

YIELD STABILITY AND FARMER PREFERENCE OF COWPEA (*VIGNA UNGUICULATA*) LINES IN SEMI-ARID EASTERN KENYA

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Stability in yields of agronomically acceptable cultivars is generally regarded as the ultimate goal in cowpea improvement. Nine advanced cowpea lines and 3 local checks were evaluated for grain yield in eastern Kenya with the aim of identifying stable genotypes and integrating farmer preferences. The study was conducted in 3 locations over 2 years under a randomized complete block design with 3 replications. Stability was estimated using additive main effects and multiplicative interaction (AMMI) and genotype by environment (GGE) models. There was variation among genotypes, locations and their interactions for grain yield. Genotype G5, G9 and G2 were found to be stable and high yielding. Environments Kit16 and Kit15 were considered as the most suitable for selecting superior genotypes for adaptability and stability. Farmers' criteria for selecting genotypes included early maturing, pod length, disease tolerant and high yielding varieties. Cowpea performance for grain yield was greatly influenced by inherent genotypic factors, environment and their interaction effects.

KEY WORDS: COWPEA, ENVIRONMENT, GENOTYPE BY ENVIRONMENT INTERACTION, STABILITY, GRAIN YIELD

Introduction

Cowpea (*Vigna unguiculata*) is the second most important legume crop after common beans in Kenya, and is cultivated predominately in warm climates in the semi-arid tropics and subtropics (Kariuki, 2015; Sani et al., 2014). Being a drought tolerant and warm weather crop, cowpea is well adapted to the drier regions of the tropics where other food legumes do not perform well (Agbicodo et al., 2009). This crop accounts for roughly 16% of Kenya's pulse production with 90% of the total production occurring and consumed in semi-arid (SAL) region of Eastern Kenya, mainly in Kitui, Machakos, Makueni, Embu, and Tharaka-Nithi counties (USAID, 2010). The SAL region is generally characterized by low, erratic and poorly distributed rainfall ranging from 100 – 900 mm/yearly, resulting in low yields (Miriti et al., 2012).

Cowpea grain is rich in protein with some varieties having up to 30% protein content in addition to micronutrients such as iron and zinc which are necessary for healthy living (Boukar et al., 2011). From its production, rural families derive food, animal feed and

income through the sale of the grain and fresh leaves (IITA, 2009). Further, the bacteria in its root nodules contribute to soil fertility by fixing atmospheric nitrogen in the soil (Tijjani et al., 2015) thereby reducing the need for nitrogen fertilizer and so costs.

Despite its importance, cowpea production in Kenya remains at a low level declining from about 173,000 MT in 2015 to about 146,000 MT in 2017 even though there was an increase in area planted in the year 2017 with 260,000 hectare (ha) compared to 238,000 in the year 2015 (FAOSTAT, 2018). Further, in the farmers' fields cowpea cultivation is poor with less than 0.3 t ha⁻¹, compared to potential yield of more than 1.5 t ha⁻¹ to 2.5 t ha⁻¹ of grain reported in research stations (Ajeibe et al., 2010). The low yield production is attributed to climate related issues including, severe attack of pest complexes, diseases, increases in temperature, frequency of droughts, low soil fertility and the use of inappropriate cultivars (Chepkoech et al., 2018) among other limiting factors. In addition, Hutchinson et al. (2017) argue that, cowpea farmers have a high preference for local land races compared to improved varieties due to their palatability and adaptability despite their low yields attributes.

In the past decades, plant breeders developed improved varieties under controlled experimental conditions in favorable environments with no consideration of farmers' preferences and needs (Ceccarelli et al., 2012; FAO 2014). This scenario resulted in low adoption of developed improved varieties (Luna et al., 2012). A few studies have shown the role of varietal traits on the adoption of improved varieties. For instance, Salifou et al. (2017) reported that farmers adopt improved varieties that combine traits of their choice with features that correspond to their local conditions. Similarly, Saidou et al. (2011) inferred that farmers preferred early maturing varieties, with good grain size, seed coat color and high yielding potential, while Asrat et al. (2009) deduced that farmers preferred crop varieties with strong adaptability and yield stability parameters.

In Kenya there is no information on yield stability based on genotype by environment interaction (GEI) effects coupled with farmers' perceptions and needs. Stability in yields of agronomically acceptable cultivars is generally regarded as the ultimate goal in cowpea improvement (Afyeman et al., 2014). However, yield is a complex quantitative trait and such traits are often controlled by many genes influenced by prevailing environmental effects with each gene having a small effect (Quarrie et al., 2006). The effects of the genotype by environment interaction (GEI) hampers breeding by inducing variations in genotype performance in different environments thereby jeopardizing selection (Cargnin et al., 2006). One strategy for reducing GEI effects involves analyzing for adaptation and stability parameters to identify genotypes with predictable performance which are responsive to environmental variations in specific or wide conditions (Farshadfar et al., 2011; Cruz et al., 2012).

Studies by Vita et al. (2010) and Carvalho et al. (2016) depicted that genotype stability and adaptability to environment can be qualitatively assessed using graphical representation that distributes the genotypes according to their principal component (PC) values. Some of the methodologies used include AMMI (additive main effects and multiplicative interaction) bi-plots model (DDmulira et al., 2015; Santos et al., 2015) and GGE (genotype plus

genotype by environment) bi-plots (Santos *et al.*, 2016). The models combine the analysis of variance of the genotype by environment main effects, with the principal components analysis (PCA) of the G x E interactions, and simultaneously identifies genotypes with high grain yield and stability for a wide range of environments (Mehari *et al.*, 2015). For instance, the AMMI model was effective in distinguishing genotypes that performed in mega-environments and identified varieties that had stable performance in *Vigna radiata* (Singh *et al.*, 2014). Similarly, Funga *et al.* (2017) and Rashidi *et al.* (2013) used the AMMI method to analyze stability and adaptation of chickpea genotypes over eight environments in major chickpea producing areas of Ethiopia and Iran, respectively. The GGE model of analysis has helped to explain GEI in diverse agro-ecologies for cowpeas (Santos *et al.*, 2016), chickpea (Tilahuni *et al.*, 2015; Kanouni *et al.*, 2015); lentil (Idrissi *et al.*, 2019) and pigeon pea (Thanki *et al.*, 2010). The model was used to study varietal stability in mega environments assessment (Kumar *et al.*, 2012). In order to identify the most stable and high yielding genotypes it is imperative to assess the genotypes in multi-environmental trials (Raboanatahiry *et al.*, 2018).

Hence, investigation of the magnitude of the genotype-by-environment interaction as well as the genotypes adaptability and stability is a useful step in developing breeding varieties that will perform to their full potential in the target environments (Muranaka *et al.*, 2016). Therefore, this study was undertaken to evaluate advanced cowpea breeding lines for grain yield stability coupled with smallholder farmers' perceptions and needs in the semi-arid regions of Kenya. Indeed, cultivars with high yielding potential and good adaptability and stability could be recommended for release in different environments in Kenyan.

Materials and Methods

Study Sites

This study was carried out at three experimental stations of the Kenya agricultural Livestock and research organization (KALRO) in Kiboko, Kitui and Kambi Mawe during the cropping seasons of 2015 short rains (SR) and 2016 long rains (LR) representing six testing environments (location by year). The crop was grown under rainfed conditions in Kitui and Kambi mawe testing sites while Kiboko was supplemented with irrigation due to moisture stress. The locations fall under semi-arid region of eastern Kenya (Jaetzold *et al.*, 2006) which experiences a bimodal rainfall pattern with long rains occurring from March - May and short rains from October - December. The rains are usually low, erratic and poorly distributed within the cropping season.

Location	Years	Latitude	Longitude	Altitude (m. asl)	Temp (°C)		Rainfall (mm)	Soil type
					Min	Max		
Kiboko	2015SR	02° 21'S	37° 72'S	975	18	30	≈200	Sandy clay
Kitui	2015SR	01° 37'S	38° 01'S	1155	15	28	≈500	Reddish Sandy loam

Kambi Mawe	2015SR	01° 37'S	37° 40'S	1125	18	29	≈500	Sandy clay
Kiboko	2016LR	02° 21'S	37° 72'S	975	18	30	≈200	Sandy clay
Kitui	2016LR	01° 37'S	38° 01'S	1155	15	28	≈300	Reddish Sandy loam
Kambi Mawe	2016LR	01° 37'S	37° 40'S	1125	15	29	≈300	Sandy clay

* LR= Long rain and SR= Short Rain: Cropping seasons

Table 1: Description of the cowpea study sites in Eastern region

Plant materials and Experimental design

Nine cowpea advanced breeding lines, along with 3 improved check varieties were laid out in a randomized complete block design with three replications. Each breeding line was planted in a 4 row plot of 4 m length with inter-row spacing of 0.6 m and intra-row spacing of 0.2 m. Two seeds were planted per hill and later thinned to one plant per hill two weeks after emergence. Foliar and pod pests were controlled using Imidacloprid + Betacyflutherin and Flubendiamide 480 g/L) whereas fungal and bacterial disease were controlled using copper-oxychloride. The plots were maintained weed free by hand hoeing.

Yield data was collected in two middle rows (net plots) according to International Board for Plant Genetic Resources (IBPGR) cowpea descriptors and extrapolated to grain yield per hectare (t ha⁻¹).

Code	Breeding line	Pedigree
G1	1003	Kvu27-1 (Local check)
G2	1005/1002/1/1/1	IT99K-573-1-1 x M66/1/1/1
G3	1004	K80 (Local check)
G4	1005/1004/5	IT99K-573-1-1 x K80
G5	1003/1001/3	Kvu27-1 x B301
G6	1005/1004/1	IT99K-573-1-1 x M66/1
G7	1002/1005/3	M66 x IT99K-573-1-1/3
G8	1004/1001/3	K80 x B301/3
G9	1005/1003/3	IT99K-573-1-1 x Kvu27-1/3
G10	1005/1002/1	IT99K-573-1-1 x M66/1
G11	1001 (check)	B301 (IITA Check)
G12	1005/1002/2/1/1	IT99K-573-1-1 x M66/2/1/1

Table 2: Cowpea advanced breeding lines tested during the 2015SR and 2016LR season

Data was subjected to analysis of variance (ANOVA) using the Genstat software (Genstat, 2012) statistical programme to determine significance of main effects consisting of year (Y), Location (L) and Genotypes and their interactions (GEI). Grain yield (t ha⁻¹) per en-

vironment was analyzed separately to observe the mean performance. The ANOVA model used was:

$$X_{ijk} = \mu + G_i + L_j + Y_k + (GL)_{ik} + (LY)_{jk} + (GLY)_{ijk}$$

Where, X_{ijk} is the mean yield over r replications of the i^{th} genotype in the j^{th} location in year k with the right side of the equation giving grand mean yield μ and respective main and interaction effects of the genotypes (G), locations (L) and years (Y). The magnitude of variance components was computed as the percentage of total variation to determine the contribution of the main and interaction effects in total variations of yield. Combined mean performance of genotypes for 3 locations and 2 years, treated as six (6) environments, was computed to generate a genotype by environment two-way table data for the bi-plot analysis

Additive main effect and multiplicative interaction analysis

The AMMI model was applied with additive main effect of the 12 cowpea genotypes (G) and six testing environments (3 growing sites and 2 seasons) and multiplicative term for GEI. The AMMI model first fits additive effects for genotypes and environments by ANOVA procedure and then fits multiplicative effects for G x E (genotype environment) by principal component analysis (PCA). The AMMI model according to Farshadfar et al., (2011) is represented as:

$$\gamma_{ij} = \mu + g_i + e_j + \sum_{k=1}^N \lambda_k \alpha_{ik} \gamma_{jk} + \varepsilon_{ij}$$

Where: γ_{ij} is yield of the i^{th} genotype in the j^{th} environment, μ is the overall mean, g_i is the i^{th} genotype mean deviation, e_j is the j^{th} environment mean deviation, λ_k is the square root of the eigen value of PCA axis k , α_{ik} and γ_{jk} are the principal components scores for PCA axis k of the i^{th} genotype and j^{th} environment, respectively, and ε_{ij} is the residual.

The AMMI bi-plot graphic interpretation was based on the variation caused by the main additive effects of genotype and environment and the multiplicative effect of G x E interaction. The abscissa represents the main effects and the ordinate is the first interaction axis (IPCA1). The lower the IPCA value (absolute values), the lower its contribution to the G x E interaction, and therefore, the more stable the genotype. Desirable genotype is a high yielder with IPCA1 scores close to zero while, undesirable genotype has low stability associated with low yield (Ferreira 2006).

Genotype plus genotype by environment Analysis

The Genotype plus genotype by environment (GGE) bi-plots were constructed from the firsts two principal components (PC1 & PC2) derived by subjecting the environment centered yield data which contains G and GE to singular valued composition (Yan and Rajcan, 2002). The first principal component is highly correlated with the main effect of the genotype while the second component represents the part of the yield that results from G x E interaction (Yan et al 2000 ;Yan, 2011). The GGE Bi-plot model maintains the terms G

and G X E together in two multiplicative terms which is shown in the following equation:

$$Y_{ij} - \bar{y}_j = \lambda_1 \xi_{i1} \eta_{j1} + \lambda_2 \xi_{i2} \eta_{j2} + \varepsilon_{ij}$$

Where Y_{ij} is the average yield of genotype i in environment j ; \bar{y}_j is the average yield over all genotypes in environment j ; and $\lambda_1 \xi_{i1} \eta_{j1}$ and $\lambda_2 \xi_{i2} \eta_{j2}$ are the first principal component (PC1) and the second principal component (PC2); λ_1 and λ_2 are the singular values for the first and second principal components PC1 and PC2, respectively, for ξ_{i1} and ξ_{i2} are the PC1 and PC2 scores respectively; for genotype i ; η_{j1} and η_{j2} are the PC1 and PC2 scores respectively, for environment j ; and ε_{ij} is the residual of the model associated with genotype i in the environment j .

The genotype plus genotype and environmental interaction (GGE) bi-plot analysis (Yan, 2001) was used to generate all bi-plot graphs showing (i) ranking of genotypes on basis of mean yield and stability and (ii) which genotype won where pattern (Yan et al., 2007)

Farmers' perceptions and preferences

At the full pod development stage, the research team invited farmer groups who are actively engaged in cowpea production to participate in a variety selection exercise to identify and select farmer preferred genotypes. Stakeholders from the ministry of agriculture and seed merchants were also invited to participate in the exercise. Stakes were placed with a bag attached in front of each plot of the trial to serve as a ballot box for casting the vote. Farmers were allowed to walk through the trial to familiarize themselves with varieties planted before voting. The male and female farmer-participants were provided with different colors of ballots to signify, positive or negative variety of choice by gender. Each farmer was presented with 5 ballots for casting the best and 5 ballots for worst cultivars. After the exercise the votes were tallied by the researchers and a few farmers and the results were presented to the whole group for discussion. Through probing questions guided by a single page questionnaire farmers were requested to outline the criteria of how and why they chose the best varieties and the reasons why they disliked a variety. Each criterion was scored on a scale of 1 to 5 (1= Excellent; 2 = Very Good; 3 = Good; 4= Fair; 5 = Worst) for each variety. Preference score (PS) for each cowpea line was generated by calculating data on positive votes cast minus the negative votes divided by the total number of votes that were cast by the farmers (Paris et al, 2011)

Preference scores (PS) for each variety is calculated as:

$$PS = \frac{\text{Number of positive votes} - \text{negative votes}}{\text{Total number of positive and negative votes}}$$

Results

Combined Analysis of Variance and Cowpea Mean Grain Yield

Results of the combined analysis of variance for grain yield are presented in Table 3 which gives an overall picture of the relative magnitude of genotype (G), year (Y), location (L) and their interactions variance terms. Mean square (MS) associated with genotype (G), year (Y) and location (L) main effects as well as interactions effects of genotype-by-loc-

tion (GL), genotype-by-year-by location (GYL) were highly significant ($p < 0.001$). The partitioning of interactions variance components effects L x Y, G x L and G x Y x L explained 10%, 10% and 8%, total sum of squares (TSS), respectively (Table 3). In contrast, total grain yield variation due to location, year and genotype explained 24%, 15% and 7%, respectively.

The mean grain yield of genotypes differed from year to year ranging between 2.49 t ha⁻¹ to 1.49 t ha⁻¹ in 2015SR cropping season while in 2016LR the performance ranged between 1.62 t ha⁻¹ to 0.90 t ha⁻¹ (Table 4). Overall the mean grain yield value over environments indicated that genotype (G6) 1005/1004/1 had the highest mean of 1.82 t ha⁻¹ with a margin of 35% advantage higher than the lowest grain yield genotype (G10) 1005/1002/1 and with over 5.5% of the highest yielding check variety.

Source of variation	DF	SS	MS	%TSS
Year (Y)	1	17.62	17.61***	15
Location (L)	2	29.27	14.63***	24
L x Y/Environment	2	11.61	5.80***	10
Genotype (G)	11	8.05	0.73***	7
Genotype x Year (GY)	11	5.51	0.5 ^{ns}	5
Genotype x Location (GL)	22	12.64	0.57***	10
Genotype x Year x Location (GYL)	22	9.59	0.44***	8
Error	132	21.66	0.16	

*** Significance at $p \leq 0.001$; ns: non-significant $p > 0.05$

Table 3: Combined analysis of variance of grain yield of 12 cowpea genotypes tested in 3 locations in 2015 and 2016

Genotype	E1 (Kib16LR)	E2 (Kit16LR)	E3 (Kbm16LR)	E4 (Kib15SR)	E5 (Kbm15SR)	E6 (Kit15SR)	Mean	2015	2016
G1	1.04	1.51	0.30	1.80	1.16	1.90	1.28	1.6	0.97
G2	2.16	1.65	0.42	1.93	1.54	2.03	1.62	1.81	1.43
G3	2.52	1.63	0.44	1.88	1.87	2.03	1.73	1.88	1.58
G4	1.82	1.71	0.67	1.93	2.34	2.18	1.77	2.2	1.35
G5	1.76	1.79	0.58	2.08	1.58	2.18	1.66	1.98	1.34
G6	1.44	1.74	0.80	1.94	2.72	2.27	1.82	2.49	1.14
G7	1.77	1.37	0.22	1.62	1.58	1.79	1.39	1.73	1.05
G8	2.89	1.50	0.38	1.72	2.22	1.94	1.77	1.92	1.62

G9	1.93	1.68	0.45	1.97	1.46	2.05	1.59	1.88	1.29
G10	0.85	1.64	0.35	1.97	0.77	1.98	1.26	1.63	0.89
G11	0.88	1.40	0.37	1.62	1.89	1.88	1.34	1.49	1.19
G12	2.38	1.85	0.40	2.22	0.68	2.11	1.61	1.65	1.57
mean	1.78	1.62	0.45	1.89	1.65	2.03	1.57	1.86	1.29

Table 4: Mean grain yield of cowpea genotypes tested in 6 environments (LY) over two years

AMMI analysis of variance for G, E and GEI

The AMMI analysis of cowpea grain yield in six testing environments showed that both IPCA₁ and IPCA₂ were highly significant ($p < 0.001$) (Table 5). IPCA₁ explained 40.68% of genotype by environment (GE) interaction sum of squares, whereas IPCA₂ explained 36.57%. Significant effects ($p < 0.001$) were detected for genotype, environments and the G, GE interactions (Table 5). The environment effect was responsible for greatest proportion of variation (62%), followed by effects of GE interactions and genotypes.

Source of variation	DF	SS	MS	%TSS
Treatments	71	94.28	1.33***	
Genotypes	11	8.05	0.73**	8.5
Environments	5	58.5	11.70***	62.0
Block	12	5	0.42**	
Interactions	55	27.73	0.50***	29.4
IPCA	15	11.28	0.75***	40.68
IPCA	13	10.14	0.78***	36.57
Error/residue	132	21.66	0.16	

Table 5: Additive Main Effect and Multiplicative Interaction analysis for yield of 12 cowpea genotypes

Stability and adaptability analysis

Bi-plot graphs of the AMMI (IPCA₁ & IPCA₂ versus additive effects from genotypes and environments) are shown in Figure 1. The characterization of each promising genotype based on mean grain yield and contribution to GEI by mean of IPCA₁ (Figure 1) indicates that genotype G6 (1005/1004/1) and G4 (1005/1004/5) specifically adapted to environments Kbm15 and Kit15 (Figure 1). In regard to their contribution to GEI (i.e. stability) the IPCA₁ score, genotypes G4 was most stable in Kit15 while genotype G6 in environment Kbm15 amongst the high yielding environments. On the other hand, genotypes G5 (1005/1003/3), G9 (1005/1003/3) and G2 (1005/1002/1/1/1) were most stable and broadly adapted, as indicated by values near origin of the IPCA₁ and had smaller contribution to genotype by environmental interactions (GEI) as indicated IPCA₂ scores. Genotype G7 was a relatively stable but had a grain yield lower than the grand mean.

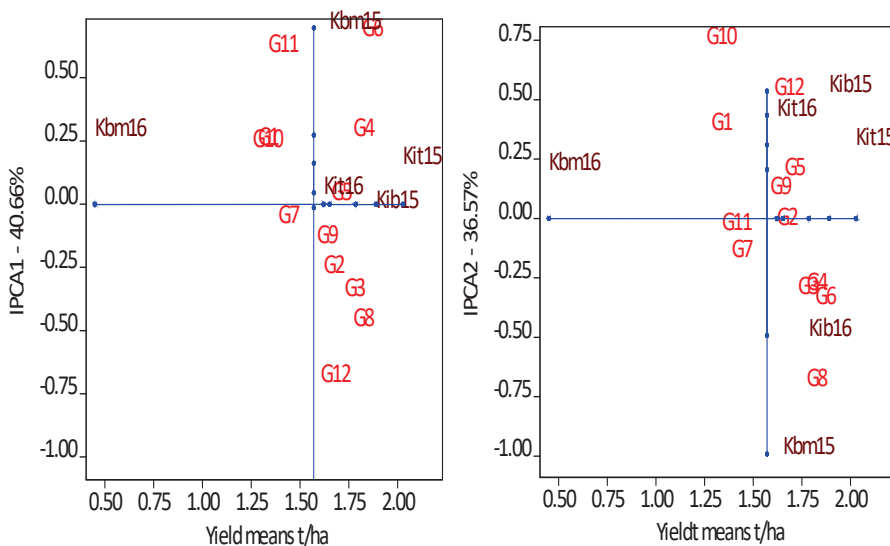


Figure 1: AMMI Bi-plot cowpea genotype and environment of IPCA1 & 2 versus grain yield (t ha⁻¹) of 12 genotypes in 6 environments.

The lowest yielding environment Kbm16 (Kambi mawe 2016 LR) recorded positive IPCA 1 & 2 (Fig 1) scores and was located at some distance from all genotypes showing that it interacted poorly with genotypes. Environment Kit16 (Kitui 2016LR) elicited low interactions with most of the genotypes as it was located near point of origin (low IPCA scores).

Genotype and Genotype by Environment yield performance

The Genotype and Genotype by Environment (GGE) bi-plots describes the genotypic main effects (G) and genotype-by-environment interactions (GE) effect. In this study, the results of GGE bi-plots showed that the first two principal components (PC1 and PC2) accounted for 75.2% total variation caused by G + GEI. PC1 accounted for 44.37% while PC2 32.82 % of the total variation (Figure 2[i & ii]). Figure 2(i) shows mean yield and stability performance of the tested genotypes based on the average tester coordinate (ATC) axis. The stability and mean yield performance of genotype is measured by the projections of their markers on the ATC axis. Short projections to the axis indicate genotypes with high stability while long vectors elicit unstable genotypes. Genotypes G5, G7 and G3 had very short vectors in relation to the ATC axis indicating high stability while G10 and G1 depicted least stability with poor performance (Figure 2[i]). Genotype G5, G2, G9, and G3 exhibited the highest stability and achieved a grain yield above the overall mean. However, genotypes G6, G4, G8 and G12 though high yielding were unstable genotypes across environments as explained by long projection vectors on the ATC axis.

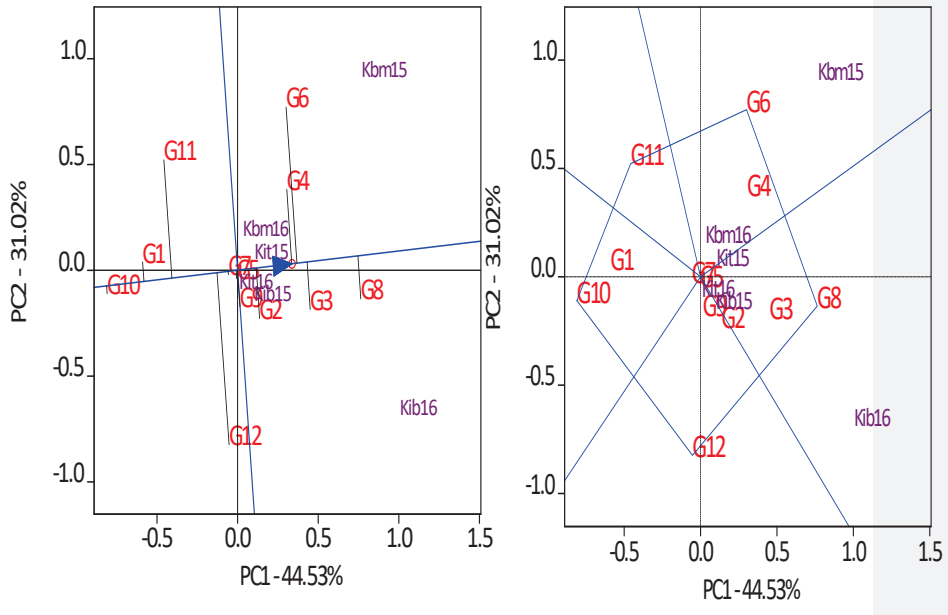


Figure 2: AEC results of GGE bi-plot for (i) Yield stability (ii) Which-won-where. Environments Kib16 reps. Kiboko 2016 Long Rain, Kib15 Kiboko 2015 Short Rain, Kbm16 for Kambi Mawe 2016 Long Rain, Kbm15 = Kambi Mawe 2015 Short Rain,

Figure 2(ii) shows the vertices of the polygon with genotype markers located farthest away from the bi-plot origin, such that all the genotypes are contained within the polygon. The test environments fell into three cowpea growing mega-environments out of five sectors outlined in polygon view. The first grouping of mega-environments was represented by Kbm16 and Kbm15, while the second mega-environment by Kib16 and Kit15SR and third with Kib15 and Kit16.

Genotype G6 and G4 was associated with mega-environment groups Kbm15 and Kbm16 with G6 being at the vertex. The second mega environments Kib16 and Kit15 contained genotype G8 as the most responsive genotype and G3, while the third mega-environmental group was Kib15 and Kit16 with G5, G9 and G2, with winning genotype (G12) 1005/1002/2/1/1 at the vertex. Two vertex genotypes G11 (1001) and G10 (1005/1002/1) without any environment were the poorest genotypes in most of the environments with the lowest mean yield.

Farmer preferences in selection of cowpea genotypes

Figure 3 shows the farmer preference score (PS) and perceptions of best and least preferred genotypes by male and female participants (Fig 3). Both genders agreed on their preferences for the best performing genotypes tested in cowpea trials. For example, genotypes G7, G8, and G5 were preferred by both male and female farmers (Fig. 3). Similarly, comparing the farmers' results and yield data calculated by the researcher in Table

4, female farmers chose genotypes G4, G8, G7 and G6 which were superior genotypes in yield attributes whereas male participants selected genotypes G5, G7 and G3 (Fig 3).

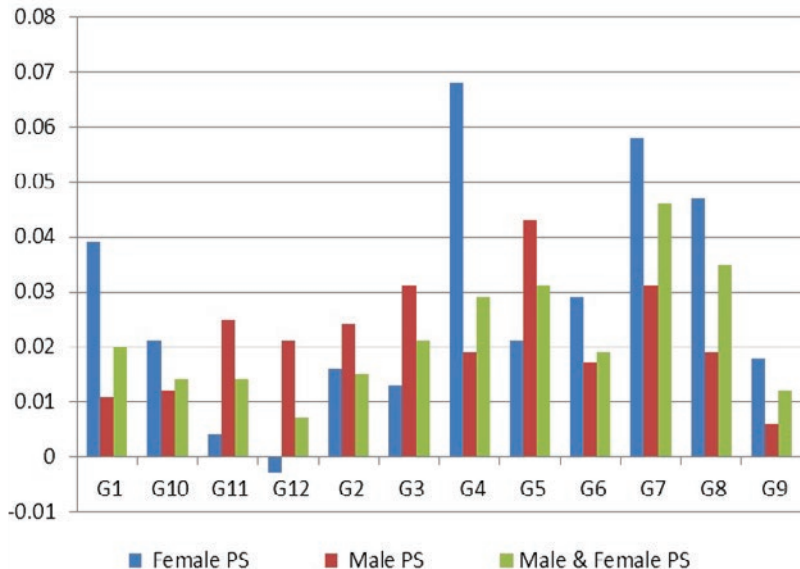


Figure 3: Preference scores of cowpea genotypes preferred by male and female farmers and combined perceptions in eastern Kenya

Figure 4, shows criteria of how both male and female farmers selected best and preferred cowpea genotypes for growing in their own environments. Early maturing long pods, high yielding and disease resistant varieties were the criteria adopted by farmers. Women selected genotypes with large grain with good seed color as significant criteria.

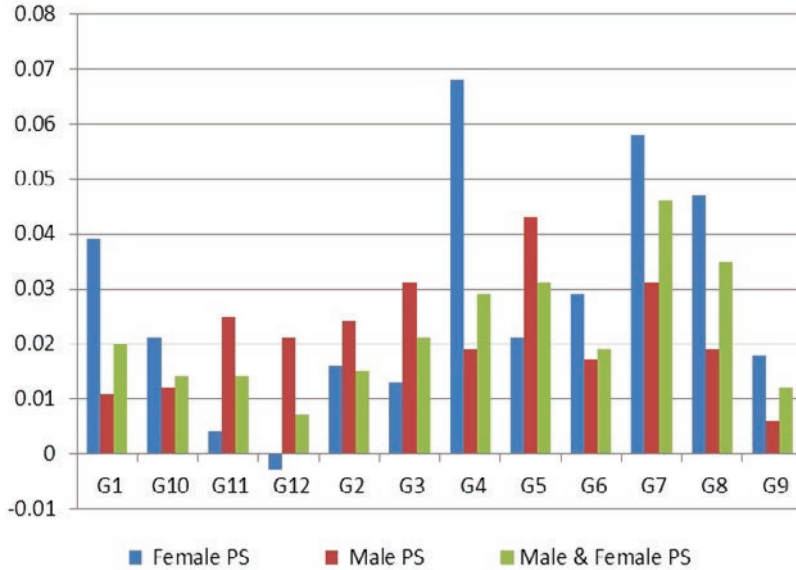


Figure 4: Farmers' criteria in selecting preferred cowpea genotypes

Discussion

The presence of significant genotype (G), years (Y, location (L) main effects and genotype by environment (GE) in ANOVA suggests differential responses of the genotypes and the need to identify high yielding and stable genotypes across test environments. Sousa et al., (2018) found similar results for these three sources of variation in cowpea genotypes. The location (L) variation (24%) indicated that the tested locations in this current study were diverse with the largest differences among locations effects causing the most variation in genotype performance. The magnitude of genotype by location interactions (10%) for yield per hectare ($t\ ha^{-1}$) was larger than that of genotype (7%). The G x L interactions effects demonstrated that genotypes responded differently to different locations, confirming the importance of testing cowpea genotypes at multi-locations in Eastern Kenya. Oladosu et al., (2017) reported differences in responses of genotype across locations in different seasons. In addition variation due to locations and years (LY/ environment) and genotype by environment interaction (GEI) in relation to genotype effect suggested that there was possibility of existence of mega environments with different genotypes.

Differences in grain yield ($t\ ha^{-1}$) means were observed in genotypes evaluated in different environments. The highest grain yield was detected by genotype 1005 x 1004/1 (G6) which had a yield advantage of 35% compared to the worst performing genotype 1005 x 1002/1 (G10). Muranaka et al., (2016) suggested that high grain yield variation could be due to greater differences between the genotypes and seasons. Nonetheless, yield levels above the mean alone is not sufficient for cultivar selection, but cultivars should be stable and perform much better than the check varieties (Kaya et al., 2006). In addition, Olayi-

wola et al. (2015) and Olayiwola & Arroyo (2013) reported the consequences of selecting high yielding but unstable genotypes in breeding programs to avoid commercial losses. The AMMI analysis of cowpea grain yield in 6 production environments showed that 62% of the sums of squares was explained by environment (E) and 8.5% and 29.4% were attributable to genotype (G) and GEI, respectively. The large variations in environmental percentage for sum of squares reflect the significant differences in environments. The environment showed much variability in both additive main effects and interactions. Similar results were observed by Oliveira et al., (2013) and Jeberson et al., (2017) in their studies of passion fruit and bread wheat, respectively, in which most of the variation was attributed to environmental factors and G x E interaction. This was mainly due to the fact that biophysical attributes (biotic stresses, soils, temperatures and rainfall found at each location were highly variable) (Rukuni et al., 2006). In line with this, semi-arid regions of Kenya are known to have 2 agro-ecological zones that are diverse in physical properties such as soils, rainfall and temperatures (Jaetzold et al., 2006). Indeed in this study, there was relatively more rainfall in 2015SR than 2016LR as shown in Table 2.

The study of Yan, (2011) elucidated that, the closer the IPCA scores are to zero the more stable the genotypes are across environments. Genotypes G5, G9 and G2 in AMMI analysis were broadly adapted and stable since they were located near the origin and hence insensitive to environmental interactions. Environments E2 and E4 revealed low interactions as they were near the point of origin compared to E6 and E5 which were positioned far away (Fig 1). The position of genotype or environment provides some insight into GEI (Ceccarelli, 2012). Similarly, the GGE bi-plot results showed genotypes G5, G2, G9, G7 and G3 had very short vectors in relation to ATC axis indicating high stability. Similar results were also described by Krzysztof & Marcin, (2016). A genotype which has a shorter absolute length of projection in either of the two directions of the AEC ordinate (located closer to AEC abscissa), represents a smaller tendency of GEI which means it is the most stable genotype across different environments or vice versa (Ceccarelli, 2012; Yan et al, 2007). Equally, genotype G11 (1001) and G7 (1002/1005/3) exhibited stable characteristics, though with lower mean grain yield. Oliviera & Godoy (2006), suggested most stable genotypes do not always have the best yield.

The response of genotypes in different locations and Genotype by environment interaction (GEI) in relation to genotype effect suggested the possibility of mega environments with different genotypes (Oladosu et al., 2017). The bi-plot detected 3 mega-environments: first Kbm16LR (E3) and Kbm15SR (E5), second Kib16LR (E1) and Kit15SR (E6), and third Kib15SR (E4) and Kit16LR (E2). The environmental markers that have a short vector closer to the bi-plot origin are less interactive and it is considered an effective measure for selecting genotypes with average performance and adaptations (Murphy et al., 2009). In this case, environments Kit16LR (E2) and Kit15SR (E6) are less interactive with genotypes and therefore good environments for testing cowpea genotypes for adaptability and stability. According to Akter et al. (2014), the genotypes that cluster together tend to have a similar response in all environments while genotypes that are far apart differ in response to the environments. Therefore genotypes distant from origin is

sensitive and have large interactions whereas those closer to the origin are not sensitive to environmental interactions. This method provides a more efficient exploration of the GEI to identify, select stable and adapted genotypes for specific environments and mega-environments (Safari et al., 2014). The vertex genotypes in this study were 1005/1004/1 (G6), 1004/1001/3 (G8), 1005/ 1002/2/1/1 (G12), 1001 (G11) and 1005/1002/1 (G10). These genotypes were either best or poorest performers in some or all of the sites because they were located at the furthest distance from the origin of the bi-plot (Yan et al 2002; Yan et al, 2007).

Farmer preferences for cowpea genotypes

Participatory breeding is usually conducted to ensure adoption of newly developed crop cultivars and their production packages (Ceccareli et al., 2007). Formal cultivar selection and crop improvement programmes often focus on a few economically important traits such as yield and disease resistance (Alene & Manyong, 2006). In this study, farmers generally preferred early maturing genotypes for drought escape, high yielding, pest and disease tolerant varieties with low shattering ability. During discussions with the farmers, the color of the grain and the grain size characteristics were mentioned for marketability. Tolerance to biotic and abiotic stresses, earliness, marketability, cooking characteristics, seed color and size and growth habit were important selection criterion (Assefa et al (2005), Humphries et al (2005) and Asfan et al. (2012). A lack of engagement between researchers and local farmers is a primary causes for low adoption of newly developed improved crop cultivars (Luna et al., 2011, Adesina and Baidu-Forson, 1995).

Conclusion and Recommendation

The study established that cowpea performance for grain yield is greatly influenced by inherent genotypic factors, environment and their interaction effects, indicating the usefulness of GGE and AMMI analysis in distinguishing superior and stable genotypes. Genotype G5, G9 and G2 were regarded as ideal genotypes due to their high stability and high yield potential and can be recommended for release. The study also inferred that environments (E2) Kitr6LR and (E6) Kit15SR are less interactive with genotypes and therefore, good environments for testing cowpea genotypes for adaptability and stability across eastern Kenya. Comparing farmers' preference scores with the calculated results for mean grain yield, it was concluded that farmers can predict strong performing varieties attributed to yield potential. Understanding farmer knowledge regarding varietal preference is important in the breeding of cowpea improvement for acceptance and eventual adoption. This study deduced that there are varied preferences and needs among the end users of the cowpea. Production of cowpea with consumer preferred attributes could enhance adoption and boost its cultivation in Kenya.

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