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## Influence of genotype and environment on grain yield among cowpea (*Vigna unguiculata* (L.) Walp) genotypes under dry land farming system

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### ABSTRACT

The identification of high-yielding and stable genotypes for cultivation across differential production regions is among the key breeding objectives in cowpea improvement programs. This study was aimed to determine genotype-by-environment interaction (GEI) for grain yield to select high-yielding and stable cowpea genotypes for production in South Africa and identical agro-ecologies, and for cultivar development. Fifty cowpea genotypes were tested for grain yield across seven environments of South Africa using a 10 × 5 alpha lattice design replicated three times, during the 2019/2020 and 2020/2021 planting seasons. Grain yield data were subjected to analysis of variance (ANOVA), additive main effects and multiplicative interaction (AMMI) and the genotype-by-environment interaction (GGE) biplot analyses. ANOVA and AMMI showed significant genotype, environment and GEI effects. High grain yield was recorded for genotypes G35 (0.47 t ha<sup>-1</sup>), G1 (0.45 t ha<sup>-1</sup>) and G47 (0.43 t ha<sup>-1</sup>) across test environments. AMMI stability values (ASV); identified Acc-Cowp44 as the most stable genotype across all sites, recording the lowest ASV of 0.03. The comparison view of GGE biplot revealed Acc-Cowp29, Acc-Cowp38 and Acc-Cowp5 as ideal genotypes, possessing high grain yield of 0.19, 0.47 and 0.36 t ha<sup>-1</sup>, respectively. The identified genotypes are recommended for production and inclusion in subsequent breeding activities.

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### KEYWORDS



AMMI; ASV; GEI; GGE biplot; stability; *Vigna unguiculata*; yield

## Introduction

Cowpea (*Vigna unguiculata* [L.] Walp), a Fabaceae, is a widely cultivated vegetable and forage crop in the tropical and subtropical agro-ecologies of the world (Awurum et al. 2013; Alemu et al. 2016; Odeseye et al. 2018; Owade et al. 2020). Globally, ~8.9 million metric tonnes of cowpea grains are produced annually on about 14.4 million hectares of land (FAOSTAT 2020). In 2019, ~95% of total global cowpea production was in West Africa, with Nigeria as a leading producer (Herniter et al. 2020). Cowpea is ranked the fourth most important food legume after dry beans (*Phaseolus vulgaris* L.), groundnuts (*Arachis hypogaea*) and soybean (*Glycine max*), with an annual production of 4801 tonnes over 10,990 hectares of land (FAOSTAT 2020). The vegetable crop is cultivated for its fresh leaves, green pods and grain which are sources of macro- and micronutrients required for human nutrition (Gerrano et al. 2017; Martos-fuertes et al. 2017; da Silva et al. 2018; Gerrano

et al. 2019; ElMasry et al. 2021). The following quantities of macronutrients were reported in cowpea dry grain: 50–66% carbohydrate, 9–14% starch, 1–35% protein and 0.6–3.7% fat (Giami et al. 2005; Rengadu et al. 2020a, b). Micronutrients such as calcium (0.11 mg kg<sup>-1</sup>), copper (5.85 mg kg<sup>-1</sup>), iron (74.64 mg kg<sup>-1</sup>), potassium (13247 mg kg<sup>-1</sup>), magnesium (2064 mg kg<sup>-1</sup>), manganese (11.68 mg kg<sup>-1</sup>), sodium (361.60 mg kg<sup>-1</sup>), phosphorus (5315.00 mg kg<sup>-1</sup>) and zinc (40.16 mg kg<sup>-1</sup>) are found in cowpea grain (Gerrano et al. 2017).

Cowpea shares considerable tolerance to most abiotic stresses including drought and heat stress, salinity and poor soil nitrogen status (Daryanto et al. 2015; Meena et al. 2015; Sousa et al. 2018; Nkoana et al. 2019; Gerrano et al. 2020). Further, the crop is resistant to major biotic stress factors including weeds (*Striga gesnerioides* (Willd.) Vatke and *Alectra vogelli* Benth), and animal pests such as bruchids, beetles and leaf hoppers. In addition, the crop possesses tolerance

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to viral (e.g. cowpea aphid borne mosaic, southern bean mosaic sobemovirus and mottle virus), bacterial (e.g. bacterial blight caused by *Xanthomonas campestris* pv. *vignaauiculatae*) and fungal (e.g. leaf smut, stem and root rot) pathogens (Horn and Shimelis 2020; Mbeyagala et al. 2014; Viswanatha et al. 2011). The nutritional quality and environmental stress tolerance attributes make cowpea a vital food and nutrition security suitable for cultivation using low-input agricultural production systems.

Despite the significant role of cowpea in food and nutrition security, the release of improved cultivars for wide scale-production and breeding remains unsatisfactory, partially attributable to limited breeding effort to identify and select suitable genotypes that possess superior and stable performance. The low release of improved cultivars could be partially attributed to the lengthy breeding period required to complete selection cycles in improvement programmes (Horn and Shimelis 2020). Further, GEI effect causes variable crop performance across environmental conditions (Yan and Kang 2003), limiting the selection gain in genetic improvement programs. As a result, identification and selection of high-yielding and stable breeding parents are key to speed-up genetic improvement for increased yield and productivity in cowpea. Multi-environment trial (MET) analysis to investigate genotype-by-environment interaction (GEI) effect for major selection traits is a key procedure in cultivar design and development (Cooper and DeLacy 1994).

GEI analysis is a key statistical procedure to aid the identification and selection of high-yielding genotypes possessing broad or narrow adaptations (Yan et al. 2000; Yan and Kang 2003; Yan and Tinker 2006). Genotypes with broad adaptation are associated with high stability (Yan et al. 2000), suitable for production in different environments and for genetic advancement to aid in product profile and cultivar development. GEI analysis is conducted using the additive main effect and multiplicative interaction (AMMI) for the estimation of genotype (G), environment (E) and GEI effects (Yan and Hunt 2001). Further, genotype and genotype-by-environment interaction (GGE) biplot analysis are important to identify and select high-yielding and stable genotypes with specific or wide adaptation to production environments (Yan and Kang 2003; Yan and Tinker 2006; Yan et al. 2007). To identify and select high-yielding and stable cowpea genotypes, 50 elite and genetically diverse germplasm accessions sourced from the Agricultural Research Council (ARC), South Africa, were subjected to GEI analysis using METs conducted in South Africa. Other studies used GEI analysis in cowpea to identify high-yielding genotypes with narrow and

wide adaption for production and breeding (Ddamulira et al. 2015; Horn et al. 2018, Gerrano et al. 2020; Mbuma et al. 2021; Iseki et al. 2021). The objective of this study was to determine GEI interaction for grain yield to select high-yielding and stable cowpea genotypes for production in South Africa and identical agro-ecologies, and for cultivar design and development.

## Materials and methods

### Plant materials

Fifty cowpea genotypes obtained from the ARC gene bank collections from South Africa and Nigeria were used in this study (Table 1). The genotypes used were selected based on suitable agronomic attributes and origin.

### Study environments

The trials were conducted in the agro-ecological regions of South Africa, including Brits (25.6276° S, 27.7816° E), Loskop (25.1773° S, 29.3936° E), Roodeplaat (25.6080° S, 28.3525° E), Mafikeng (25.8201° S, 25.6298° E) and Polokwane (24.0295° S, 29.7425° E) during the 2019/2020 and 2020/2021 summer cropping seasons. The following seven test environments were defined, i.e. E1 = Brits 2019/2020, E2 = Loskop 2019/2020, E3 = Roodeplaat 2019/2020, E4 = Brits 2020/2021, E5 = Loskop 2020/2021, E6 = Mafikeng 2020/2021 and E7 = Polokwane 2020/2021. Environmental conditions of the studied environments are presented in Table 2.

### Experimental design and data collection

The cowpea genotypes were evaluated using a 10 × 5 alpha-lattice experimental design replicated three times. Each genotype was sown in a 6-m<sup>2</sup> plot comprised of two 3 m rows. The intra- and inter-row spacings were 0.3 and 1 m, respectively. Two seeds were hand sown per hole and later thinned to one seedling 2 weeks after emergence. The plants were cultivated under rainfed conditions, with supplemental moisture supplied using a sprinkler irrigation system when the rainfall was not enough for optimal growth and development. Data was recorded on three randomly selected plants per plot in each replication. Agronomic practices such as weeding, insects and diseases control were carried out using chemical and cultural practices as per recommendation for cowpea. To simulate low-input soil conditions, no fertiliser's application was performed (Gerrano et al. 2019). At physiological maturity, when the

**Table 1.** Name and geographic origin information cowpea genotypes evaluated in the present study.

Genotype code	Genotype name	Origin	Genotype code	Genotype name	Origin
G1	Acc-Cowp2	South Africa	G26	Acc-Cowp29	South Africa
G2	Acc-Cowp3	South Africa	G27	Acc-Cowp30	South Africa
G3	Acc-Cowp4	South Africa	G28	Acc-Cowp31	South Africa
G4	Acc-Cowp5	South Africa	G29	Acc-Cowp32	South Africa
G5	Acc-Cowp6	South Africa	G30	Acc-Cowp33	South Africa
G6	Acc-Cowp7	South Africa	G31	Acc-Cowp34	South Africa
G7	Acc-Cowp9	South Africa	G32	Acc-Cowp35	South Africa
G8	Acc-Cowp10	South Africa	G33	Acc-Cowp36	South Africa
G9	Acc-Cowp11	South Africa	G34	Acc-Cowp37	South Africa
G10	Acc-Cowp12	South Africa	G35	Acc-Cowp38	South Africa
G11	Acc-Cowp13	South Africa	G36	Acc-Cowp39	South Africa
G12	Acc-Cowp14	South Africa	G37	Acc-Cowp40	South Africa
G13	Acc-Cowp15	South Africa	G38	Acc-Cowp41	South Africa
G14	Acc-Cowp16	South Africa	G39	Acc-Cowp43	South Africa
G15	Acc-Cowp17	South Africa	G40	Acc-Cowp44	South Africa
G16	Acc-Cowp18	South Africa	G41	Acc-Cowp45	South Africa
G17	Acc-Cowp19	South Africa	G42	Acc-Cowp46	South Africa
G18	Acc-Cowp20	South Africa	G43	Acc-Cowp47	South Africa
G19	Acc-Cowp21	South Africa	G44	Acc-Cowp48	South Africa
G20	Acc-Cowp22	South Africa	G45	Acc-Cowp49	South Africa
G21	Acc-Cowp24	South Africa	G46	Acc-Cowp50	South Africa
G22	Acc-Cowp25	South Africa	G47	98K-5301	Nigeria
G23	Acc-Cowp26	South Africa	G48	Glenda	South Africa
G24	Acc-Cowp27	South Africa	G49	TVU13953	Nigeria
G25	Acc-Cowp28	South Africa	G50	VegCowDakCream	South Africa

Note: VegCowDakCream = Vegetable cowpea Dakama Cream.

**Table 2.** Soil characteristics, altitude and mean annual weather data for average rainfall, and minimum ( $T_{\min}$ ) and maximum ( $T_{\max}$ ) air temperature information for the studied environments. Source: SA Weather Services (weathersa.co.za).

Environment	Soil type	Altitude (masl)	Average rainfall (mm)	$T_{\min}$ (°C)	$T_{\max}$ (°C)
Brits	Clay loam	1083	629	18.3	28.9
Loskop	Loamy	920	497	18.6	30.0
Roodeplaat	Clay loam	1168	772	10.0	21.0
Mafikeng	Sandy	1359	571	17.6	28.8
Polokwane	Clay loam	1310	495	16.7	27.6

Note: Masl = meters above sea level, Min = Minimum, Max = Maximum.

plants and pods turned brown, grain yield data were recorded in grams plant<sup>-1</sup> for each genotype, and later converted to t ha<sup>-1</sup>.

## Data analysis

### Analysis of variance

Following analysis of variance (ANOVA), the additive main effect and multiplicative interaction (AMMI) analysis were performed to infer the effects due to genotype (G), environment (E) and genotype-by-environment interaction (GEI) (Gauch et al. 2008; Gauch 2006; Gauch 2013). The AMMI analysis was done using the following statistical AMMI model:

$$\bar{Y}_{ij} = \mu - G_i + E_j + \sum_{k=1}^m \lambda_k \alpha_{ik} \gamma_{jk} + \rho_{ij}$$

where  $\bar{Y}_{ij}$  is the yield of genotype  $i$ th in the  $j$ th environment,  $\mu$  is the grand mean,  $G_i$  is the mean of the  $i$ th genotype minus the grand mean,  $E_j$  is the mean of the  $j$ th environment minus the grand mean,  $\lambda_k$  is the square root of the eigenvalue of the  $k$ th interaction principal component axis (IPCA) axis of the  $i$ th genotype and  $j$ th environment, and  $\rho_{ij}$  is the deviation from the model. Further, AMMI stability values (ASVs) were computed to rank genotypes based on stability using Genstat® version 20 according to Purchase (1997) using the following formula:

$$ASV = \sqrt{\left[ \left( \frac{SSIPCA1}{SSIPCA1} (IPCA1) \right)^2 + [IPCA1]^2 \right]}$$

where  $\frac{SSIPCA1}{SSIPCA1}$  denotes the weighted value assigned to the first interaction principal component score due to its high contributions in the GE model. SSIPCA1 and SSIPCA2 are the sum of squares for IPCA1 and IPCA2, respectively.

Further, grain yield data were subjected to genotype and genotype environment (GGE) biplot analysis to identify high-responsive and stable genotypes (Yan and Tinker 2006) using Genstat® version 20 (Payne 2014).

## Results

### Genotype, environment and genotype-by-environment interaction effects

AMMI showed significant ( $P \leq 0.01$ ) G, E and GEI effects for grain yield (Table 3). The first, second, third, fourth and fifth IPCAs were significant ( $P \leq 0.01$ ) for grain yield,

**Table 3.** Additive main effects and multiplicative interaction analysis of variance for grain yield among the studied cowpea genotypes across environments.

Source of variation	d.f.	SS	MS	Total variation explained (%)	GEI explained (%)
Treatments	349	26.58	0.07		
Genotypes (G)	49	7.78	0.15**	29.27	
Environments (E)	6	3.57	0.59**	13.42	
G x E	294	15.23	0.05**	57.03	
IPCA1	54	7.61	0.14**		49.96
IPCA2	52	4.04	0.08**		26.54
IPCA3	50	1.78	0.04**		11.65
IPCA4	48	0.99	0.02**		6.52
IPCA5	46	0.53	0.01**		3.44
Block	14	2.93	0.01**	0.00	
Residual	188	3.58	0.019**		1.87
Total	1049	26.58	0.03		

Note: d.f. = degrees of freedom; SS = sum of squares, MS = mean squares, IPCA1, IPCA2, IPCA3, IPCA4, IPCA5 = interaction principal component axes 1, 2, 3, 4 and 5, respectively; \*\* = significant at  $P \leq 0.01$ .

explaining 98.11% total GEI signal. IPCA1, IPCA2, IPCA3, IPCA4 and IPCA5 explained 49.96%, 26.54%, 11.65%, 6.52% and 3.44% GEI signal of the AMMI model, respectively. Further, AMMI revealed high variation of 57.03% due to GEI effect, followed by 29.27% and 13.42% for genotype and environment main effects, respectively.

### Performance of cowpea genotypes for grain yield

Mean performances, IPCA scores and ASVs for grain yield among 50 cowpea genotypes evaluated in seven environments are shown in Table 4. The highest grain yield values were recorded for G47 (0.64 t ha<sup>-1</sup>) under E1, G41 (0.55 t ha<sup>-1</sup>) under E2, G15 (0.62 t ha<sup>-1</sup>) under E3, G46 (0.43 t ha<sup>-1</sup>) under E4, G12 (0.20 t ha<sup>-1</sup>) under E5, G6 (0.51 t ha<sup>-1</sup>) under E6 and G43 (0.79 t ha<sup>-1</sup>) under E7. Across the environments, grain yield ranged from 0.13 to 0.47 t ha<sup>-1</sup> which were recorded for genotypes G10 and G35, respectively. High grain yield values were recorded for genotypes G35, G1, G47, G15 and G7 (i.e. 0.47, 0.45, 0.43, 0.41 and 0.37 t ha<sup>-1</sup>, in that order). Genotypes G10, G30, G21, G45 and G6 recorded low grain yield values of 0.13, 0.14, 0.15, 0.16 and 0.17 t ha<sup>-1</sup>, respectively, across test environments. Based on ASV analysis, G40 was the most stable genotype recording the lowest ASV of 0.03, followed by G9 (0.04), G38 (0.05), G26 (0.07) and G48 (0.08). The following genotypes (i.e. G41, G17 and G29) recorded high ASVs of 0.87, 0.74 and 0.70, respectively.

### GGE biplot analysis of which genotypes were superior in which environment

A 'which-won-where' GGE biplot showing which genotypes won in which environment is presented in

Figure 1. The biplot consists of an irregular polygon and a set of lines drawn from the origin to perpendicularly dissect each side of the polygon. The set of lines divide the biplot into sectors. Identifying winning genotypes for each sector (Yan et al. 2007). The 'which-won-where' biplot explained 78.26% total variation of which PC1 and PC2 accounted for 52.73% and 25.52% of the total variation, respectively. The biplot depicted eight sectors and environments were clustered into three of the eight sectors. Genotypes such as G28, G43, G31, G3, G50, G12, G18, G11, G37, G27 and G42 constituted the largest sector and were associated with environments E4, E5, E6 and E7 which formed a mega-environment. Genotypes G47, G15, G14, G7 and G8 formed the second sector which involved environments E1, E2 and E3. The genotypes which were located at the vertices of the polygon were G1, G35, G47, G41, G10, G6 and G28.

### GGE biplot analysis for the studied environments

GGE biplot analysis revealing the test environments' discriminating power and representativeness of the target environment is presented in Figure 2. Vector lines are drawn from the biplot origin to each test environment marker, measuring the discriminative power of the environment. Long vectors indicate test environments with more discriminating power. Further, the average environment axis (AEA) is the dotted vertical and horizontal line indicating points where the PC1 and PC2 axes had respective values of zero. Test environments with small angles with the AEA are more representative of the mega-environment (Yan et al. 2007). AMMI revealed a total variation of 76.51% contributed by IPCA1 (49.96%) and IPCA2 (26.54%). Environment E7 showed the longest vector line, suggesting high discriminating ability for this environment. The other test environments were plotted closer to the origin, signifying that most genotypes performed similarly in these environments. Environment E5 showed the smallest angle with the AEA, signifying high representativeness of the mega-environment involving E4, E5, E6 and E7. Also, environment E1 showed the most representativeness in the mega-environment involving E1, E2 and E3.

### Comparison view of GGE biplot analysis of ideal cowpea genotype

The GGE biplot clustering of the studied genotypes relative to the ideal genotype is presented in Figure 3. The ideal genotype is located at the innermost concentric circle, indicated by an arrowhead in the biplot (Yan and Tinker 2006). The two principal components accounted for 78.26% total variation among genotypes,



**Table 4.** Mean values of grain yield (t ha<sup>-1</sup>) among the studied cowpea genotypes across tested environments.

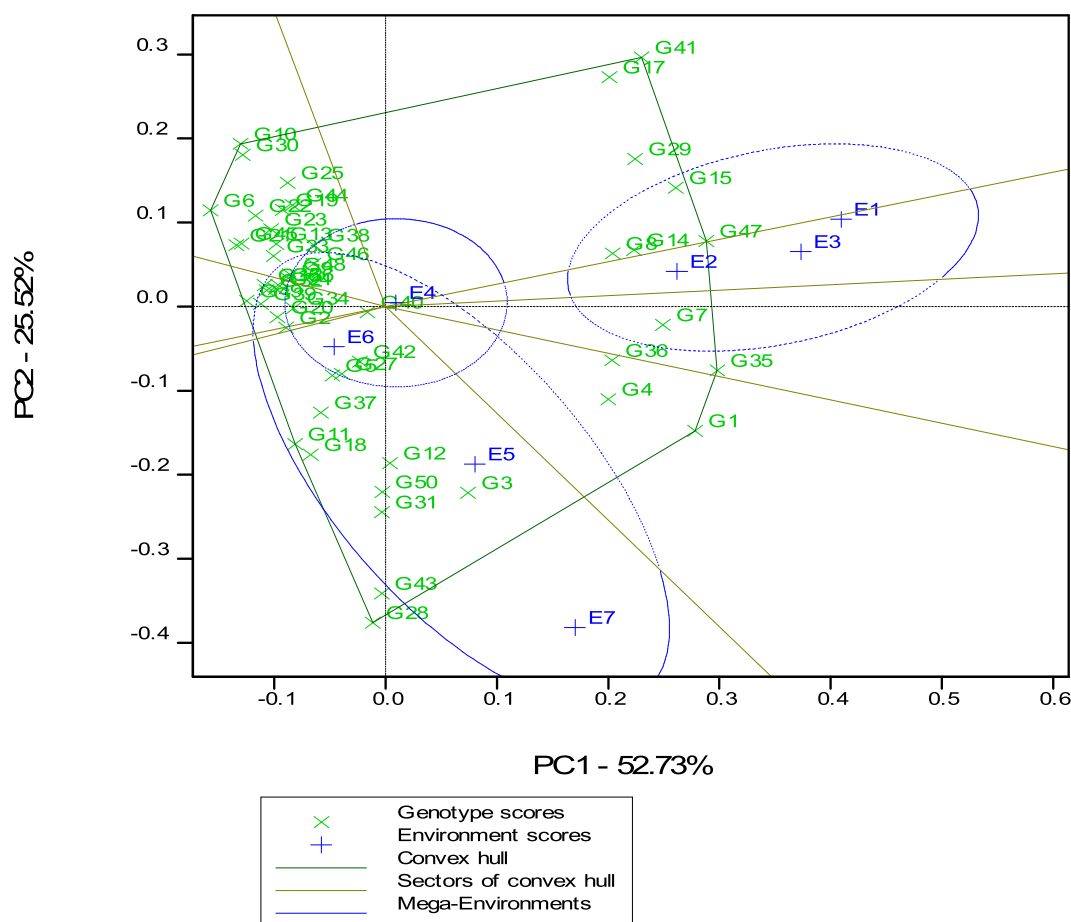
	Environments										
Genotype	Brits 2019/ 2020	Loskop 2019/2020	Roodeplaat 2019/2020	Brits 2020/ 2021	Loskop 2020/2021	Mafikeng 2020/2021	Polokwane 2020/2021	Mean	IPCA1	IPCA2	ASV
G1	0.58	0.45	0.50	0.20	0.52	0.23	0.67	0.45	−0.14	0.26	0.38
G2	0.12	0.15	0.11	0.35	0.36	0.16	0.33	0.23	0.12	−0.05	0.23
G3	0.17	0.20	0.45	0.25	0.55	0.37	0.61	0.37	0.14	0.12	0.29
G4	0.55	0.15	0.50	0.22	0.27	0.14	0.70	0.36	−0.15	0.32	0.43
G5	0.11	0.21	0.17	0.26	0.37	0.08	0.45	0.24	0.09	0.09	0.19
G6	0.09	0.16	0.09	0.05	0.11	0.50	0.17	0.17	0.07	−0.21	0.25
G7	0.50	0.50	0.53	0.13	0.26	0.11	0.59	0.37	−0.26	0.27	0.57
G8	0.50	0.43	0.48	0.25	0.34	0.07	0.41	0.36	−0.26	0.10	0.50
G9	0.11	0.14	0.17	0.20	0.23	0.09	0.32	0.18	0.02	0.02	0.04
G10	0.18	0.10	0.10	0.09	0.28	0.11	0.03	0.13	−0.06	−0.16	0.19
G11	0.09	0.13	0.10	0.15	0.36	0.20	0.54	0.23	0.18	0.15	0.37
G12	0.13	0.25	0.23	0.20	0.76	0.13	0.44	0.31	0.16	0.09	0.31
G13	0.18	0.17	0.10	0.23	0.33	0.24	0.19	0.20	0.05	−0.14	0.17
G14	0.53	0.47	0.50	0.16	0.23	0.19	0.45	0.36	−0.29	0.12	0.55
G15	0.58	0.50	0.61	0.25	0.31	0.28	0.32	0.41	−0.33	−0.04	0.63
G16	0.09	0.19	0.10	0.20	0.28	0.17	0.28	0.19	0.07	−0.05	0.14
G17	0.62	0.45	0.50	0.27	0.33	0.21	0.09	0.35	−0.38	−0.18	0.74
G18	0.10	0.19	0.09	0.15	0.46	0.24	0.52	0.25	0.20	0.12	0.39
G19	0.15	0.10	0.24	0.26	0.21	0.38	0.17	0.22	0.03	−0.21	0.22
G20	0.10	0.17	0.11	0.17	0.26	0.15	0.36	0.19	0.07	0.03	0.14
G21	0.08	0.12	0.08	0.20	0.35	0.05	0.18	0.15	0.04	−0.07	0.10
G22	0.12	0.17	0.10	0.34	0.24	0.15	0.18	0.19	0.03	−0.17	0.18
G23	0.09	0.23	0.17	0.18	0.42	0.35	0.10	0.22	0.07	−0.24	0.28
G24	0.13	0.16	0.11	0.24	0.28	0.20	0.30	0.20	0.07	−0.06	0.15
G25	0.19	0.18	0.16	0.30	0.32	0.30	0.09	0.22	0.01	−0.27	0.27
G26	0.13	0.11	0.13	0.25	0.25	0.07	0.32	0.18	0.04	0.02	0.07
G27	0.18	0.24	0.14	0.41	0.38	0.32	0.43	0.30	0.15	−0.08	0.29
G28	0.11	0.27	0.09	0.23	0.82	0.36	0.66	0.36	0.36	0.14	0.70
G29	0.61	0.48	0.47	0.15	0.35	0.09	0.25	0.34	−0.37	0.02	0.70
G30	0.11	0.13	0.15	0.19	0.26	0.10	0.05	0.14	−0.04	−0.17	0.18
G31	0.16	0.20	0.18	0.20	0.41	0.23	0.69	0.30	0.18	0.23	0.42
G32	0.12	0.12	0.11	0.16	0.23	0.17	0.32	0.18	0.06	0.00	0.11
G33	0.16	0.16	0.09	0.32	0.29	0.14	0.24	0.20	0.05	−0.11	0.14
G34	0.12	0.21	0.12	0.25	0.40	0.16	0.28	0.22	0.08	−0.05	0.17
G35	0.61	0.45	0.55	0.36	0.72	0.10	0.49	0.47	−0.19	0.13	0.38
G36	0.56	0.25	0.45	0.19	0.51	0.06	0.52	0.36	−0.17	0.23	0.40
G37	0.12	0.24	0.10	0.24	0.38	0.23	0.49	0.26	0.16	0.06	0.31
G38	0.16	0.12	0.23	0.26	0.27	0.11	0.25	0.20	−0.01	−0.05	0.05
G39	0.09	0.17	0.08	0.35	0.31	0.22	0.29	0.22	0.13	−0.11	0.26
G40	0.19	0.23	0.23	0.27	0.35	0.15	0.36	0.25	0.02	0.01	0.03
G41	0.55	0.55	0.58	0.24	0.28	0.06	0.10	0.34	−0.46	−0.10	0.87
G42	0.15	0.17	0.25	0.19	0.30	0.13	0.46	0.24	0.04	0.12	0.14
G43	0.11	0.27	0.12	0.17	0.50	0.30	0.78	0.32	0.27	0.27	0.58
G44	0.16	0.20	0.18	0.26	0.41	0.28	0.08	0.22	0.02	−0.25	0.25
G45	0.10	0.13	0.09	0.16	0.29	0.13	0.20	0.16	0.04	−0.07	0.11
G46	0.20	0.18	0.15	0.43	0.34	0.26	0.24	0.26	0.07	−0.19	0.23
G47	0.64	0.54	0.55	0.31	0.31	0.21	0.44	0.43	−0.32	0.05	0.60
G48	0.14	0.22	0.10	0.23	0.28	0.13	0.28	0.20	0.04	−0.04	0.08
G49	0.11	0.11	0.10	0.18	0.25	0.42	0.30	0.21	0.14	−0.13	0.29
G50	0.17	0.20	0.19	0.27	0.31	0.25	0.70	0.30	0.17	0.21	0.38
G.M	0.24	0.24	0.24	0.24	0.35	0.20	0.35	—	—	—	—
Min	0.08	0.10	0.08	0.05	0.11	0.05	0.03	0.13	−0.46	−0.27	0.03
Max	0.64	0.55	0.61	0.41	0.82	0.50	0.78	0.47	0.36	0.32	0.87
CV%	17.9	11.9	19.1	11.2	18.9	23.7	20.9	—	—	—	—
LSD	0.98	0.70	0.54	0.84	0.54	0.62	0.74	—	—	—	—

Note: G.M = grand mean; Min = minimum; Max = maximum; CV% = percentage coefficient of variation; LSD = least significant differences.

contributed by PC1 (52.73%) and PC2 (25.52%), respectively. G35 was identified as an ideal genotype for grain yield, given its position at the epicentre of the concentric circles. G1, G35, G4 and G36 were the next genotypes next to the ideal genotype, in that order. G6, G10 and G30 were the furthest from the ideal genotype, signifying low stability.

### Comparison view of GGE biplot analysis of ideal environment

GGE biplot visualising comparing test environments relative to the ideal environment is presented in Figure 4. Environments E3, E1 and E2 were plotted closest to the epicentre of the concentric circles, in that order,



**Figure 1.** The 'Which-won-where' view of GGE biplot showing which genotypes performed best in which environment and the delineation of mega-environments. E1 = Brits 2019/2020; E2 = Loskop 2019/2020; E3 = Roodeplaat 2019/2020; E4 = Brits 2020/2021; E5 = Loskop 2020/2021; E6 = Mafikeng 2020/2021; E7 = Polokwane 2020/2021.

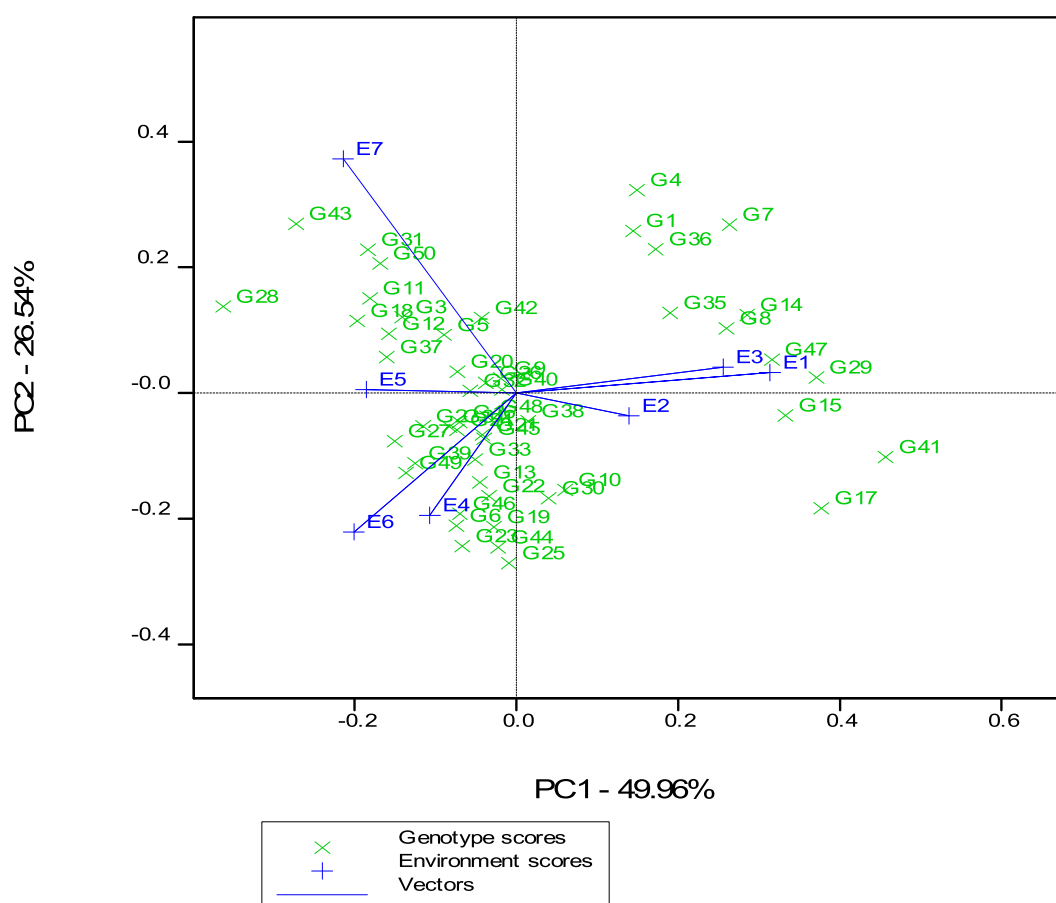
providing the most ideal production conditions for grain yield. Environments E6, E4, E7 and E5 were plotted farthest from the epicentre, in that order, considered the worst discriminatory environments.

## Discussion

The development and release of high-yielding and stable cowpea genotypes for farmer adoption and breeding are key to sustainable production and food security. This study determined genotype-by-environment interaction effect for grain yield among cowpea genotypes across seven environments of South Africa to identify and select high-yielding and stable genotypes for production, and for use as breeding parents in cultivar design and development. The AMMI analysis of variance revealed significant genotype (29%), environment (13%) and genotype-by-environment interaction (57%) effects for grain yield (Table 3). The high GEI effect of 57% indicates the larger influence of environment on grain yield among the tested cowpea genotypes, allowing identification of environment-

specific genotypes with narrow adaptation. Significant GEI effect on grain yield in cowpea was reported by other studies (Mbumba et al. 2021; Shiringani and Shimeilis 2011; Martos-Fuentes et al. 2017), signifying the importance of GEI analysis to select high-yielding and stable genotypes. Contrary to the present findings, Simion et al. (2018) reported genotype effect as the largest contributor to total phenotypic variation, recording 78% variance. Furthermore, Mohammed et al. (2016) reported the highest phenotypic variance of 75% due to environment effect in cowpea grain yield. Nevertheless, the significant genotype effect of 29% observed in the present study is useful to identify and select high-yielding cowpea genotypes.

In the present study, cowpea genotypes such as Acc-Cowp38, Acc-Cowp2 and 98K\_5301 recorded high grain yield values of 0.47, 0.45 and 0.43 t ha<sup>-1</sup>, respectively, across the test environments (Table 4). Grain yield ranged between 0.13 and 0.47 t ha<sup>-1</sup> across the tested environments which is higher than the range of 0.048–0.23 t ha<sup>-1</sup> reported by Mbumba et al. (2021), which could be attributable to favourable environmental



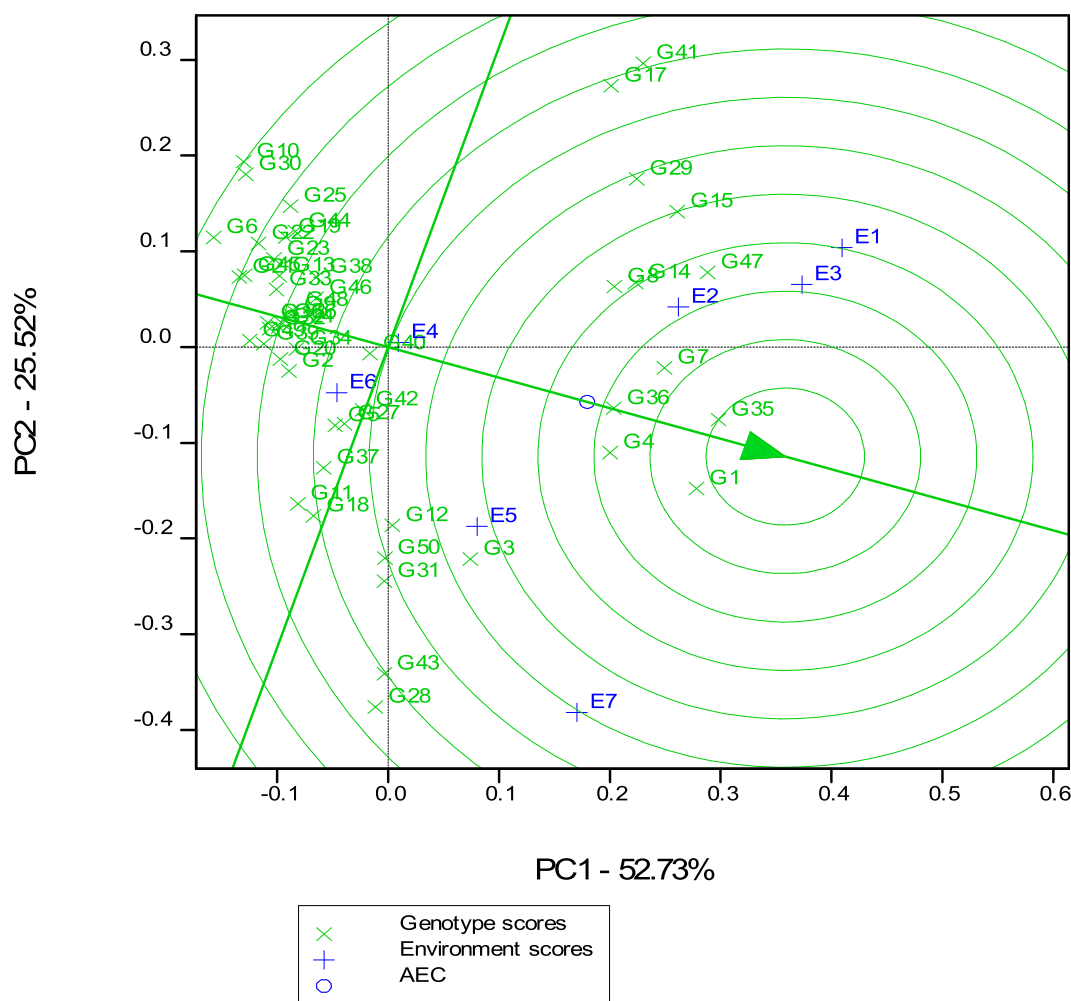
**Figure 2.** The ‘discriminating power vs. representativeness’ view of GGE biplot showing the relationship between studied environments. E1 = Brits 2019/2020; E2 = Loskop 2019/2020; E3 = Roodeplaat 2019/2020; E4 = Brits 2020/2021; E5 = Loskop 2020/2021; E6 = Mafikeng 2020/2021; E7 = Polokwane 2020/2021.

conditions in the tested locations. For instance, the environment evaluated by Mbuma et al. (2021) (i.e. Rustenburg) was comprised of sandy clay soils, whereas locations evaluated in the present study consisted mainly of clay loam soils (Table 2). Andrade et al. (2013) also reported a high grain yield range of between 0.6 and 1.1 t ha<sup>-1</sup> in cowpea, which was associated with the application of biofertilisers. The cowpea genotypes identified with superior grain yield could be important to enhance genetic improvement for grain yield. ASV analysis is a salient statistical procedure to estimate genotype stability across test locations, whereby a low ASV value indicates high stability (Purchase 1997). Smaller ASV indicates wide adaptation of genotype across environments, whereas high ASV indicates narrow adaptation of genotype to a certain environment (Purchase 1997; Mahmodi et al. 2011). Based on ASV analysis, genotypes such as G40 (Acc-Cowp44), G9 (Acc-Cowp11), G38 (ACC-41), G26 (Acc-Cowp29) and G48 (Acc-Glenda) were identified as the most stable for grain yield, recording low ASV values of below a unit (i.e. 0.03, 0.04, 0.05, 0.07 and 0.08

respectively) (Table 4). These genotypes are widely adapted for suitable grain yield in various agroclimatic conditions, possessing grain yield of a range from 0.18 to 0.28 t ha<sup>-1</sup> (Table 4). Genotypes such as G17 (Acc-Cowp19), G28 (Acc-Cowp31), G29 (Acc-Coep32) and G41 (Acc-Cowp45) with high ASVs of >0.70 were characterised with narrow adaptation for grain yield (Table 4). For example, G28 (Acc-Cowp31) recorded high grain yield of 0.82 t ha<sup>-1</sup> in Loskop during the 2020/2021 season, higher than the values of 0.23 and 0.36 t ha<sup>-1</sup> that were recorded Brits and Mafikeng during the similar season (Table 4).

IPCA scores are an important statistical measure to indicate genotype stability, whereby high IPCA scores, whether negative or positive, indicate the presence of narrow adaptation and vice versa. Further, IPCA scores that are closer indicate more genotype stability across various agroclimatic conditions (Horn et al. 2018). In the present study, the following genotypes (i.e. G9 [Acc-Cowp11], G26 [Acc-Cowp29], G29 [Acc-Cowp32] and G30 [Acc-Cowp33]) were observed as the most stable genotypes, recording low IPCA2 scores of a





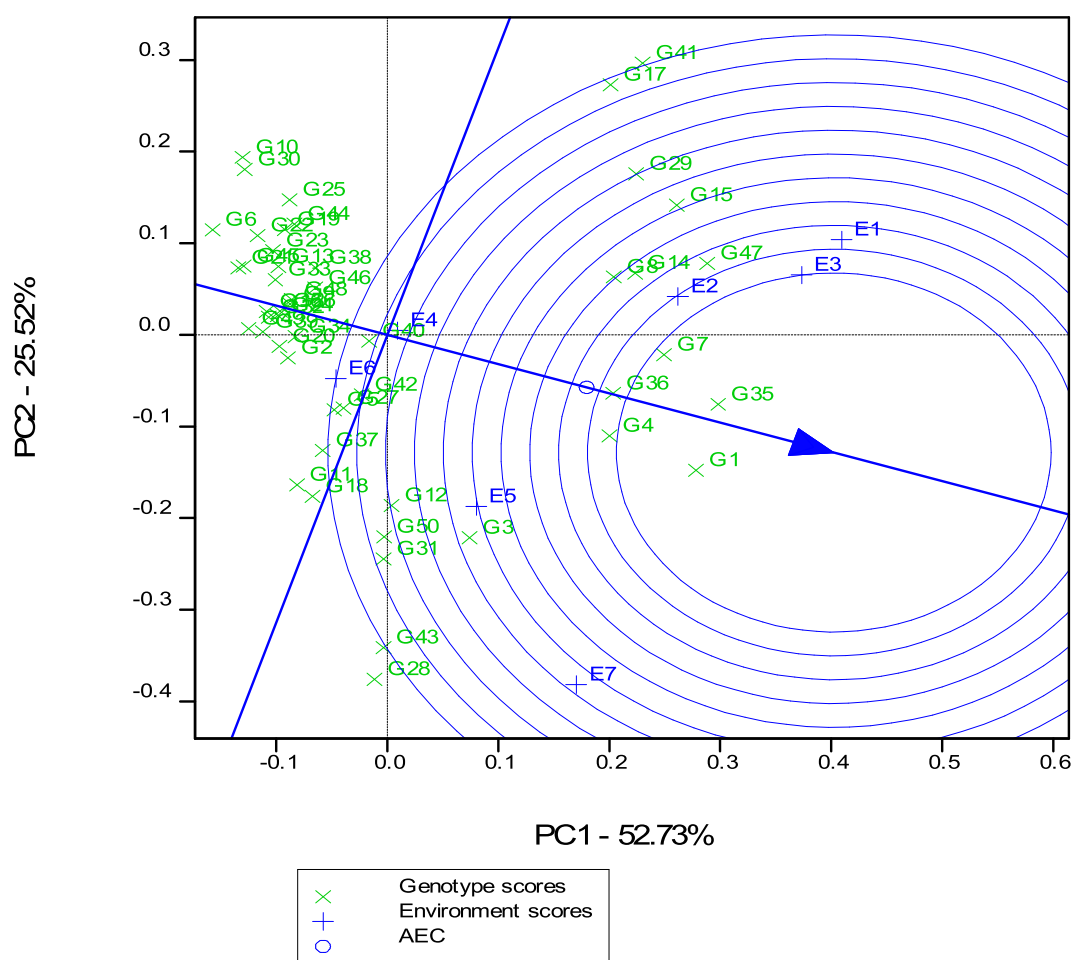
**Figure 3.** The comparison view of GGE biplot showing an ideal genotype for grain yield. E1 = Brits 2019/2020; E2 = Loskop 2019/2020; E3 = Roodeplaat 2019/2020; E4 = Brits 2020/2021; E5 = Loskop 2020/2021; E6 = Mafikeng 2020/2021; E7 = Polokwane 2020/2021.

range between 0.00 and 0.02 (Table 4). Numerous studies used ASV values and IPCA scores to identify widely- and specifically-adapted cowpea genotypes (Horn et al. 2018; Gerrano et al. 2020; Goa et al. 2022). The genotypes identified with high stability can be recommended for production under diverse environments of South Africa or in identical agroclimatic conditions to enhance cowpea productivity and for breeding.

The visualisation of the 'which-won-where' GGE biplot is an important statistical technique to identify mega-environments and their corresponding winner genotypes (Gauch and Zobel 1997; Yan et al. 2000; Yan and Hunt 2001). The GGE biplot revealed two mega-environments of which the first mega-environment involved environments E4 (Brits 2020/2021), E5 (Loskop 2020/2021), E6 (Mafikeng 2020/2021) and E7 (Polokwane 2020/2021), within which there is an overlapping mega-environment involving environment E4 (Brits 2020/2021) and E6 (Mafikeng 2020/2021) (Figure 1). This could be due to the close association between the

environments Mafikeng and Brits based on the agroclimatic conditions. For example, annual rainfall ranged between 571 and 629 mm in Brits and Mafikeng, with minimum and maximum temperature ranges of 17.6–18.3°C and 28.8–2.89°C, respectively (Table 2). In agreement with the present findings, Gerrano et al. (2020) also argued that precipitation and temperature affected the delineation of mega-environments.

Based on the 'discriminating power vs. representativeness' view of the GGE biplot, environment E7 (Polokwane 2020/2021) possessed the most discriminating power for grain yield, whereby environments E5 (Loskop 2020/2021) and E1 (Brits 2019/2020) were the most representative in the first and second mega-environments, respectively (Figure 2). These environments (i.e. E1 and E5) could substitute for the other environments in subsequent breeding activities. Further, genotypes such as G1 (Acc-Cowp2), G6 (Acc-Cowp7), G10 (Acc-Cowp12), G28 (Acc-Cowp31), G35 (Acc-Cowp38), G41 (Acc-Cowp45) and G47 (98K-5301)



**Figure 4.** The comparison view of GGE biplot showing the ideal environment for grain yield. E1 = Brits 2019/2020; E2 = Loskop 2019/2020; E3 = Roodeplaat 2019/2020; E4 = Brits 2020/2021; E5 = Loskop 2020/2021; E6 = Mafikeng 2020/2021; E7 = Polokwane 2020/2021.

were located at the vertices of the polygon in the ‘which-won-where’ GGE biplot, indicating poor stability and specific adaptation for these genotypes (Figure 1). For instance, G6 (Acc-Cowp7) recorded high grain yield of  $0.50 \text{ t ha}^{-1}$  under E6 (Mafikeng 2020/2021), whereas low grain yield of  $0.09$ ,  $0.09$  and  $0.05 \text{ t ha}^{-1}$  were recorded for the same genotype in E1 (Brits 2019/2020), E3 (Roodeplaat 2019/2020) and E4 (Brits 2020/2021), respectively (Table 4). This indicated poor stability for grain yield in these genotypes as well as the importance of narrow adaptation. In contrast, G40 (Acc-Cowp44), G34 (Acc-Cowp37) and G2 (Acc-Cowp3) were located close to the origin, indicating that these genotypes were least responsive to differential environmental conditions. These genotypes (i.e. G40, G34 and G2) can be used in breeding for wide adaptation. According to Yan and Rajcan (2002), genotypes which are located closer to the origin are less susceptible to the GEI effect due to differential environmental conditions.

The comparison view of the GGE biplot revealed the following ideal genotypes: G35 (Acc-Cowp38), G1

(Acc-Cowp2), G7 (Acc-Cowp9), G4 (Acc-Cowp5) and G36 (Acc-Cowp39), in that order (Figure 3). These genotypes (i.e. G35, G1, G7, G4 and G36) possessed suitable grain yield of  $0.47$ ,  $0.45$ ,  $0.37$ ,  $0.36$  and  $0.36 \text{ t ha}^{-1}$ , respectively, across the test environments (Table 4). The cowpea genotypes identified as ideal could be released for production or subjected to further genetic advancement to increase selection gain for grain yield in breeding programs. The comparison view of GGE biplot analysis revealed environments E1 (Brits 2019/2020) and E3 (Roodeplaat 2019/2020) as ideal environments, possessing high discriminatory power for grain yield among the studied cowpea genotypes (Figure 4). For example, wide ranges of grain yield of  $0.09$ – $0.64 \text{ t ha}^{-1}$  and  $0.08$ – $0.55 \text{ t ha}^{-1}$  were observed under environments E1 (Brits 2019/2020) and E3 (Roodeplaat 2019/2020), in that order (Table 4), suggesting the presence of wide phenotypic variation for grain yield among the tested genotypes in these environments.

In conclusion, the present study determined genotype-by-environment interaction for grain yield to

select high-yielding and stable cowpea genotypes for production in South Africa and identical agro-ecologies, and for cultivar design and development. Significant genotype-by-environment interaction effect was detected for grain yield among the test genotypes. Cowpea genotypes Acc-Cowp38, Acc-Cowp2, Acc-Cowp9, Acc-Cowp5 and Acc-Cowp39 were identified as ideal for grain yield, in that order. The selected cowpea genotypes are recommended for production in South Africa or in similar agro-ecologies, and for incorporation in future breeding programs targeting genetic improvement for grain yield.

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