



Genotype by environment interaction and grain yield stability of drought tolerant cowpea landraces in Ethiopia

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Abstract Cowpea is one of the most important indigenous food and forage legumes in Africa. It serves as a primary source of protein for poor farmers in drought-prone areas of Ethiopia. The crop is used as a source of food, and insurance crop during the dry season. Cowpea is adaptable to a wide range of climatic conditions. Despite this, the yield of the crop is generally low due to lack of stable and drought-tolerant varieties. In this study, 25 cowpea genotypes were evaluated in five environments using a lattice design during the 2017 and 2018 main cropping seasons. The objectives of this study were to estimate the magnitude of genotype by environment interaction (GEI) and grain yield stability of selected drought-tolerant cowpea genotypes across different environments. The additive main effect and multiplicative interaction (AMMI) model indicated the contribution

of environment, genotype and GEI as 63.98, 2.66% and 16.30% of the total variation for grain yield, respectively. The IPCA1, IPCA2 and IPCA3 were all significant and explained 45.47%, 28.05% and 16.59% of the GEI variation, respectively. The results from AMMI, cultivar superior measure, genotype plus genotype-by-environment biplot yield stability index, and AMMI stability value analyses identified NLLP-CPC-07-145-21, NLLP-CPC-103-B and NLLP_CPC-07-54 as stable and high yielding genotypes across environments. Thus, these genotypes should be recommended for release for production in drought-prone areas. NLLP-CPC-07-143, Kankeki and CP-EXTERETIS were the least stable. The AMMI1 biplot showed that Jinka was a high potential and favorable environment while Babile was an unfavorable environment for cowpea production.

Keywords AMMI stability value · Environment · GGE biplot · Yield stability index · Yield

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Introduction

Cowpea [*Vigna unguiculata* (L.) Walp.] is one of the most important food and forage legumes grown in the semi-arid tropics and some temperate regions of the world (Timko and Singh 2008). Cowpea, at all stages of growth, serves as food source (Ahenkora et al. 1998; Singh et al. 2003). Poor people in developing countries of the tropics derive their protein, animal

feed and cash income from the production of the crop (Diouf 2011). The young leaves, green pods and green grains are used as vegetables, and the dry grains are used in various preparations for both human food and livestock feed (Filho et al. 2017; Owade et al. 2020). The cowpea grain is highly nutritious and contains about 22.8–28.9% protein with an average of 25.6% (Weng et al. 2019). The portion of the cowpea crop above ground (except for pods) serves as a useful source of nutrient-rich fodder for livestock in many areas of the world (Singh et al. 2003; Weng et al. 2019). Cowpea can withstand harsh growing conditions, particularly temperature and moisture stress in comparison to other crops (Agbicodo et al. 2009; Goufo et al. 2017; Fatokun et al. 2012).

Environment, growing season, and rainfall distribution and intensity may have positive or negative impacts on cowpea genotypes (Marina et al. 2017). Plant breeders evaluate genotypes in multi-environments, representing favorable and unfavorable growing conditions, to estimate and understand the complexity of the genotype across environments (Mohammadi and Amri 2008).

Cowpea is greatly influenced by seasonal environmental fluctuations and shows large genotype by environment interaction (GEI), which is a major challenge in obtaining a full understanding of genetic control of varieties when compared across a series of environments (Kuruma et al. 2019; Olajide and Ilori 2017; Gerrano et al. 2020; Simion 2018; Simion et al. 2018). Studying and understanding of GEI is important to plant breeding programs for improving yield and yield components (Yan and Tinker 2006) and is also used for identifying the basic causes of differences between genotypes for yield stability (Yan and Tinker 2006). GEI exists when the ranks of genotypes show an obvious shift from one environment to another (Leflon et al. 2008). Measuring GEI is important to determine the optimum breeding strategy for releasing genotypes with adequate adaptation to target environments (Das et al. 2019; Yan 2016).

The methods commonly used for quantifying GEI and stability include; principal component analysis (PCA) (Zobel et al. 1988), additive main effect and multiplicative interaction (AMMI) (Zobel et al. 1988), genotype plus genotype-by-environment (GGE) biplot analysis (Yan and Tinker 2006), cultivar superiority measure (Pi) (Lin and Binns 1988), AMMI stability value (ASV) (Purchase et al. 2000)

and yield stability index (YSI) (Tumuhimbise et al. 2014). Understanding the magnitude of effects of the environment, genotype and their interaction on yield and stability performance of cowpea genotypes across environments are important because it reduces the efficiency of the genetic gain through the development of high yielding genotypes with desirable agronomic traits (Hall et al. 2003; Simion et al. 2018). Ethiopia is a victim of repeated droughts that cause partial or total crop failure, and subsequently, famine in the country. Cowpea can be used to reduce the consequence of drought.

Knowledge on the effect of genotype, environment, and their interactions on drought tolerant cowpea grain yield is limited in Ethiopia. The objectives of the present study, therefore, were to estimate the magnitude of GEI and grain yield stability of selected drought tolerant cowpea genotypes across drought prone environments.

Materials and methods

Study area

The field experiments were conducted during the 2017 and 2018 main cropping season at five environments namely Babile, Melkassa, Mieso, Jinka and Sirnka (Kobo) (Table 1).

Plant materials

A total of 25 genotypes were used for this study (Table 2). Of these, two released varieties were used as standard checks and 23 genotypes were selected as drought tolerant from a drought stress experiment, which included 324 genotypes (data not shown).

Experimental Design and Procedures

The experiments were laid out using a 5×5 lattice design with three replications. The plot size was 4 m long, 0.75 m between rows and 0.2 m between plants. Plots consisted of four rows with 20 plants per row. The distance between plots, intra blocks and replications was 1 m, 1.5 m and 2 m, respectively. The data were collected from the middle two rows.

Table 1 Description of experimental sites

Experimental sites	Soil type	Altitude (m.a.s.l)	Geographical location		Rainfall (mm)	Temperature (°C)	
			Latitude (N)	Longitude (E)		Min T	Max T
Babile	Sandy	1647	9° 13' 09"	42° 19'	432	13.85	28.9
Melkassa	Andosols	1550	8°3 0'	39° 24'	763	15.73	27.31
Miesso	Vestisol	1470	9°14'	40°45'	787	18.4	30.70
Jinka	Vestisol	1383	5° 52'	36° 38'	1247.7	17.60	30.00
Sirnka (Kobo)	Euric Fluvsol	1470	12° 09'	39° 28'	637.3	13.00	34.00

m.a.s.l = meters above sea level, N = North, E = east, mm = millimeter, °C = degree Celsius Min T = minimum temperature, Max T = maximum temperature, Weather data accessed from meteorological stations at each site

Table 2 List of genotypes used for genotypes by environment interaction

Genotypes	Genotype code	Source	Breeding status of the genotypes
NLLP-CPC-07-10	G1	MARC	Landrace
CP-EXTERETIS	G2	MARC	Landrace
NLLP-CPC-07-169	G3	MARC	Landrace
Dass 001	G4	MARC	Landrace
ACC-215-821	G5	MARC	Landrace
ACC-216-747	G6	MARC	Landrace
NLLP-CPC-07-139	G7	MARC	Landrace
NLLP-CPC-07-145-21	G8	MARC	Landrace
NLLP-CPC-07-143	G9	MARC	Landrace
ACC-215-762	G10	MARC	Landrace
NLLP-CPC-103-B	G11	MARC	Landrace
NLLP-CPC-07-156	G12	MARC	Landrace
NLLP-CPC-07-54	G13	MARC	Landrace
NLLP-CPC-07-28	G14	MARC	Landrace
NLLP-CPC-07-36	G15	MARC	Landrace
NLLP-CPC-07-19	G16	MARC	Landrace
NLLP-CPC-07-03-B	G17	MARC	Landrace
NLLP-CPC-07-167	G18	MARC	Landrace
NLLP-CPC-07-166	G19	MARC	Landrace
NLLP-CPC-07-157	G20	MARC	Landrace
NLLP-CPC-07-140	G21	MARC	Landrace
NLLP-CPC-07-57	G22	MARC	Landrace
ACC-211-490	G23	MARC	Landrace
MARC = Melkassa Agricultural Research Center	Bole (Standard check)	G24	Released variety
	Kanketi (Standard check)	G25	Released variety

Data Collection and Analyses

According to the descriptors of cowpea (IBPGR 1983), yield on a plot basis was collected and converted to grain yield per hectare (kg ha^{-1}).

SAS (SAS 2013) software was used for combined analysis of variance (ANOVA) over environments and seasons. A mixed linear model was used for ANOVA (Gomez & Gomez 1984). Environment and season were considered as random and genotypes as

fixed effects (Hartley 1950). F-Max ratio was used to test the homogeneity of error variances before analyzing the combined data. GEA-R was used for AMMI, GGE biplot, and Pi analysis (Pacheco et al. 2016).

The AMMI model analysis proposed by Zobel et al., (1988) was used for analyzing GEI. AMMI partitions the sum of squares into interaction principal component (IPC) axes.

GGE biplots were constructed from the data (Yan et al. 2000, 2007; Yan and Rajcan 2002; Yan 2011). The GGE biplot has many visual interpretations, which the AMMI does not have. It also allows visualization of crossover GEI (Yan et al. 2007). Moreover, the GGE biplot is more logical for biological objectives in terms of explaining the first PC score, which represents genotypic level rather than additive level (Yan et al. 2000). The GGE biplot is based on the first two major components of a PCA using the Site Regression (SREG) model. When the first component is highly correlated with the genotype main effect, the proportion of the yield is considered to be due only to the characteristics of the genotype. The second component represents the variation in the yield due to the GEI (Yan 2011). The GGE biplots were generated using a singular value decomposition model of the first two principal components (Yan 2002; Yan and Rajcan 2002).

GEA-R was used for AMMI, GGE biplot analysis and Pi (Pacheco et al. 2016). According to Purchase et al. (2000) and Farshadfar et al. (2011) the ASV would be essential to quantify and rank genotypes according to their yield stability (Farshadfar et al. 2011).

$$ASV = \sqrt{\left[\left[\frac{IPCA1 \text{ Sum of squares}}{IPCA2 \text{ Sum of squares}} (IPCA1 \text{ scores}) \right]^2 + [IPCA2 \text{ scores}]^2 \right]}$$

where ASV = AMMI's stability value, IPCA1 = interaction of first principal component, IPCA2 = interaction of second principal component.

YSI incorporates both mean yield and stability in a single criterion. Low values of both parameters show desirable genotypes with high mean yield and stability (Tumuhimise et al. 2014). The YSI was calculated using the following formula:

$$YSI = RASV + R$$

where: RASV is the ranking of the AMMI stability value and R the ranking of genotypes in all environments.

Pi measures the deviation from the yield of a given genotype in relation to the maximum in each environment. The significant difference of Pi was compared by computing a cutoff point for each value. Even though distributional properties of the cultivar superiority measure is not exactly known, the cut-off point was calculated by multiplying the 5% or 1% significant F-values for Pi at environment (E) and genotype (E-2) degrees of freedom by the deviation from regression mean squares, where G and E denote the number of genotypes and environments respectively (Lin and Binns 1988). The Pi measures were calculated using the following formula:

$$Pi = \frac{n(\bar{X}_i - \bar{M})^2 + \sum_j (X_{ij} - \bar{X}_i - \bar{M}_j + \bar{M})^2}{2n}$$

where: \bar{X}_i = is the mean of genotype i in the environments, \bar{M} = is the genotype with maximum response among all genotypes in the jth environment, X_{ij} = is the response of the ith genotype in the jth environment, \bar{M}_j = is the genotype with maximum response among all genotypes in the jth environment.

Results

Analysis of variance for grain yield across environments

The results of the combined ANOVA across the tested genotypes showed that environment (E) and season (Y) main effects, G × E, G × Y, E × Y, G × E × Y were all highly significant ($p < 0.0001$) for grain yield, and the genotype main effect (G) was significant ($p < 0.05$) for grain yield

Table 3 Sum of squares from combined ANOVA for grain yield of 25 cowpea genotypes

Source of variation	DF	Mean square
Replication	2	71,291.20
Genotype (G)	24	208,390.70*
Environment (E)	4	30,026,430.10**
Season (Y)	1	57,369,811.20**
Genotype* Environment	96	318,675.40**
Genotype* Season	24	334,214.70**
Environment* Season	4	25,866,297.40**
Genotype* Environment* Season	96	301,461.90**
Error	498	121,728.80

(Table 3). *P ≤ 0.05, ** P ≤ 0.01, DF = degree of freedom.

Grain yield performance across the environments

G2, G8, G10, G3 and G 18 had high yield performance at specific environments Sirnka, Jinka, Melkassa, Miesso, and Babile, respectively. However, G20, G9, G12, G15, G11, and G9 were the poorest performers at Sirnka, Jinka, Melkassa, Miesso, and Babile, respectively (Table 4). The highest grain yielding was recorded at Jinka (2445.7 kg ha⁻¹), while the poorest grain yield was recorded at Babile

Table 4 Grain yield performance across the environments

N/S	G	Sirnka	G	Jinka	G	Melkassa	G	Miesso	G	Babile	G	GM
1	G2	1804.7 ^A	G8	2445.7 ^A	G10	1905.4 ^A	G3	2252.2 ^A	G18	909.77 ^A	G8	1641.25
2	G11	1757.7 ^{BA}	G6	2333.3 ^{BA}	G13	1769.3 ^{BA}	G19	2192.7 ^A	G5	898.4 ^B	G17	1595.47
3	G24	1693.0 ^{BAC}	G12	2282.7 ^{BAC}	G7	1748.4 ^{BA}	G12	2166.6 ^{BA}	G20	896.94 ^{BA}	G13	1582.33
4	G4	1602.8 ^{BDAC}	G13	2240.2 ^{BDAC}	G8	1696.6 ^{BAC}	G8	2163.4 ^{BA}	G9	852.86 ^{BAC}	G6	1566.2
5	G16	1597.4 ^{BDAC}	G5	2150.6 ^{BDAC}	G17	1694.9 ^{BAC}	G23	2156.2 ^{BAC}	G22	834.36 ^{BAC}	G14	1551.03
6	G13	1584.0 ^{BDAC}	G1	2139.4 ^{EBDAC}	G14	1691.0 ^{BAC}	G21	2049.4 ^{BDAC}	G25	824.45 ^{BAC}	G12	1529.22
7	G10	1555.6 ^{EBDAC}	G15	2109.4 ^{EBDACF}	G21	1656.3 ^{BDAC}	G25	2015.5 ^{EBDAC}	G23	821.78 ^{BAC}	G11	1523.12
8	G17	1549.7 ^{EBDAC}	G22	2106.9 ^{EBDACF}	G16	1544.8 ^{BDEC}	G11	1979.5 ^{EBDACF}	G15	821.02 ^{BAC}	G21	1521.99
9	G7	1536.5 ^{EBDAC}	G14	1973.4 ^{EBDAGCF}	G1	1541.0 ^{BDEC}	G14	1975.4 ^{EBDACF}	G17	817.86 ^{BAC}	G1	1515.8
10	G15	1517.2 ^{EBDAC}	G3	1972.0 ^{EBDAGCF}	G11	1516.2 ^{BDEC}	G17	1966.1 ^{EBDACF}	G21	787.9 ^B	G19	1513.18
11	G6	1503.3 ^{EBDAC}	G19	1971.1 ^{EBDAGCF}	G20	1489.4 ^{FBDEC}	G20	1936.9 ^{EBDACF}	G4	783.2 ^{BDAC}	G3	1489.99
12	G12	1449.7 ^{EBDACF}	G17	1948.8 ^{EBDAGCF}	G24	1476.9 ^{FBDEC}	G6	1886.6 ^{EBDACF}	G2	770.67 ^{BDAC}	G15	1486.16
13	G18	1430.0 ^{EBDACF}	G11	1806.3 ^{EBDHGCF}	G15	1466 ^{FBDEC}	G4	1832.8 ^{EBDACF}	G13	770.05 ^{BDAC}	G7	1480.54
14	G3	1404.3 ^{EBDCF}	G4	1786.5 ^{EDHGCF}	G6	1393.1 ^{FGDEC}	G1	1815.9 ^{EBDACF}	G7	756.3 ^{BDEC}	G4	1471.45
15	G21	1401.0 ^{EBDCF}	G16	1778.2 ^{EDHGCF}	G4	1352.0 ^{FGDE}	G10	1804.5 ^{EBDACF}	G12	746.35 ^{BDEC}	G10	1468.25
16	G25	1382.8 ^{EBDCF}	G7	1746.7 ^{EDHGF}	G22	1342.1 ^{FGDE}	G5	1794.5 ^{EBDACF}	G14	734.93 ^{DEC}	G5	1459.13
17	G14	1380.5 ^{EBDCF}	G21	1715.4 ^{EDHGF}	G18	1329.1 ^{FGDEH}	G18	1704.2 ^{EBDCF}	G1	734.75 ^{DEC}	G16	1450.65
18	G19	1349.2 ^{EDGCF}	G18	1615.8 ^{EHGF}	G19	1321.7 ^{FGHEH}	G2	1671.3 ^{EDCF}	G19	731.19 ^{DEC}	G23	1432.33
19	G1	1348.0 ^{EDGCF}	G23	1610.8 ^{EHGF}	G9	1281.1 ^{FGHEH}	G9	1655.4 ^{EDF}	G10	728.84 ^{DEC}	G18	1397.76
20	G5	1347.3 ^{EDGCF}	G20	1594.5 ^{HGF}	G2	1278.9 ^{FGHEH}	G16	1615.2 ^{EDF}	G16	717.69 ^{DEC}	G2	1397.63
21	G23	1316.2 ^{EDGCF}	G24	1594.3 ^{HGF}	G23	1256.7 ^{FGHEH}	G7	1614.8 ^{EDF}	G8	717.22 ^{DEC}	G22	1396.82
22	G9	1223.7 ^{EDGF}	G25	1527.7 ^{HG}	G25	1178.8 ^{FGH}	G22	1586.8 ^{EDF}	G6	714.69 ^{DEC}	G24	1390.28
23	G8	1183.4 ^{EGF}	G2	1462.6 ^{HG}	G3	1168.7 ^{FGH}	G24	1577.2 ^{EDF}	G3	652.89 ^{FDE}	G25	1385.84
24	G22	111.4 ^{GF}	G10	1346.9 ^H	G5	1104.9 ^{GH}	G13	1548.2 ^{EF}	G24	610.0 ^{FE}	G20	1379.77
25	G20	981.2 ^G	G9	1324.9 ^H	G12	1000.8 ^H	G15	1517.2 ^F	G11	555.81 ^F	G9	1267.62
	GM	1440.52		1863.36		1448.16		1858.13		767.6		1475.75
	LSD	380.87		529.94		333.77		488.26		15,248		176.99
	R2	59.72		55.53		79.99		88.33		93.34		
	CV	23.08		24.82		20.12		22.92		17.34		

G = genotype, GM = grand mean, LSD = least significant difference, R2 = coefficient of determination, CV = coefficient of variation, LSD = least significant difference. Values in columns followed by different letters are statistically different at P ≤ 0.05

(555.81 kg ha⁻¹). The highest yielding genotype across the environments and seasons was G8 with a yield of 1641.25 kg ha⁻¹ while the poorest yielding genotype was G9 with a yield of 1267.62 kg ha⁻¹.

Additive main effect and multiplicative interaction analysis (AMMI)

AMMI analysis (Table 5) showed that environment and GEI effects were highly significant ($p < 0.0001$), and genotype effect was significant ($p < 0.05$) for grain yield. The test environments contributed 63.98% of the total variation in yield. Genotype and GEI accounted for 2.66% and 16.30% of the total variation for grain yield, respectively. The ratio of genotype effect to genotype + genotype × environment ($G + G \times E$) was 0.14. The magnitude of the GEI sum of squares was 6.12 times that of the genotype sum of squares for grain yield. The AMMI model extracted three highly significant ($p < 0.0001$) IPCA's from the interaction PC axes (Table 5). Those three IPCA's accounted for a total of 90.11% of the observed variation due to GEI. IPCA1, IPCA2, and IPCA3 captured 45.47%, 28.05%, and 16.59% of the sum of squares, respectively.

Lin and Binns Cultivar superiority measure (Pi)

According to this stability model, the three most stable genotypes with the lowest Pi values were G8, G17 and G13, which ranked 1st, 2nd and 3rd for grain yield

(Table 6). The most unstable genotypes were G9, G2, and G25 which ranked 25th, 20th and 24th for grain yield.

GGE biplots

Which-won-where and what

The polygon view of the genotypes in the GGE biplot for 25 genotypes is presented in Fig. 1. The cumulative variation contributed by PC1 (AXIS 1) and PC2 (AXIS2) was 69.16%, both of which were highly significant. The biplot showed that two environments (Babile and Sirnka) grouped in the same mega-environments. The other three environments (Jinka, Melkassa, and Miesso) each fell in a different mega-environment. The plot showed that G8, G13, G3, G16 and G4 recorded the highest grain yield in Jinka, Melkassa, Miesso, Sirnka, and Babile. On the other hand, G9, G25, and G23 did not fall in a specific environment and were poor yielders.

Ideal genotypes (ranking genotypes)

The first two principal components (PC1 and PC2) were highly significant ($p < 0.0001$) and explained 42.31% and 26.85% of the yield variation among the genotypes, respectively (Fig. 2). The GGE biplot, which identifies ideal genotypes that are high yielding and stable across the test environments, identified G8, G6 and G1, which fell close to the center of the concentric circle as ideal genotypes. Based on the

Table 5 AMMI analysis of variance for grain yield (kg ha⁻¹) of 25 cowpea genotypes evaluated at five environments

Source of variation	DF	SS	MS	Total VE	Sum of squares explained (%)	
					GEI E	GEI cum
Treatments	124	77,849,952	627,822			
Genotypes	24	2,500,687	104,195*	2.66		
Environments	4	60,052,810	15,013,202**	63.98		
Block	10	559,100	55,910			
Interactions	96	15,296,455	159,338**	16.30		
IPCA 1	27	6,710,300	248,530**		45.47	45.47
IPCA 2	25	4,336,683	173,467**		28.05	73.52
IPCA 3	23	2,668,520	116,023*		16.59	90.11
Residuals	21	1,580,952	75,283			
Error	240	15,453,907	64,391			
Total	374	93,862,959	250,970			

* $P \leq 0.05$, ** $P \leq 0.01$,
DF = degree of freedom,
SS = sum of squares,
MS = mean squares,
Total VE = total variation explained,
GEI E = GEI explained,
GEI cum = GEI cumulative.

Table 6 Grain yield and cultivar superiority value (Pi)

Genotypes	y Mean	R ²	y Rank	Pi	Pi Rank
G1	1515.80	0.94	9	65,612.64	20
G2	1397.63	0.61	20	171,567.2	2
G3	1489.99	0.90	11	99,346.36	14
G4	1471.45	0.95	14	97,339.92	15
G5	1459.13	0.78	16	114,667.1	10
G6	1566.2	0.91	4	53,755.99	23
G7	1480.54	0.79	13	101,497.7	12
G8	1641.25	0.88	1	47,458.89	24
G9	1267.61	0.83	25	234,259.9	1
G10	1468.25	0.50	15	150,238.8	5
G11	1523.12	0.90	7	76,205.07	19
G12	1529.22	0.82	6	100,484	13
G13	1582.331	0.73	3	62,452.33	21
G14	1551.03	0.96	5	55,618.29	22
G15	1486.16	0.79	12	93,679.66	16
G16	1450.65	0.88	17	106,111.3	11
G17	1595.47	0.98	2	44,651.05	25
G18	1397.76	0.97	19	146,153.6	7
G19	1513.18	0.93	10	80,879.75	18
G20	1379.77	0.69	24	167,535.7	3
G21	1521.99	0.90	8	81,427.34	17
G22	1396.83	0.76	21	135,756	9
G23	1432.33	0.80	18	137,337.8	8
G24	1390.28	0.76	22	146,642	6
G25	1385.85	0.79	23	161,189.5	4

y = grain yield

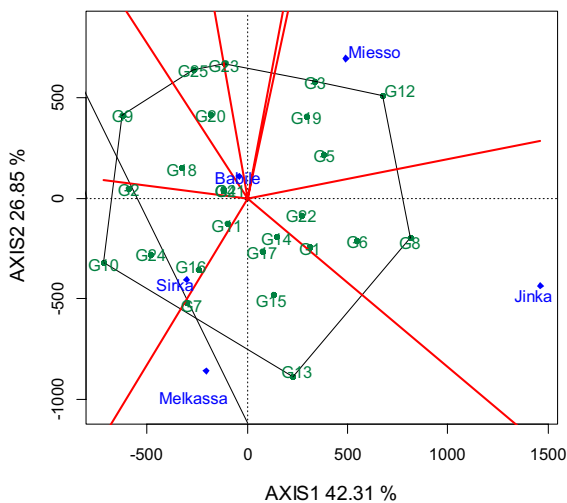


Fig. 1 Polygon view of GGE-biplot for 25 genotypes evaluated across five environments during 2017 and 2018

average environment coordination (AEC) method, G9, G25 and G23 were the most unstable and low yielding genotypes across the environments (Fig. 2).

Ideal environment (ranking environment)

Jinka was close to the concentric circle and provided the most ideal environment and the most powerful to discriminate performance of the tested genotypes (Fig. 3). In contrast, Babile was located far from the center of the concentric circle, indicating poor discriminating power.

Mean vs stability

The GGE biplot visualizes performance and effectively identifies the best performing genotypes across environments with the help of the AEC. The mean of PC1 and PC2 scores of the tested environments is represented by the arrowhead, and the AEC ordinate is the line that passes through the biplot origin and it is perpendicular to the AEC abscissa (Fig. 4).

The length of the abscissa discriminates the grain yield of genotypes that are above and below average yield if right and left of the biplot origin, respectively (Fig. 4). The length of the ordinate approximates the GEI associated with the genotype stability, and a longer ordinate corresponds to higher variability and

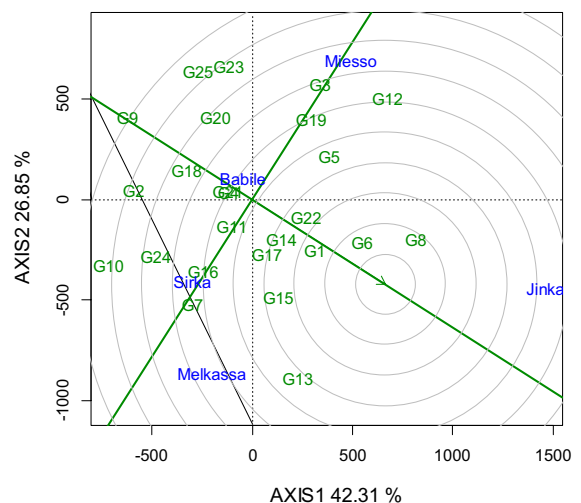


Fig. 2 GGE-biplot showing the ideal genotypes based on mean grain yield performance across environments

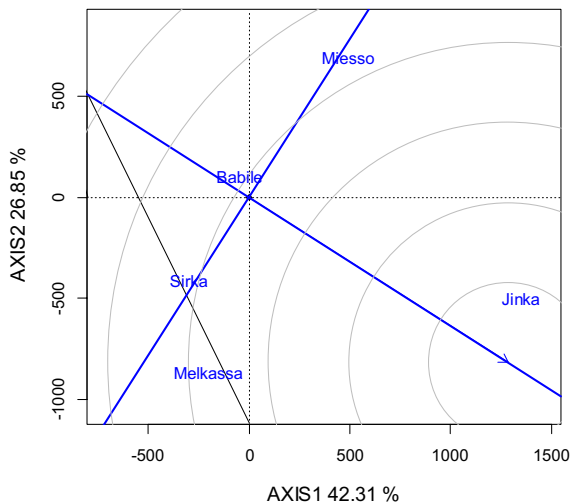


Fig. 3 GGE-biplot showing the ideal environments for the 2017 and 2018 seasons

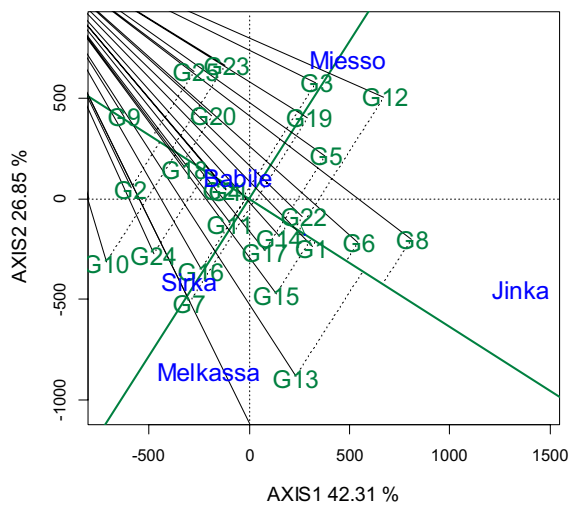


Fig. 4 Mean vs. Stability view of GGE biplot showing the mean performance and stability of 25 genotypes

lower stability and vice-versa. NLLPP-CPC-07-10 (G1), NLLP-CPC-07-57 (G20), ACC-216-747 (G6), NLLP-CPC-07-145-21 (G8), NLLP-CPC-07-28 (G14), NLLP-CPC-07-36 (G15), and NLLP-CPC-103-B (G11) were above average yielders with higher stability, however, NLLP-CPC-07-169 (G3), ACC-215-821 (G5), NLLP-CPC-07-156 (G12), NLLP-CPC-07-54 (G13), and NLLP-CPC-07-03-B (G17) had above average yield but with lower stability.

Furthermore, CP-EXTERETIS, Dass 001 (G4), NLLP-CPC-07-143 (G9), NLLP-CPC-07-166 (G19), NLLP-CPC-07-167 (G18), NLLP-CPC-07-157 (G7), and NLLP-CPC-07-140 () were stable but their yield below average, and NLLP-CPC-07-139 (), ACC-215-762 (G10), NLLP-CPC-07-19 (G16), ACC-211-490 (G23), Bole (G24) and Kanketi (G25) were not stable and their yield also below the average.

AMMI stability value (ASV) and yield stability index (YSI)

Utilizing YSI, the combination of AMMI stability values and average grain yield was estimated to quantify and classify the genotype (Table 7). According to the YSI model, G14, G17, and G21 were the most stable genotypes across environments and high grain yielders. On the other hand, genotypes G10, G2, and one check (Bole) were unstable as indicated by high YSI values of 40, 41, and 45 respectively, and those genotypes had poor productivity and lower stability.

Discussion

The majority of cowpea growing environments are extremely vulnerable to moisture stress, and the farmers use this crop as an insurance crop as they experience prolonged drought in this area. The higher yield variation contributed by the environment over genotype and GEI, indicates that the test environments were highly variable and had a great impact on genotypes. The significant GEI necessitates the need to identify adaptable genotypes with consistent high grain yield (Yan and Tinker 2006).

In addition, the response of genotypes varied considerably for grain yield due to the genetic makeup of the materials and the interaction between genetic constitution and environmental influences. This is in agreement with Gerrano et al. (2020) who reported that genotype and environment directly affect the yield potential of cowpea. From this study, the effect of environment, season, and environment \times season was high as it was responsible for 33.98%, 16.23%, and 29.27% of the total variation for grain yield, respectively. Thus, the environment and the season effects were very high, contributing to diverse cowpea grain yield. Cowpea grain yield will therefore also be largely affected by climate change. A previous study also reported variation in responses of genotype

Table 7 AMMI stability value (ASV), yield stability index (YSI), ranks and IPCA scores

Genotypes	IPCA1	IPCA2	ASV	rASV(A)	YLD	r YLD(B)	YSI (A + B)
G1	-0.41	-0.36	0.73	13	1515.80	9	22
G2	1.00	0.01	0.92	21	1397.63	20	41
G3	0.33	0.13	0.84	19	1489.99	11	30
G4	-0.67	0.46	0.34	6	1471.45	14	20
G5	-0.05	-0.84	0.80	16	1459.13	16	32
G6	-0.09	-0.11	0.81	17	1566.20	4	21
G7	-0.18	-0.62	0.74	14	1480.54	13	27
G8	0.16	-0.41	0.96	22	1641.25	1	23
G9	0.19	-0.03	0.68	11	1267.62	25	36
G10	0.16	0.03	1.55	25	1468.25	15	40
G11	-0.45	0.35	0.53	8	1523.12	7	15
G12	0.59	0.10	1.13	24	1529.22	6	30
G13	-0.10	0.23	0.84	20	1582.33	3	23
G14	0.13	0.15	0.17	1	1551.03	5	6
G15	-0.48	-0.39	0.68	10	1486.16	12	22
G16	0.06	0.70	0.48	7	1450.65	17	24
G17	0.66	-0.15	0.30	5	1595.47	2	7
G18	0.15	0.61	0.25	3	1397.76	19	22
G19	-0.39	0.59	0.77	15	1513.18	10	25
G20	0.21	0.11	0.27	4	1379.77	24	28
G21	-0.52	0.01	0.24	2	1521.99	8	10
G22	-0.50	-0.24	0.83	18	1396.82	21	39
G23	0.38	-0.46	0.70	12	1432.33	18	30
G24	-0.62	-0.09	1.03	23	1390.28	22	45
G25	0.41	0.25	0.65	9	1385.84	23	32

across environments in different seasons (Kuruma et al. 2019).

Generally, the existing variation due to environment, season, genotype performance and GEI in relation to genotype effect suggested to there was the possibility of mega-environment effects for different genotypes. Therefore, based on the variable response of genotypes, it would help to map the mega-environments suitable for the improvement of grain yield to combat the rapid climate change.

Grain yield increment is the goal of cowpea for any stressed environment because yield is governed by multi traits with different levels of expression for various environments and their interaction. In the present study, 52% of the tested genotypes recorded a higher yield than the standard checks (Bole and Kankei). Genotype NLLP-CPC-07-145-21 (G8) had a yield advantage of 15.26% and 22.25% compared to the worst genotype NLLP-CPC-07-143 (G9), and the standard checks, respectively. Therefore identification

of the highest yielding and adaptable genotypes for the specific range of environments is important for the selection and evaluation of superior genotypes in multi-environment studies and are the main targets of cowpea breeding programs. Kuruma et al. (2019) and Muranaka et al. (2016) reported that high grain yield variation could be due to greater differences between the genotypes.

AMMI analysis showed that the environmental effects accounted for the most (63.98%) of the total variation compared to the other components, implying that differential cowpea yield performance was typically caused by environmental changes. This is in agreement with the findings of Gerrano et al. (2020) and Simion (2018) that indicated the environment made the largest contribution to grain yield variation in cowpea. The magnitude of the GEI sum of squares was 6.12 times that of the genotype sum of squares for grain yield of cowpea, indicating that there were

considerable differences in genotypic responses across environments.

In the present investigation, the three IPCA's accounted for 90.11% of the interaction sum of squares. Zobel et al. (1988) stated that AMMI with the first two multiplicative terms was the best predictive model. In this study, the high (45.47%) and significant contribution of IPCA1 to the total variation across the tested environments implies that IPCA1 could identify stable and unstable genotypes based on the value scores or nearest or furthest to zero, which is in line with the findings of previous investigations (Muranaka et al. 2016; Gerrano et al. 2020; Simion 2018; Yaw et al. 2020). The positive and negative IPCA scores of genotypes in AMMI analysis are the best indicators of stability or adaptation over environments. High positive interaction of the genotypes like NLLP-CPC-07-169 (G3) in IPCA1 in an environment can exploit the agro-ecological conditions of the specific environment (Sirnka). Therefore, it would be possible to identify adaptable and suitable genotype/s for the specific environment. Kandus et al. (2010) and Yan et al. (2007) reported that the different high yielding genotypes fall in a specific environment, and it shows crossover GEI, suggesting that the test environment could be classified into mega-environments.

Using Pythagorean Theorem the distance from the origin (0:0) in a two-dimensional scattergram indicates the most stable genotypes (Purchase et al. 2000). In the ASV method, a genotype with the lowest ASV score is the most stable; accordingly, G14, G17, and G21 were stable and these genotypes were the highest yielding among the tested genotypes, indicating that the yield performance and stability showed a similar trend. Oliveira et al. (2014) noted that the dynamics of stable genotype and yield response are always parallel to the mean response of the tested environments. Unstable genotypes like Bole, CP-EXTERETIS (G2), and ACC-215-762 (G10) had high ASV values, and they were adapted to a specific favorable environment. Likewise, Oladosu et al. (2017) reported that the higher the IPCA score, and ASV the more specifically adapted a genotype is to a certain environment. In this study, crossover stability and yield did not have the same trend for all genotypes across season and environment. Jadhav et al. (2019) and Mohammadi and Amri (2008) suggested that principle stability per se should, however, not be the only selection parameter because the most stable genotypes would

not necessarily give the best yield performance. Therefore, there is a need for approaches that incorporate both mean yield and stability in a single index.

The lowest YSI value is considered as the most stable, with high grain yield (Bose et al. 2014). NLLP-CPC-07-28 (G14), NLLP-CPC-07-145-21 (G8) and NLLP-CPC-07-54 (G13) were the most stable genotypes with good yield performance. Thus, according to the YSI method, the most desirable genotypes can be considered as widely adapted and with grain yield above the grand mean among 25 genotypes. Similarly Zali et al. (2012) also indicated that both yield and stability of performance should be considered simultaneously to exploit the useful effect of GEI and to select genotypes for diverse environments.

The polygon view of the “which-won-where and what” GGE-biplot (Fig. 1) showed that genotypes NLLP-CPC-07-143 (G9), ACC-215-762 (G10), NLLP-CPC-07-156 (G12), NLLP-CPC-07-54 (G13), NLLP-CPC-07-145-21 (G8) and ACC-211-490 (G23) were genotype markers located farthest from the biplot origin in various directions and it shows that the genotypes were well adapted to specific environments. If the environment markers fall in different sectors it shows that different cultivars won in different environments (Oladosu et al. 2017; Gerrano et al. 2020). In addition, because of long environment vectors, the rest of the genotypes scattered around the biplot origin. This clearly explained that the environment effect was higher than the genotype effect. This implies that the genotype had less response for GEI because of high environment exertion to the GEI. The GGE-biplot showed that the tested environments occurred in different sectors, indicating that the particular environment had different high yielding genotypes for those sectors, this indicating the existence of crossover GEI. It also indicated the possibility to classify the environments into mega-environments for cowpea production. Yan and Rajcan (2002) stated that the presence or absence of crossover GEI indicates the existence of different mega-environments. Generally, the GGE biplot effectively identified the best performing genotypes across environments and best genotypes for specific environments, whereby specific genotypes can be recommended for specific environments and can be used to evaluate the yield and stability of genotypes, which is not possible with AMMI analysis (Kaya et al. 2006; Yan and Tinker 2006).

GGE biplots help visualize and compare the distance between each genotype and the ideal genotype located at the center of the concentric circle (Yan and Rajcan 2002). The ideal genotypes, based on proximity to the center of the concentric circle of the GGE biplot were ACC-216-747 (G6) and NLLP-CPC-07-145-21 (G8), with high yield and stability (Fig. 2). In addition, NLLP-CPC-07-10 (G1) was located on the next homocentric circle and might be considered as a desirable genotype. In principle, the ideal genotype should have the longest vector, highest mean performance and with zero GEI, and/or it should perform consistently in all environments. Because of the genetic background or nature of the traits (yield) and level of expression, the ideal genotype does not always exist in reality. Therefore, such like genotypes the breeders can be used as a reference for genotype for further study. Genotypes which were high yielding but were not stable across environments could be recommended for a particular environment.

Yan and Rajcan (2002) and Yan et al. (2007) specified that the environments with long vectors (PC1 scores) and relatively small angles or absolute with the AEC abscissa are valuable for greater discriminatory capacity (in terms of the genotype main effect) and is representative of the other environments. Therefore, Jinka was in the epicenter of the concentric circle, and it was identified as a highly discriminating environment for these genotypes, thus this environment is considered as an ideal environment for developing high yielding genotypes, or for identify ideal genotypes. Hence, Jinka allowed the genotype to express genetic potential, minimizing population development expenses by discriminating the worst genotypes at an early stage.

Conclusions

The present study showed that genotype, environment, and genotype \times environment, genotype \times season and environment \times season interaction effects were significant for grain yield. The performance of tested genotypes was largely affected by the environment. Jinka was the most ideal environment and it had discriminatory power for genotype performance in all seasons. The AMMI showed that the environmental effects accounted for 63.98% of the total yield variation. The GGE biplot showed that the tested environments occurred in different sectors which could

be used for classifying the environments into mega-environments for cowpea production. In terms of ideal genotypes (having a long vector), good yielding capacity and stability, NLLP-CPC-07-145-21 (G8), NLLP-CPC-103-B (G11) and NLLP_CPC-07-54 (G13) were identified as ideal genotypes for drought-prone environments for the country and could be proposed for release for production. The results of this study confirmed that the ideal genotype should have a long vector, high yield performance, but such genotypes do not always exist in reality.

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Declarations

Conflict of interest The authors declare that they have no conflict of interest.

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