicchiarico, 2002) (Tables 5 and 6).

**Table 3.** Combined analysis of variance for yield and yield related traits.

Source of variation	Degree of freedom	DF	DM	PH (cm)	PPP	GY (kg)
Replication (R)	14	0.8	2.5	33.0	16.1	206.8
Genotype (G)	15	52.4**	122.8**	479.0**	107.4**	210611.0**
Environment (E)	6	2387.4**	1611.6**	14274.5**	1894.7**	6251125.2**
G × E	90	35.8**	65.8**	774.0**	69.2**	195706.1**
Error	335	8.5	6.1	81.8	23.7	4788.8
CV%		4.8	2.7	15.3	23.4	5.6
SEM		1.7	1.4	5.2	2.8	39.9
Mean		61.0	90.3	59.0	20.5	1237.4

\*\* : Significant at  $p \leq 0.01$ , DF= days to flowering, DM=days to maturity, PH (cm) = plant height in centimeters, PPP= pods per plant, GY (kg) = grain yield in kilo gram, CV (%) =coefficient of variation in percent and SEM=mean standard error.

**Table 4.** Mean grain yield (kg/ha) of genotypes.

Genotype	Environment								R
	Arbaminch	Babile	Sekota	Kobo	Melkassa	Jinka	Meisso	Gm	
Kenketi	1206.7 <sup>ef</sup>	856.0 <sup>c</sup>	1766.3 <sup>c</sup>	1415.0 <sup>gh</sup>	645.3 <sup>g</sup>	1013.7 <sup>e</sup>	996.7 <sup>ef</sup>	1128.5 <sup>hi</sup>	14
86D-378	1947.7 <sup>a</sup>	524.0 <sup>fg</sup>	2078.7 <sup>a</sup>	1736.7 <sup>e</sup>	851.0 <sup>de</sup>	1478.3 <sup>b</sup>	1023.7 <sup>ef</sup>	1377.1 <sup>a</sup>	2
IT-89KD	1520.7 <sup>d</sup>	450.3 <sup>g</sup>	1795.7 <sup>c</sup>	2351.7 <sup>a</sup>	783.0 <sup>def</sup>	977.7 <sup>ef</sup>	1033.7 <sup>de</sup>	1273.2 <sup>cde</sup>	7
MEL-NURL-96-3	1222.3 <sup>ef</sup>	848.3 <sup>cd</sup>	1951.7 <sup>b</sup>	2069.7 <sup>b</sup>	799.7 <sup>def</sup>	766.7 <sup>gh</sup>	1254.7 <sup>b</sup>	1273.3 <sup>cde</sup>	6
IT-96D-610	1563.0 <sup>cd</sup>	1026.0 <sup>b</sup>	1523.3 <sup>e</sup>	1332.3 <sup>h</sup>	614.7 <sup>g</sup>	674.0 <sup>h</sup>	1054.3 <sup>cde</sup>	1112.5 <sup>i</sup>	15
IT-93K-556-4	1011.7 <sup>g</sup>	780.3 <sup>cd</sup>	2139.7 <sup>a</sup>	1541.3 <sup>f</sup>	693.3 <sup>fg</sup>	1620.7 <sup>a</sup>	1056.0 <sup>cde</sup>	1263.3 <sup>cde</sup>	8
IT-97K-568-18	900.7 <sup>h</sup>	879.7 <sup>c</sup>	1395.7 <sup>f</sup>	1134.0 <sup>i</sup>	840.3 <sup>de</sup>	706.0 <sup>h</sup>	1192.7 <sup>bc</sup>	1007.0 <sup>j</sup>	16
IT-99K-1060a	1629.0 <sup>c</sup>	802.7 <sup>cb</sup>	1754.3 <sup>c</sup>	1985.7 <sup>bc</sup>	1514.0 <sup>a</sup>	1020.3 <sup>e</sup>	1085.3 <sup>cde</sup>	1398.8 <sup>a</sup>	1
95K-1095-4A	1727.7 <sup>b</sup>	610.0 <sup>ef</sup>	1593.7 <sup>de</sup>	1734.3 <sup>e</sup>	1115.3 <sup>c</sup>	1009.7 <sup>e</sup>	1461.7 <sup>a</sup>	1321.8 <sup>b</sup>	3
IT-87D-1137	1208.0 <sup>ef</sup>	1149.3 <sup>a</sup>	1819.3 <sup>c</sup>	1512.7 <sup>fg</sup>	709.3 <sup>efg</sup>	749.7 <sup>gh</sup>	1013.3 <sup>ef</sup>	1166.0 <sup>gh</sup>	13
IT-96D-604	1544.0 <sup>cd</sup>	752.0 <sup>d</sup>	1648.0 <sup>d</sup>	1723.0 <sup>e</sup>	816.0 <sup>def</sup>	1336.3 <sup>c</sup>	883.3 <sup>f</sup>	1243.2 <sup>def</sup>	9
93K-619-1	2014.3 <sup>a</sup>	626.3 <sup>e</sup>	1845.3 <sup>c</sup>	1925.0 <sup>cd</sup>	819.0 <sup>def</sup>	876.0 <sup>fg</sup>	990.0 <sup>ef</sup>	1299.4 <sup>bc</sup>	4
IT-93K-293-2-2	1490.0 <sup>d</sup>	780.7 <sup>cd</sup>	1430.7 <sup>f</sup>	1183.7 <sup>i</sup>	1273.3 <sup>b</sup>	1043.0 <sup>e</sup>	1479.3 <sup>a</sup>	1240.1 <sup>ef</sup>	10
IT-99K-1060	1142.7 <sup>f</sup>	1066.0 <sup>ab</sup>	1566.7 <sup>de</sup>	1411.7 <sup>gh</sup>	790.3 <sup>def</sup>	1286.7 <sup>cd</sup>	1176.3 <sup>bcd</sup>	1205.8 <sup>fg</sup>	11
IT-960-604	1255.3 <sup>e</sup>	985.7 <sup>b</sup>	1540.7 <sup>e</sup>	1501.0 <sup>fg</sup>	863.3 <sup>d</sup>	1010.0 <sup>e</sup>	1241.3 <sup>b</sup>	1199.6 <sup>fg</sup>	12
TVU	1543.3 <sup>cd</sup>	994.3 <sup>b</sup>	1426.7 <sup>f</sup>	1850.3 <sup>d</sup>	831.7 <sup>def</sup>	1171.0 <sup>d</sup>	1199.3 <sup>bc</sup>	1288.1 <sup>bcd</sup>	5
Overall mean	1432.9	820.7	1704.8	1650.5	872.5	1046.2	1133.9	1237.4	
CV (%)	4.1	7.4	3.4	4.2	7.5	7.9	6.7		
SEM	32.17	31.27	30.78	37.55	42.5	42.9	45.5		

Means in the same column followed by the same letters are not significantly different at 5% level of significance, Gm=grand mean of genotypes, R=mean grain yield rank of genotype in descending order and CV (%) =coefficient of variation in percent, SEM=mean standard error.

### Stability analysis for grain yield estimates of stability parameters from Eberhart and Russell's model

The six genotypes viz.; IT-960-604, Kenketi, IT-99K-10609, TVU, IT-96D-604 and IT-97K-568-18 with non-significant  $S^2_{di}$  values from zero indicated the genotypes were stable. However, all genotypes had lower yield than overall mean of genotypes (1237.4 kg/ha) except TVU and IT-96D-604 which indicated the genotypes were not desirable for cultivation though they were stable. The desirable genotypes are expected not only to be stable in

all environments but also have (high mean values). Ten genotypes viz.; 86D-378, IT-89KD, MEL-NURL-96-3, IT-96D-610, IT-93K-556-4, IT-99K-1060a, 95K-1095-4A, IT-87D-1137, 93K-619-1 and IT-93K-293-2-2 had significant  $S^2_{di}$  values from zero indicating the genotypes were unstable. TVU was the desirable genotype for cultivation in all environments having static stability evident from non-significant value  $S^2_{di}$  from zero, with non-significant  $b_i$  value ( $b_i=1$ ) from unity/one and higher mean grain yield above average mean grain yield of genotypes. IT-99K-1060 was a low responsive genotype to varied

**Table 5.** AMMI analysis of variance for grain yield.

Source of variation	DF	SS	MS	Sum of square explained		
				%Total	% G x E	% G x E cumulative
Total	335	59287984	176979			
Treatments	111	58279428	525040**	98.3		
Genotypes	15	3159168	210611**	5.3		
Environments	6	37506751	6251125**	63.3		
Interactions (G x E)	90	17613509	195706**	29.7		
IPCA 1	20	6680777	334039**	11.3	37.93	
IPCA 2	18	4349683	241649**	7.3	24.67	62.6
IPCA 3	16	2946860	184179**	4.97	16.73	79.33
Residuals	36	3636189	101005**	6.1		
Error	335	908139	4324			

ns and \*\*, nonsignificant and significant at  $p < 0.01$ , respectively. DF = Degree of freedom, SS = Sum of square, MS = Mean square, G = Genotype, E = Environment, G x E = Genotype by environment interaction, IPCA 1, IPCA 2 and IPCA 3 = Interaction principal component axis one, two and three, respectively. In the joint regression analysis of variance, all effects were significant ( $p < 0.01$ ), which indicated contrasts between the environments and the occurrence of differential response of genotypes across environment (Table 6). These results are similar to those reported by Akande (2009), Sarvamangala et al. (2010) and Nunes et al. (2014) in cowpea.

**Table 6.** Joint regression analysis of variance for grain yield.

Source of variation	DF	SS	MS
Total	111	19426476.1132	175013.3
Genotype	15	1053056.1030	70203.74**
Environment+ (Genotype x Environment )	96	18373420.0102	191389.8**
Environment linear	1	12502250.2023	12502250**
GxE (linear)	15	1721084.0049	114738.9**
Pooled deviation	80	4150085.8030	51876.07**
Kenketi	5	99553.9451	19910.79**
86D-378	5	386414.6073	77282.92**
IT-89KD	5	257322.7465	51464.55**
MEL-NURL-96-3	5	252998.3918	50599.68**
IT-96D-610	5	281839.2433	56367.85**
IT-93K-556-4	5	739493.2260	147898.6**
IT-97K-568-18	5	176478.3714	35295.67**
IT-99K-1060a	5	385325.1075	77065.02**
95K-1095-4A	5	268299.5908	53659.92**
IT-87D-1137	5	280016.9027	56003.38**
IT-96D-604	5	173031.5005	34606.3**
93K-619-1	5	248038.7147	49607.748**
IT-93K-293-2-2	5	289537.9642	57907.59**
IT-99K-1060	5	129666.3231	25933.26**
IT-960-604	5	35612.2136	7122.443**
TVU	5	146456.9544	29291.39**
Pooled error	224	336185.3234	1500.827**

\*\* : Significant at  $p < 0.01$ , DF = Degree of freedom SS = Sum of square and MS = Mean square.

environments and suitable only for unfavorable environments with  $b_i$  value significantly different from one/unity ( $b_i < 1$ ).

Seven genotypes 86D-378, IT-89KD, MEL-NURL-96-3, IT-93K-556-4, 95K-1095-4A, IT-96D-604 and 93K-619-1 had mean yield greater than the mean yield of genotypes

over seven environments ranging from 2.1 to 11.3%. However, all genotypes had  $S^2_{di}$  values significantly different from zero and significant  $bi$  values ( $bi > 1$ ) from unity/one. This suggested that the genotypes were not stable and highly responsive to favorable environments. These were desirable genotypes for cultivation in favorable environments for the crop having dynamic stability (mean value higher in favorable environments than the average yield of favorable environments).

Two genotypes (IT-99K-1060 and IT-97K-568-18) had non-significant  $S^2_{di}$  value from zero ( $S^2_{di} > 0$ ), significant  $bi$  value ( $bi < 1$ ) from unity/one and lower mean yield than average mean yield of genotypes. These genotypes were stable and more responsive to unfavorable environments for the crop, but the low yield of these genotypes did not promote its being recommended for cultivation in environments where they perform.

IT-96D-604 had non-significant  $S^2_{di}$  value from zero ( $S^2_{di} > 0$ ), significant  $bi$  value ( $bi > 1$ ) from unity/one and high mean yield above average mean yield of genotypes which suggested it was a desirable genotype for cultivation in all environments and more responsive in favorable environments. TVU had yield advantage of 4.01% over grand mean yield of genotypes and fifth ranking mean yield, zero (0) IPCA 1 score and relatively low IPCA 2 (negative); also, ASV suggested that this genotype could be considered for cultivation in unfavorable environments. This result indicated a proportionate genotype response (Silveira et al., 2013).

The genotypes with lower IPCA1 scores would produce a lower G×E interaction effect than those with higher IPCA1 scores and have less variable yields (more stable) across environments (Oliveira et al., 2014). The second group of genotypes consisted of IT-99K-1060a, 86D-378, 95K-1095-4A, 93K-619-1, MEL-NURL-96-3, IT-89KD and IT-96D-604 of which the first four ranked 1 - 4 high yields in the experiment while the last three ranked 6, 7 and 9 high yields. All had higher mean yields above the grand mean yield of genotypes, negative IPCA 1 scores, low ASV ranked 1 - 6 except 95K-1095-4A and MEL-NURL-96-3 with ASV ranked 11 and 14, respectively. The first four high yielding genotypes (IT-99K-1060a, 86D-378, 95K-1095-4A, 93K-619-1) except (86D-378) had same sign of IPCA 1 and IPCA 2 scores while the other genotype was suitable in unfavorable environments with opposite sign of IPCA 1 and IPCA 2. Therefore, the three genotypes could be considered for cultivation in all environments. Other genotype (86D-378) could be considered for cultivation in environments where it performed well. Dynamic stability implies for a stable genotype, a yield response that is always parallel to the mean response of the tested environments, that is, zero GEI (Annicchiarico, 2002). The third group of genotypes consisted of IT-99K-1060, IT-960-604, IT-87D-1137, Kenketi, IT-96D-610 and IT-97K-568-18 which had mean yields lower than grand mean yield of genotypes, with mean yield ranked 11 - 16 having relatively high and

positive IPCA 1 scores, of which IT-96D-610, IT-99K-1060 and IT-87D-1137 had high ASV ranked 12, 13 and 15, respectively. The results suggested that these genotypes could not be considered for cultivation. Usually, in crop improvement programs, tests of performance across a wide range of environments is conducted to reduce the effect of GEI and to ensure that the selected genotypes have a high yield and stable performance across several environments (Stanley et al., 2005) (Table 7).

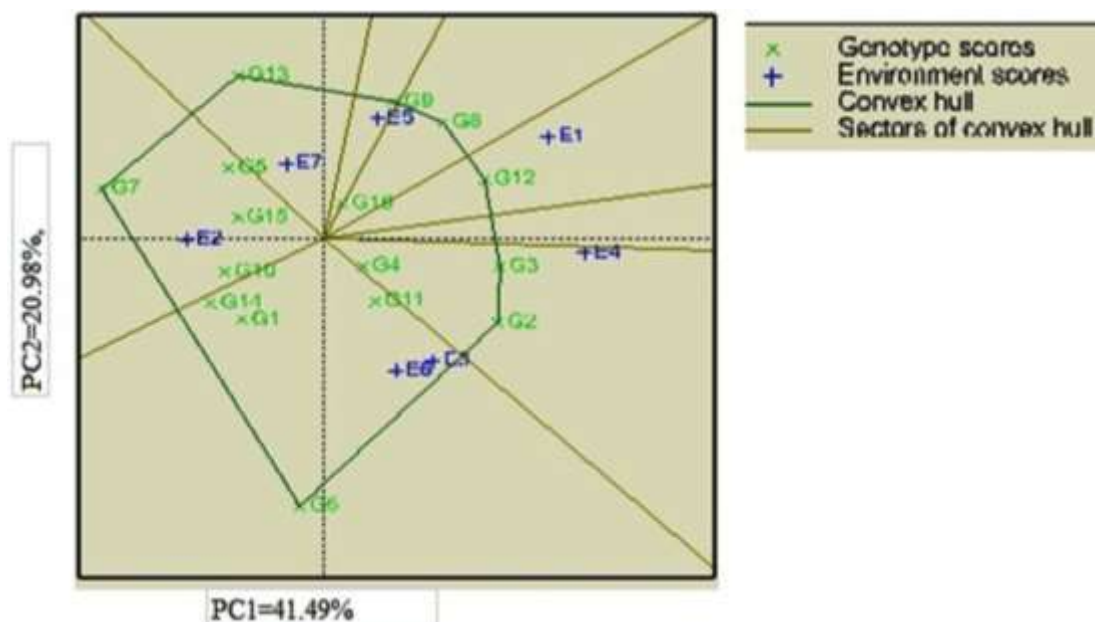
### Which-Won-Where” Patterns

In Figure 1, a polygon view of GGE was formed by connecting the vertex genotypes with straight lines and the rest of the genotypes were placed within the polygon. The vertex genotypes were 86D-378 (G2), IT-89KD (G3), IT-93K-556-4 (G6), IT-97K-568-18 (G7), IT-99K-1060a (G8), 95K-1095-4A (G9) and IT-93K-293-2-2 (G13) and 93K-619-1 (G12) having the largest distance from the origin which were more responsive to environmental change and gave high yield except IT-97K-568-18 (G7) which was considered as specially adapted genotypes. The vertex genotypes in each sector are the best genotype at environments whose markers fall into the respective sector. Environments within the same sector share the same winning genotypes, and environments in different sectors have different winning genotypes. The genotypes within the polygon and nearer to origin were less responsive than vertex genotypes (Yan and Hunt, 2001; Yan and Tinker, 2006). Accordingly, the genotypes Kenketi (G1), MEL-NURL-96-3 (G4), IT-96D-610 (G5), IT-87D-1137 (G10), IT-96D-604 (G11), IT-99K-1060 (G14), IT-960-604 (15) and TVU (G16) were located within polygon which were less responsive. Genotype TVU (G16), located near to the origin indicated stability. Winner and higher yielder genotype at Jinka (E6) and Sekota (E3) was IT-93K-556-4 (G6). IT-89KD (G3) and IT-99K-1060a (G8) were winners and highest yielders at Kobo (E4) and Melkassa (E5) respectively. Genotype 93K-619-1 (G12) and IT-93K-293-2-2 (G13) were winner and high yielder genotypes at Arbaminch and Meisso, respectively. Genotype IT-97K-568-18 (G7) was winner but lowest yielder at Babile (E2) which was relatively not conducive for cowpea genotypes to express their potentials. Yan et al. (2000) and Yan and Kang (2003) reported the polygon view of GGE biplot as the best way for identification of winning genotypes with visualizing the interaction patterns between genotypes and environments. The GGE biplot has therefore, been used in crop genotypes trials to effectively identify the best-performing genotype(s) across environments, identify the best genotypes for specific environments delineation, whereby specific genotypes can be recommended to specific environments and can be used to evaluate the yield and stability of genotypes (Yan and Kang, 2003;

**Table 7.** Stability parameters from AMMI analysis and Eberhart and Russel's models for grain yield.

Genotype	Pooled mean over seven environments	AMMI model stability parameter				ER's model stability parameter		
		IPCA 1	IPCA 2	IPCA 3	ASV	bi	S <sup>2</sup> di	S <sup>2</sup> di R
Kenketi	1128.5 (14)	4.2	6.8	1.18239	8.55 (5)	0.97	18409.9617 <sup>ns</sup>	2
86D-378	1377.1 (2)	-12.8	7.1	11.4536	8.72 (6)	1.48	75782.0941 <sup>**</sup>	15
IT-89KD	1273.2 (7)	-18.5	1.3	-6.7099	8.105 (3)	1.7163	49963.722 <sup>*</sup>	9
MEL-NURL-96-3	1273.3 (6)	-4.1	1.8	-0.6522	20.292 (14)	1.3881	49098.851 <sup>*</sup>	8
IT-96D-610	1112.5 (15)	4.6	-6.3	-12.365	18.941 (12)	0.8685	54867.0213 <sup>*</sup>	12
IT-93K-556-4	1263.3 (8)	3.9	23.3	-2.2022	15.423 (10)	1.0717	146397.8179 <sup>**</sup>	16
IT-97K-568-18	1007 (16)	15.2	-4	1.67856	10.067 (7)	0.4678	33794.8469 <sup>ns</sup>	6
IT-99K-1060a	1398.8 (1)	-5.7	-9.6	0.83635	2.8393 (1)	0.9791	75564.1942 <sup>**</sup>	14
95K-1095-4A	1321.8 (3)	-3.5	-11.4	-14.602	17.424 (11)	1.0162	52159.0908 <sup>**</sup>	10
IT-87D-1137	1166 (13)	6.7	2.7	8.33403	23.019 (15)	0.9288	54502.5532 <sup>**</sup>	11
IT-96D-604	1243.2 (9)	-5	5.2	17.1131	5.4225 (2)	1.0573	33105.4728 <sup>ns</sup>	5
93K-619-1	1299.4 (4)	-15.7	-5.9	3.0611	8.4902 (4)	1.5643	48106.9156 <sup>*</sup>	7
IT-93K-293-2-2	1240.1 (10)	11.3	-12.8	-4.9588	23.775 (16)	0.3926	56406.7655 <sup>**</sup>	13
IT-99K-1060	1205.8 (11)	11.4	6.2	3.28577	19.295 (13)	0.5615	24432.4373 <sup>ns</sup>	3
IT-960-604	1199.6 (12)	8	-1.5	0.15715	11.908 (8)	0.6894	5621.6154 <sup>ns</sup>	1
TVU	1288.1 (5)	0	-2.8	-5.6117	12.19 (9)	0.8542	27790.5636 <sup>ns</sup>	4

ns, \* and \*\*, non-significant, significant at p<0.05 and p<0.01, respectively. Numbers in parenthesis represent the pooled mean and ASV rank of genotypes in descending and ascending order, respectively. IPCA 1, IPCA 2 and IPCA 3 = interaction principal component axis one, two and three, respectively, ASV = AMMI stability value, ER's = Eberhart and Russel's model, bi and S<sup>2</sup>di, regression coefficient and deviation from regression, respectively, S<sup>2</sup>di R= rank of deviation from regression.

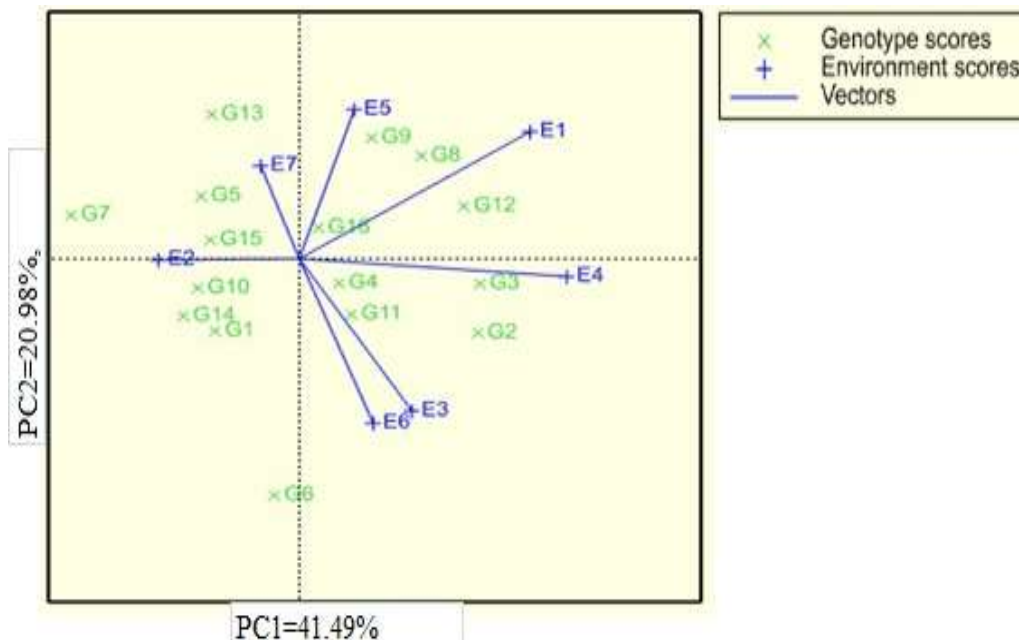


**Figure 1.** Polygon view of genotype by environment interaction for cowpea genotypes.

Yan and Tinker, 2006).

Figure 2 shows the discriminating ability and representativeness of test environments. Accordingly, Melkassa, Sekota and Jinka were more discriminating environments with longer vector and larger angle which

provides much more information about differences among genotypes. These environments cannot be used in selecting superior cowpea genotypes, but are useful in culling unstable genotypes. Babile and Meisso had relatively short vectors and close to origin that all



**Figure 2.** Discriminating power and representativeness of test environments.

genotypes performed similarly, and therefore provides little or no information about the genotypes difference.

Thus, it should not be used as test environments for cowpea genotypes. However, identification and removal of non-informative test environments as well as identification of test environments for yield evaluation trial requires multiyear data (Yan et al., 2007). Arbaminch and Kobo had long vectors and small angles with the abscissa and were ideal for selecting superior genotypes. If budgetary constraints allow only a few test environments, these test environments would be the first choice.

According to Yan and Hunt (2001), discriminating ability and representativeness are the important properties of test environments. An ideal environment should be highly differentiating for the tested genotypes and at the same time representative of the target environment (Yan et al., 2007). Representativeness of the test environment is visualized by the angle formed between the environment vector and abscissa of average environment axis. The smaller the angle, the more representative the environment is (Yan et al., 2007). Environments with longer vectors are more discriminating of the genotypes, whereas environments with very short vectors are little or not informative on the genotype difference (Yan et al., 2007).

## CONCLUSION

TVU (check variety) was identified as the most stable with mean yield above the mean grain yield of genotypes.

Two genotypes, IT-99K-1060a (1398.8 kg/ha) and 86D-378 (1377.1 kg/ha) had first and second highest yield, identified as responsive to favorable environments suggested the need to further test to develop as varieties. Other two genotypes, 95K-1095-4A and 93K-619-1, identified as unstable and highly responsive to environments suggested considering the genotypes as candidate varieties where they performed best. Melkassa, Sekota and Jinka were identified as more discriminating environments, Arbaminch and Kobo were ideal for selecting superior genotypes, but Babile and Meisso were not discriminating environments.

## CONFLICT OF INTERESTS

The authors have not declared any conflict of interests.

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