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Yield stability among cowpea genotypes evaluated in different environments in Uganda

E. K. Mbeyagala1,2*, J. B. Ariko1, A. O. Atimango1 and E. S Amuge1

Abstract: Cowpea (Vigna unguiculata) is one of the important legume crops in Uganda especially in the eastern and northern regions. Its productivity in the country is, however, still low. Environmental constraints and occurrence of genotype × environment interactions (G × E) contribute greatly to the low production. In this study, an additive main effects and multiplicative interaction analysis (AMMI) model was used to assess the yield stability of 30 cowpea genotypes planted in five locations for three consecutive seasons. Also, the relationship of G × E interaction with genotypic/weather variables was analysed. AMMI analysis of variance indicated that environment had the highest contribution to the variation in grain yield. Postdictive success method indicated AMM1-3 as the best model since the first three interaction principal component axes (PCA1, PCA2, PCA3) were significant (p = 0.0000). Together, the first three PCAs explained 75.1% of the G × E interaction sum of squares. However, according to the predictive success method, AMMI-1 was the best model. The AMMI stability value (ASV) identified five genotypes; UCR 5279, Ayiýi, IT07K-257-33, ACC122*WC66 and IT06K-281-1 as being more stable. These

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PUBLIC INTEREST STATEMENT

Cowpea is widely grown in Uganda mainly for its fresh leaves and edible dry grain and is a major leguminous crop after common bean, groundnuts and soybean. Despite its importance, productivity at farm level is still low partly due to lack of varieties that can suit a wide range of farmers’ contexts/conditions. This study has identified five cowpea genotypes with a good combination of high yield and stability across a range of environments. Release of these genotypes as varieties and their adoption by farmers would contribute greatly to enhanced cowpea productivity.
are recommended for release as varieties after confirmation of their preference by farmers. Results in this study also showed that $G \times E$ interaction was associated with the interaction of temperature, rainfall, relative humidity, days to maturity, number of seeds per pod, number of pods per plant and yield per plant.

**Subjects:** Crop Science; Environmental Sciences; Agriculture and Food

**Keywords:** AMMI stability value; Vigna unguiculata; $G \times E$; Stability; GGE; PCA

1. **Introduction**

Cowpea (*Vigna unguiculata* (L.) Walp) is a multipurpose legume providing food for humans and livestock and it is also a key source of income for farmers and grain traders especially in the tropical environments (Timko & Singh, 2008). The species *Vigna unguiculata* includes cultivated forms (*Vigna unguiculata* ssp. *Unguiculata var. unguiculata*), wild annual forms (*ssp. Unguiculata var. spontanea*) and wild perennial subspecies (Pasquet, 2000). Cultivated cowpea, subspecies *Unguiculata* is divided into five cultivar-groups (*Cv-gr.*); *Cv-gr.* *Unguiculata*, *Cv-gr.* *Biflora*, *Cv-gr.* *Sesquipedalis* (yard long bean), *Cv-gr.* *Textilis* and *Cv-gr.* *Melanophthalmus* (Pasquet, 1998). The cultivated forms include both the grain type grown for dry grains (pulse) as well as the vegetable type grown for green pods (fresh shell peas and immature, fresh pods or snaps) (Som & Hazra, 1993; Uguru, 1996; Fery et al., 2007). The distribution of these cultivar-groups is based on their roles and forms of utilization with most commonly grown cowpea varieties in Africa belonging to *Cv-gr.* *Unguiculata* (pulse/dry grain), cultivars grown in Asia for seed and fodder are intergrades of *Cv-gr.* *Unguiculata* and *Cv-gr.* *Biflora*, while those grown for green pods are intergrades of *Cv-gr.* *Unguiculata* and *Cv-gr.* *Sesquipedalis*. *Cv-gr.* *Textilis* is mainly grown in West Africa for fibre extracted from its long peduncles (Som & Hazra, 1993). In Uganda like many other African countries, varieties belonging to *Cv-gr.* *Unguiculata* are predominantly grown. Farmers desire varieties that display temporal stability, that is, performing consistently from year to year as opposed to varieties that perform consistently from location to location (spatial stability) (Kang, 2002; Okori et al., 2019). While several factors are known to influence variety adoption by farmers, the most important one is the yield potential (real/perceived) (Ghimire et al., 2015; Langyintuo & Mungoma, 2008). However, expression of yield trait is subject to modification due to environment/management practices and genotype by environment interactions ($G \times E$) (Kang, 2002). Large $G \times E$ makes it difficult to accurately partition the contributions of cultivars and improved management/environment and therefore highlights the need for cultivar testing in multiple environments to obtain reliable results. Yield data from multi-environmental trials (METs) make it possible to identify genotypes with consistent year-to-year (temporal variation) performance and those with consistent location-to-location (spatial variation) performance (Kang, 2002). However, yield data from METs often have both significant main effects and significant $G \times E$ interactions which render traditional statistical approaches inadequate for instance, analysis of variance (ANOVA) gives no insights into the patterns of environment or genotypes that lead to $G \times E$, principal component analysis (PCA) despite being a multiplicative model is less effective in analysing $G \times E$ since it omits additive main effects (Zobel et al., 1988). The linear regression model (LR) was reported to be effective in analysing both main effects and interaction since it combines both additive and multiplicative components (Finlay & Wilkinson, 1963). However, effectiveness of LR can only be achieved if the pattern of interaction terms fits a specific regression model (Westcott, 1986; Becker and Leon, 1988; Zobel et al., 1988). Malosetti et al. (2013) in their study of a maize data set, the additive main effects and multiplicative interaction analysis (AMMI) and genotype main effects and genotype by environment interaction biplots (GGE) were both useful in exploring $G \times E$. However, previous studies show that AMMI is a superior and powerful approach in deciphering agronomically important as well as statistically significant $G \times E$ interactions in yield trials (Zobel et al. 1988; Gauch & Zobel, 1997; Gauch, 2006). AMMI partitions the overall variation into genotype main effects, environment main effects and $G \times E$ interactions. Additionally, the principal component parts of AMMI can accurately separate key signal-rich portion of the interaction from early
components while discarding the noise-rich portion in late components (Gauch et al., 2008). In this study, G × E interaction for grain yield among cowpea genotypes in Uganda was analysed using AMMI method. This is because AMMI analysis is very efficient in identifying both high yielding and stable genotypes (Asio et al., 2005). AMMI analysis has been extensively used to determine stable cowpea genotypes (Asio et al., 2005; Ddamulira et al., 2015; Horn et al., 2018; Tariku et al., 2018; Kuruma et al., 2019; Abiriga et al., 2020; Haisirikul et al. 2020). The AMMI method has also been used to assess the causes of G × E interactions in crops like rye grass (van Eeuwijk and Elgersma, 1993) and wheat (Mohammadi et al., 2017) but not cowpea. Thus, this study also investigated the relative influence of genotypic traits and weather variables on G × E among cowpea genotypes under rainfed conditions.

2. Materials and methods

2.1. Cowpea germplasm

Twenty-seven cowpea lines obtained from cowpea-breeding programmes at the National Semi-Arid Resources Research Institute (NaSARRI) and Makerere University Centre for Crop Improvement (MARCCI) were used in this study. Three released varieties; SECOW2W, NAROCOWPEA 3 and NAROCOWPEA 5 were included as checks in all the trials. The checks were obtained from the cowpea breeding programme at NaSARRI. Descriptions of the genotypes evaluated in this study are given in Table 1 below.

2.2. Test sites

The study was conducted in five locations (Serere, Mayuge, Lira, Kitgum and Arua) that are representative of cowpea-growing areas in the country (Figure 1). The study was conducted for three consecutive cropping seasons: second season of 2018 (2018B), first season of 2019 (2019A), and second season of 2019 (2019B). Each location and season constituted an environment resulting in a total of 13 environments in which data was collected. The characteristics of trial sites are given in Table 2.

2.3. Experiment design and management of trials

Each test material was planted in four rows, spaced at 60 cm between rows and 30 cm within rows. Test materials were planted in plots ranging from 3.6 to 5.4 square metres per plot. In 2018B, trials were planted on 8 October, 11 October and 16 October in Arua, Lira and Serere, respectively. In 2019A, trials were planted on 24 April, 2 May, 4 May and 16 May in Serere, Mayuge, Lira and Kitgum, respectively. In 2019B, planting was done on 27/9/2019, 28/9/2019, 29/9/2019, 1/10/2019, 30/9/2019 in Serere, Mayuge, Lira, Kitgum and Arua, respectively. Harvesting of 2018B trials was carried out on 8 January, 10 January, and 24 January 2019 in Arua, Lira and Serere, respectively, while harvesting of 2019A trials was done on 15th July, 25th July, 26th July and 27th July 2019 in Serere, Mayuge, Lira, and Kitgum, respectively. Harvesting of 2019B trials was carried out on 15/12/2019, 18/12/2019, 19/12/2019, 20/12/2019, 21/12/2019 in Serere, Mayuge, Lira, Kitgum and Arua, respectively. The trials were laid out in an alpha lattice (resolvable incomplete block) design with three replicates at each trial site. Experimental layout/designs were generated using Breeding Management System (BMS) of the Integrated Breeding Platform (IBP) available at https://www.integratedbreeding.net. Recommended agronomic practices for weeding, thinning, pest management and harvesting were followed. Harvesting and postharvest operations were carried out manually on a plot basis. Harvested pods from each plot were sun-dried before threshing.

2.4. Data collection

At maturity, pods from all plants from each plot were harvested, sun-dried and threshed, and plot yield was established. Plot seed yield was then used to determine yield per hectare. Data on other yield traits such as pod length, number of seeds per pod, pod weight per plant, seed weight per plant, 100 seed weight and reaction to fungal, bacterial and viral diseases were also recorded in all the trials.
Meteorological data for monthly average temperature, monthly minimum temperature, monthly maximum temperature, monthly total precipitation, monthly radiation, average monthly relative humidity, minimum monthly relative humidity, monthly maximum relative humidity, monthly average wind speed, monthly maximum wind speed and monthly minimum wind speed were obtained from Automatic Weather Stations installed by Uganda National Meteorological Authority (UNMA) across the country. For locations where weather data were not available, data from a nearby station was used.

2.5. Data analysis
Combined analysis of variance (ANOVA) for grain yield data was carried out across all environments. The environments were treated as random variables while genotypes were treated as fixed variables. Additive Main Effects and Multiplicative Interaction (AMMI) analysis was carried out using agricolae package version 1.3-3 (Mendiburu, 2020). All analyses were undertaken with R statistical software Version 4.0.2 (R Core Team, 2020). The following AMMI model was used:

\[ Y_{ij} = \mu + g_i + \epsilon_j + \sum_{n=1}^{N} \lambda_n g_i \epsilon_j + \rho_{ij} + \epsilon_{ijk} \]

Where \( Y_{ij} \) is the yield of the \( i \)th genotype in the \( j \)th environment; \( \mu \) is the grand mean; \( g_i \) and \( \epsilon_j \) are the genotype and environment deviations from the grand mean, respectively; \( \lambda_n \) is the eigenvalue of the principal component (PCA) analysis \( n \); \( \gamma_m \) and \( \delta_n \) are the genotype and environment PCA scores (eigenvectors) for axis \( n \); \( n \) is the number of PCs retained in the model; \( \rho_{ij} \) is the interaction residual and \( \epsilon_{ijk} \) is the random error.

Since the AMMI method does not provide for a measure to quantify and rank genotypes according to their yield stability, we used AMMI’s stability value (ASV) proposed by Purchase (1997) as stated below:

\[ ASV = \sqrt{\frac{\text{IPCA1sumofSquares}}{\text{IPCA2sumofSquares}}} \left( \frac{\text{IPCA1score}}{\text{IPCA1score}} \right)^2 + \left( \frac{\text{IPCA2score}}{\text{IPCA2score}} \right)^2 \]

3. Results

3.1. Analysis of variance and principal components analysis of cowpea grain yield data
ANOVA showed genotypes differed significantly \( (P < 0.000001) \) in mean yields. Environmental effects were significantly different \( (P = 0.000000) \). \( G \times E \) interactions were also significant \( (P < 0.000001) \) showing that genotypes responded differently to variations in environmental conditions during the study period. The postdictive success through the multiplicative terms indicated three significant PCAs (Table 3), which indicated AMMI-3 as the best model. The three PCAs accounted for 37%, 21% and 17.3% of the total \( G \times E \) interaction for PCA1, PCA2 and PCA3, respectively. Taken together, the first three PCAs accounted for 75.1% of the total \( G \times E \) variation in grain yield among the cowpea genotypes evaluated. The remaining nine PCAs accounted for 24.9% of the \( G \times E \) interaction although their contributions were non-significant \( (P > 0.05) \).

To characterize the \( G \times E \) interaction, a biplot was generated using genotype and environmental mean yields and their PCA1 scores (Figure 2). Environments with scores near zero had little \( G \times E \) interaction across genotypes and thus had low discrimination among genotypes. This trend was observed for environments Lira18B, Serere18B and Kitgum19B. On the other hand, environments Arua19A and Kitgum19A had high interaction across genotypes and therefore provided the highest discrimination among genotypes. Genotypes or environments on the same parallel line relative to the abscissa have the same yield (Figure 2) and genotypes or environments on the right side of the midpoint axis have high yields than those on the left side. Thus, environments, Mayuge19B, Serere19B, Arua18B, Lira19B, Kitgum19B and Lira18B had low yields. Mayuge19B and Serere19B were the lowest yielding environments as well as low interaction. On the other hand, environments with high yields were Arua19A, Kitgum19A, Mayuge19A, Serere19A, Lira19A and Kitgum19A. The
Table 1. List of cowpea genotypes evaluated

| Genotype | Entry No | Type            | Institution | Country of Origin |
|----------|----------|-----------------|-------------|-------------------|
| IT98K-503-1 | 1         | Breeding line   | IITA        | Nigeria           |
| Ayiyi     | 2         | Cultivar        | CSIR-CRI    | Ghana             |
| MU9       | 3         | Landrace        | NaSARRI     | Uganda            |
| CP 4      | 4         | Landrace        | MARCCI      | Uganda            |
| Videza    | 5         | Cultivar        | CSIR-CRI    | Ghana             |
| WC35C     | 6         | Landrace        | NaSARRI     | Uganda            |
| Danila    | 7         | Landrace        | IITA        | Nigeria           |
| WC66*SEC5T | 8      | Advanced line   | MARCCI      | Uganda            |
| SEC1*TIT93K-45-1 | 9 | Advanced line   | MARCCI      | Uganda            |
| WC35B*WC10 | 10     | Advanced line   | MARCCI      | Uganda            |
| ACC122*WC66 | 11     | Advanced line   | MARCCI      | Uganda            |
| SEC3B*TIT99K | 12   | Advanced line   | MARCCI      | Uganda            |
| TVu-1348S | 13       | Landrace        | IITA        | Kenya             |
| TVu-1544S | 14       | Landrace        | IITA        | Swaziland         |
| IT93K-503-1 | 15*     | Breeding line   | IITA        | Nigeria           |
| TVu-8923  | 16       | Landrace        | IITA        | Nigeria           |
| UCR 5279  | 17       | Breeding line   | UCR         | USA               |
| IT07K-309-44 | 18    | Breeding line   | IITA        | Nigeria           |
| NAROCOWPEA 3 | 19     | Cultivar        | NaSARRI     | Uganda            |
| NAROCOWPEA 5 | 20     | Cultivar        | NaSARRI     | Uganda            |
| SECOW2    | 21       | Cultivar        | NaSARRI     | Uganda            |
| IT08K-149-3 | 22     | Breeding line   | IITA        | Nigeria           |
| IT06K-137-1 | 23     | Breeding line   | IITA        | Nigeria           |
| IT06K-134-1 | 24     | Breeding line   | IITA        | Nigeria           |
| IT07K-188-49 | 25   | Breeding line   | IITA        | Nigeria           |
| IT07K-211-1-8 | 26  | Breeding line   | IITA        | Nigeria           |
| IT07K-187-24 | 27    | Breeding line   | IITA        | Nigeria           |
| IT07K-257-33 | 28    | Breeding line   | IITA        | Nigeria           |
| IT06K-281-1 | 29     | Breeding line   | IITA        | Nigeria           |
| IT07K-292-10 | 30    | Breeding line   | IITA        | Nigeria           |

*Entry 15 was eliminated from analysis due to very poor plant stand in all environments.

The highest yielding environments were Arua19A and Kitgum19A and these also had the highest contribution to G × E interaction (Figure 2). By just considering PCA1 scores as an indication of stability of genotypes across environments, the most stable genotypes were 2, 8, 11, 17, and 19 since they had the lowest PCA1 scores. The less stable genotypes were 14 and two released varieties (20 and 21) as these had the highest PCA1 scores. Genotypes 14, 12, and 18 interacted positively with environments Arua19A and Mayuge19A but negatively with environments Lira19B, Kitgum19B, Arua18B and Serere19B. The high-yielding genotypes such as 28, 1, 9 interacted positively with the high-yielding environments Lira19A and Kitgum19A but negatively with the low yielding environments Serere19B, Arua18B, Lira19B and Kitgum19B.

However, since PCA2 contributed significantly (21%) to G × E interaction, the PCA1 was also plotted against PCA2 scores (Figure 3) to further explore the stability. In this biplot (Figure 3), Entry 19 appears less stable indicating its strong reaction to PCA2. Other entries that showed
Figure 1. Location of cowpea trial sites in Uganda.

Table 2. Characteristics of trials sites used in evaluation of cowpea genotypes

| Location | Longitude  | Latitude  | Altitude (m. a.s.l) | Mean annual Rainfall(mm) | Mean annual Temperature (°C) | Soil texture |
|----------|------------|-----------|---------------------|--------------------------|-----------------------------|-------------|
|          |            |           |                     | 2018 | 2019 | 2018 | 2019 |                     |            |
| Serere   | 33.447120E | 1.536744 N | 1,140              | 2,242 | 3,379 | 23.6 | 23.8 | Sandy loam       |            |
| Lira     | 32.914027E | 2.297487 N | 1,084              | 1,504.8 | 1,559.2 | 23.2 | 23.4 | Sandy loam       |            |
| Kitgum   | 32.887770E | 3.290085 N | 941                | 10,264 | 2,369.3 | 23.2 | 23.3 | Loamy sand       |            |
| Arua     | 30.947898E | 3.078586 N | 1,206              | 1.4 | 347.1 | 19.8 | 12.4 | Sandy clay       |            |
| Mayuge   | 33.476585E | 0.438806 N | 1,192              | 4,244.3 | 2,384.4 | 22.4 | 22.5 | Loam             |            |

Source: Uganda National Meteorological Authority (UNMA)

A strong reaction to PCA2 were 1, 5 and 7. The most stable entries were 2, 8, 11, 17, 28, and 29.

The correlation coefficients between the first three PCAs from the AMMI model and various genotypic/environmental variables are presented in Table 4. PCA1 scores had a strong positive correlation with weather variables of average monthly temperature (p < 0.01), minimum monthly temperature (p < 0.01) and rainfall (p < 0.05). PCA1 scores were however, negatively and strongly correlated with monthly average relative humidity (p < 0.05), monthly minimum relative humidity (p < 0.05) and monthly maximum relative humidity (p < 0.01). Among the genotypic variables, PCA1 was negatively correlated with days to 90% maturity (p < 0.05) but positively correlated with number of seeds per pod (p < 0.01). For PCA2 scores, there was significant negative correlation with monthly radiation and monthly average wind speed (p < 0.05) while among the genotypic variables, there was negative correlation with number of pods per plant and grain yield per plant.
(p < 0.05). On the other hand, PCA3 scores were not correlated with any of the genotypic or meteorological variables.

3.2. Stability ranking of cowpea genotypes

Utilizing AMMI’s stability value (ASV), we identified cowpea genotypes with improved stability. The most stable genotypes across environments were 17 (UCR 5279), 2 (Aiyi), 28 (IT07K-257-33), 11 (ACC122*WC66), IT06K-281-1 (29) with lowest ASV values of 0.946838, 1.125361, 1.379295, 1.429973 and 1.563943, respectively (Table 5). On the other hand, genotype TVU 15445 (14), and two checks [NAROCOWPEA 5 (20) and SECOW2W (21) were unstable as indicated by high ASV values of 48.16704, 29.66733 and 28.767, respectively.

4. Discussion

As breeders and geneticists worldwide continue to widen the genetic base of several crops in order to avoid problems associated with genetic vulnerability, G × E or differential responses of improved cultivars in different environments (sites and/or years) are expected (Kong, 2002). Eisemann et al. (1990) suggested that where significant G × E interactions exist, they should not be ignored but rather exploited. Exploiting G × E involves assessing the stability of performance of different genotypes across diverse environments by analysing and interpreting genotypic and environmental differences. AMMI is one of the foremost statistical models for analysing data from multi-environment yield trials for various crops (Zobel et al., 1988; Gauch, 2006; Gauch et al., 2008; Sabaghnia et al., 2008). Thus, this study employed AMMI method of analysis to determine the adaptability of cowpea genotypes to growing areas in Uganda.

In this study, three PCAs accounted for the observed variation in G × E since their F tests indicated strong significance (Table 3). Similar results were reported by Crossa (1990) and Tukamuhabwa et al. (2012) for soybean genotypes as well as Tariku et al. (2018) for cowpea genotypes. However, Sabaghnia et al. (2008) reported a more complex interaction with up to seven PCAs. The complexity of the G × E is attributed to several factors such as nature of the crop, environmental conditions as well as germplasm/genotype diversity (Crossa, 1990; Mohammadi et al., 2017; Sabaghnia et al., 2008; Zobel et al., 1988). However, an AMMI analysis of G × E interactions in eight (Asio et al., 2005) and 29 (Ddamulira et al., 2015) cowpea genotypes in Uganda only reported a single significant PCA (PCA1). Findings from this study also contrast Horn

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Table 3. Principal components analysis of cowpea grain yield data for 29 genotypes in 13 environments

| Source | % of G x E | DF | SS | MS | F value | F prob |
|--------|------------|----|----|----|---------|--------|
| Interactions | 100 | 336 | 38,856,3101 | 09,955 | | |
| PCA1 | 36.9 | 39 | 14,320,565 | 67,194 | 5.23 | 0.0000 |
| PCA2 | 20.9 | 37 | 8,108,325 | 219,143.9 | 3.12 | 0.0000 |
| PCA3 | 17.3 | 35 | 6,728,147 | 92,232.8 | 2.74 | 0.0000 |
| PCA4 | 7.7 | 33 | 3,009,249 | 91,189.36 | 1.3 | 0.1275 |
| PCA5 | 5.7 | 31 | 2,208,131 | 71,230.03 | 1.02 | 0.4397 |
| PCA6 | 5.1 | 29 | 1,963,605 | 67,710.53 | 0.96 | 0.5279 |
| PCA7 | 2.8 | 27 | 1,096,441 | 40,608.93 | 0.58 | 0.9563 |
| PCA8 | 2 | 25 | 766,780.4 | 30,671.22 | 0.44 | 0.9922 |
| PCA9 | 0.9 | 23 | 354,600.3 | 15,417.4 | 0.22 | 1.0000 |
| PCA10 | 0.6 | 21 | 250,772.9 | 11,941.56 | 0.17 | 1.0000 |
| PCA11 | 0.1 | 19 | 49,691.99 | 2615.368 | 0.04 | 1.0000 |
| PCA12 | 0 | 17 | 0 | 0 | 0 | 1.0000 |
et al. (2018), Kuruma et al. (2019) and Abiriga et al. (2020) who reported only two significant PCAs (PCA1 and PCA2) in their assessment of G × E interactions among cowpea genotypes.

While results of postdictive AMMI analysis showed that three PCAs were significant, Crossa (1990) argued that AMMI analysis with one PCA is the best predictive model as further PCAs mostly capture noise (Crossa, 1990). For this dataset, the effect of PCA1 was less than the genotypic effect thus PCA1 alone had low contribution to G × E interaction. The first three PCAs, however, accounted for the majority (75%) of the interaction in the AMMI analysis indicating the
importance of the AMMI-3 model for the interpretation of this yield dataset. However, where additional PCAs have a significant contribution to G × E interaction, they should be utilized to further characterize the nature of interaction rather than ignored (Purchase, 1997). In our study, the AMMI-3 model was found suitable and this is in agreement with Gauch (2013) who reported that AMMI-3 is useful for gaining predictive accuracy in analysis of yield trials while AMMI-1 is suitable for mega-environment delineation.

Correlation analysis between environmental/morphophysiological traits and scores of significant PC axes provides an explanation for the occurrence of G × E interactions (Annicchiarico, 2002). In this study, rainfall, average/minimum monthly temperature had a significant positive contribution to G × E suggesting that environments with greater rainfall and minimum to near average temperatures were associated with higher PCA1 scores. The high correlation coefficients are also indicative of wide differences among cowpea genotypes in response to temperature and rainfall. The impact of rainfall and air temperature on G × E interaction have been reported in durum wheat (Mohammadi et al., 2017), winter wheat (Yan & Hunt, 2001) as well as in common wheat (Annicchiarico & Perenzin, 1994). Relative humidity and wind speed on the other hand, had a strong negative correlation with PCA1 and PCA2 scores, respectively, indicating that environments with higher relative humidity and faster winds were associated with large G × E interactions. While increased production due to high relative humidity was reported in cotton (Sawan, 2018), this may not be the case in crops such as cowpea. Winds alter plant growth rates as well as the morphology of leaves (Cleugh et al., 1998). Days to maturity were the most important trait
Table 5. Ranking of cowpea genotypes according to ASV

| Genotype         | Entry No | ASV    | rASV | Yield (kgha⁻¹) |
|------------------|----------|--------|------|----------------|
| UCR 5279         | 17       | 0.946838 | 1    | 1,309.4        |
| Aylyi            | 2        | 1.125361 | 2    | 1,178.7        |
| ITO7K-257-33     | 28       | 1.379295 | 3    | 1,606.5        |
| ACC122*WC66      | 11       | 1.429973 | 4    | 1,279.6        |
| ITO6K-281-1      | 29       | 1.563943 | 5    | 1,266.2        |
| WC66*SEC5T       | 8        | 1.760628 | 6    | 1,346.8        |
| TVU 8923         | 16       | 2.564067 | 7    | 1,139.3        |
| WC35C            | 6        | 2.931932 | 8    | 1,189.2        |
| ITO7K-211-1-8    | 26       | 3.584883 | 9    | 1,068.2        |
| ITO7K-292-10     | 30       | 4.352786 | 10   | 1,046.3        |
| NAROCOWPEA 3     | 19       | 5.188583 | 11   | 1,329.5        |
| ITO6K-134-1      | 24       | 6.955823 | 12   | 1,241.1        |
| MU9              | 3        | 8.662542 | 13   | 1,120.3        |
| ITO6K-137-1      | 23       | 8.837235 | 14   | 1,283.7        |
| ITO7K-187-24     | 27       | 9.346484 | 15   | 764.4          |
| TVU 13485        | 13       | 9.900625 | 16   | 1,245.4        |
| CP 4             | 4        | 11.46118 | 17   | 1,115.9        |
| SEC1T*IT93K-45-1 | 9        | 13.07616 | 18   | 1,391.5        |
| ITO7K-188-49     | 25       | 13.20804 | 19   | 1,180.5        |
| ITO7K-309-44     | 18       | 14.81965 | 20   | 1,380.2        |
| WC35B*WC10       | 10       | 17.07622 | 21   | 1,058          |
| SEC3B*IT99K      | 12       | 17.90871 | 22   | 1,558.5        |
| ITO8K-149-3      | 22       | 22.64129 | 23   | 869.8          |
| IT98K-503-1      | 1        | 25.9178  | 24   | 1,493          |
| Danilo           | 7        | 26.92145 | 25   | 1,204.9        |
| Videza           | 5        | 27.22373 | 26   | 864.6          |
| SECOW2W          | 21       | 28.767   | 27   | 1,172.9        |
| NAROCOWPEA 5     | 20       | 29.66733 | 28   | 1,196.2        |
| TVU 15445        | 14       | 48.16704 | 29   | 1,313.1        |

responsible for the observed G × E interaction among the genotypic factors. In a study of adaptability of durum wheat germplasm, Mohammadi et al. (2017) also reported days to maturity as a key plant trait responsible for G × E interactions and recommended the need to optimize earliness during the breeding process.

While AMMI analysis is appropriate for describing G × E interaction and stability of genotypes as indicated in this study, it does not provide a simple measure for ranking genotypes based on stability (Sabaghnia et al., 2008) and as such it is regarded as too sophisticated (Becker & Leon, 1988). The use of ASV statistic, which can be ranked provided a simple measure for identifying superior genotypes. ASV is able to identify genotypes that perform consistently from year to year (dynamic stability) which are highly preferred by farmers especially in marginal environments (Sabaghnia et al., 2008). ASV uses the first two PCA scores to produce a balanced measurement between them and is therefore useful in situations where the first two PCA account for considerable G × E interactions (Mohammadi & Amri, 2013). Thus, given its predictive value, ASV is recommended for G × E analysis and cultivar identification in cereals and legumes (Purchase, 1997; Purchase et al., 2000; Sabaghnia et al., 2008). In this study, ASV identified five stable
genotypes; 17 (UCR 5279), 2 (Aiyiyi), 28 (IT07K-257-33), 11 (ACC122∗WC66), IT06K-281-1 (29). Abiriga et al. (2020) while assessing stability of cowpea lines in Uganda using both GGE biplots and AMMI analysis also reported that Aiyiyi was both high yielding and stable. In a related (Horn et al., 2018) on determining stability of mutant lines of cowpea, ASV and GGE biplot analysis gave similar results. Our results thus confirm the suitability of ASV in identifying stable and high-yielding cowpea genotypes. However, stable genotypes should be selected only when they have high mean performances since a consistently low yielding genotype can as well be stable (Yan & Tinker, 2006).

5. Conclusions
Results from this study have showed that differential performance of cowpea genotypes in the different environments is due to G × E interactions. However, environment effect had the largest contribution to the total variation in grain yield compared to genetic and G × E interactions. Variation between environments as a result of the effects of weather variables was observed along the first two PC axes. Thus, the variation in such variables needs to be considered if test environments are to be placed in meaningful groups.

In this study, the use of AMMI and ASV proved vital in characterizing G × E interactions among cowpea genotypes as well as in identification of genotypes with a good combination of stability and better yield performance. Genotypes that exhibit stability are needed in most marginal environments that are mostly variable and unpredictable. The ASV statistic identified five genotypes which if preferred by farmers/consumers could be recommended for release. These were; 17 (UCR 5279), 2 (Aiyiyi), 28 (IT07K-257-33), 11 (ACC122∗WC66), IT06K-281-1 (29). The three released varieties/checks, however, showed poor stability compared to most of the test genotypes.

Competing interests
The authors declare no competing interests.

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