



Agronomic performance and genetic variability of cowpea (*Vigna unguiculata*) accessions

D.K. Nkoana^{1,2}, Abe Shegro Gerrano*¹ and E.T. Gwata¹

Agricultural Research Council, Vegetable and Ornamental Plants
Private bag X 293, Pretoria, 0001, South Africa.

Received: 28-08-2018

Accepted: 06-05-2019

DOI: 10.18805/LR-450

ABSTRACT

Cowpea is a drought tolerant food legume but yields are generally low in South Africa due to non-availability of improved varieties. The current study was undertaken to evaluate agronomic performance of cowpea germplasm and select the candidate accessions for breeding population and cultivation by small-scale farmers in South Africa. A randomized complete block design with three replications was used for the experiment. Data were collected on the agronomic traits including days to 50% maturity, days to 95% maturity, hundred seed weight, leaf area index, number of branches, number of internodes per plant, number of seeds per plant, plant height, number of pods per plant, pod length, dry biomass weight per plant, grain yield per plant and grain yield per hectare. Highly significant differences were observed among the accessions for all the traits. The grain yield per hectare correlated positively and significantly with number of pods per plant and grain yield per plant showing a scope for simultaneous improvement of yield and yield related traits. Principal Component biplot revealed that accessions Acc2024, Acc5352, Acc2355, Acc4565, Glenda and L-cwp3 were the most genetically distinct accessions and can serve as candidate parental lines for hybridization to achieve transgressive segregation population in breeding programmes.

Key words: Farmers, Heritability, Principal components, *Vigna unguiculata*.

INTRODUCTION

Cowpea [*Vigna unguiculata* (L.) Walp] is a legume crop grown for human consumption and livestock feed (Singh, 2005). It is an integral part of cropping systems for its drought tolerance and improvement of soil nitrogen (Timko *et al.*, 2008). The existence of diverse crop morphology in cowpea serve an important role of satisfying variable needs of the value chain actors. In addition, it provides a cheap source of protein, vitamins and minerals in both rural and urban areas to replace expensive source of proteins obtained from meat and complement the carbohydrates rich stable diets obtained from cereals.

In South Africa, cowpea is predominately produced for subsistence by smallholder farmers, who obtained yield of less than 500 kg ha⁻¹ (Asiwe, 2009). Lack of improved varieties is an important production constraint in cowpea production areas despite existence of high genetic diversity among cowpea germplasm (Gerrano *et al.*, 2015). Therefore, there is a need to evaluate the cowpea accessions to identify potential parental lines for improvement in targeted environments. This project was undertaken with the objective to evaluate agronomic performance of cowpea germplasm and select the candidate accessions for breeding population and cultivation by small-scale farmers in South Africa.

MATERIALS AND METHODS

Twenty-eight cowpea accessions were used in the study (Table 1) including the local cultivar Glenda. The field experiment was conducted at ARC-Roodeplaat Research Farm, Pretoria (25.604° S, 28.345° E; 1168 m.a.s.l) in the summer cropping season. The experimental site has clay loam soil, an annual rainfall of 700 mm and maximum temperature of 30°C. Seeds of each accessions were planted in plots consisting of 3 m long rows. The experiment was arranged in a randomized complete block design with 3 replications. Two seeds were sown per each hill that were thinned to one seedling per hill 15 days after planting. The inter and intra row spacing of 0.4 m and 1 m, respectively were used. Rainfall was supplemented with irrigation and no fertilizers were applied to ensure low-input conditions for growth and development of the crop as well as to determine the yield potential of the crop (Gerrano *et al.*, 2015; Gerrano *et al.*, 2019a). Weeds were controlled manually.

Data collection and analysis: Data were collected on 13 agronomic traits using cowpea descriptors (Anonymous, 1983) for days to 50% maturity (D50), days to 95% maturity (D95), hundred seed weight (HSWt), leaf area index (LAI), number of branches (NB), number of internodes per plant (NIP), number of seeds per plant (NSPP), plant height (PH),

*Corresponding author's e-mail: agerrano@arc.agric.za

¹Agricultural Research Council Vegetable and Ornamental Plants, Private bag X 293, Pretoria, 0001, South Africa.

²University of Venda, Private Bag X5050, Thohoyandou 0950, South Africa.

Table 1: Mean agronomic traits of the 28 cowpea accessions.

Genotype	D50	D95	HSWt (g)	LAI	NB	NIP	NSPP	PH (m)	NPP	PL (cm)	PWT (g)	GYP (g)	GY (kg/ha)
Cwp4	68a	140a	14.08efghi	4.06fg	7.6bcdef	12.27de	13.00abc	1.72abc	34.37efg	16.57bcd	1123.7cd	78.75ab	2624.89a
L-cwp3	67ab	136ab	24.08a	1.91o	6hij	1.8g	13.65abcdf	1.48abcddefg	25.71h	15.83bcdef	680.8fghij	38.67gh	2528.46a
Acc1998	68a	116efghi	10.25i	4.28e	8.6b	13.47cd	14.80ab	1.4bcdefgh	50.07ab	12.94ghij	635.5ghij	65.51c	2190.04bc
Cwp2	68a	125cde	21.84b	3.85jk	6.33ghij	13.53bcd	11.00gh	1.82a	40.03cdef	19.23a	939.4de	65.11c	2168.18cd
Acc1168	61def	109ghij	14.03efghi	3.88ij	7.67bcdef	12.67cde	14.00a	1.66abcd	33.73fgh	15.7bcdef	868.6efg	64.83c	2151.84cd
Acc1179	63bcde	116efghi	15.2def	4.02g	7.93bcde	13.47cd	13.00abc	1.36cdefgh	37.4defg	16.17bcde	819.8efgh	54.52de	2147.4cd
Acc1121	68a	116efghi	14.75efg	4.02gh	6.77efghij	12.93cde	12.00bcdg	1.74abc	39.83cdef	15.63bcdef	851.4efg	58.16cd	1949.2cde
Acc2355	58f	106ij	17.54c	3.47m	8bcd	13.07cde	13.00abc	1.42bcdefgh	53.49a	17.03abc	1247.3bc	85.66a	1936.03cdef
Acc5352	53g	89k	14.17efghi	2.16n	6.87defghi	11.93e	11.00gh	0.66jk	39.17cdefg	16.32bcde	745.3efghi	54.75de	1836def
Acc4893	68a	117efgh	15.66cde	3.95hi	8.4b	13.13cde	12.00bcdg	1.07hi	35.07efg	15.49bcdefg	350.9lmn	40.65fg	1799.24efg
Phokwane1	60ef	116efghi	14.63efg	3.82jk	7.33cdefg	13.27cde	11.00dfg	1.45abcddefgh	37.27defg	15.03defg	588.7hijk	39.88fg	1787.66efg
Acc1165	68a	129bcd	12.61hijkl	4.31de	9.77a	15.01a	13.00abc	1.47abcddefg	48.97ab	15.76bcdef	872.3ef	53.31de	1578.36fgh
Acc1958	65abcd	113fghi	14.34efghi	4.39d	8.27bc	13.53bcd	11.00dfg	0.7jk	41.67cd	10.61j	576.4hijkl	47.67ef	1578.36fgh
Acc4749	66abc	112fghi	11.48kl	4.39d	8bcd	13cde	12.00bcdg	0.9lij	33g	13.48fghi	593.5hijk	42.08fg	1462.71gh
Glenda	48h	89k	11.4kl	2.07n	5.8ij	12.24e	9.00i	0.4k	25.97h	11.71j	307.5mn	20.88j	1366.19h
Acc1985	68a	108ghij	14.3efghi	4.14f	7.47bcdefg	13.53bcd	13.00abcd	0.82j	41.75cd	15.76bcdef	897.6def	41.39fg	1345.77h
Acc4565	68a	135abc	13.67fghij	1.07p	7.27cdefg	12.6cde	11.00fg	1.67abcd	23.33hi	15.93bcdef	481.5ijklm	31.43hi	831.6i
Acc1257	68a	122def	12.57ijkl	3.91ij	6.93defghi	12.07e	12.00cdfg	1.17fghi	26.23h	14.03efghi	538.8ijklm	34.9gh	789.76i
Acc3916	62cdef	131abcd	17.2c	3.72l	7.07defgh	13.2cde	11.00fg	1.64abcde	14.02jk	15.39bcdefg	419.5jklmn	24.09ij	598.3i
L-cwp2	64abcde	107hij	16.96cd	3.77kl	6.73fghij	14.87ab	13.00abc	1.3defghi	45.4bc	17.61ab	1396b	75.57b	591.9i
Acc4294	68a	130abcd	14.47efghi	4.49c	7.47bcdefg	13.8abc	11.00gh	1.21fghi	17.61jk	15.4bdefg	364.4klmn	23.58ij	552.7i
Acc4670	63bcde	114fghi	12.53ijkl	4.31de	6.8efghij	12.33de	11.00dfg	1.12ghi	20.2hij	15.82bcdef	314.3mn	40.53fg	533.16i
Acc3361	68a	131abcd	13.11ghijkl	4.77a	7.2cdefg	12.33de	11.00fg	1.53abcdef	21.47hi	14.34defgh	227.8n	17.74jk	480.06i
Acc2438	68a	118efg	14.26efghi	4.61b	7.4cdefg	12.6cde	11.00gh	1.78ab	13.79k	14.69defg	232.4n	20.62j	476.28i
Acc4663	68a	113fghi	14.54efgh	4.24e	6.93defghi	13.8abc	10.00hi	1.76ab	14.78jk	14.78defg	211.6n	11.91k	346.71i
Cwp1	61def	100j	12.97ghijkl	3.97ghi	3.67j	6.6f	13.00abcdf	1.51abcddefg	40.53cde	16.61bcd	2383.3a	55.81de	264.18i
Acc2024	68a	113fghi	11.9jkl	4.73a	8.4b	13.2cde	12.00bcdg	1.26efghi	11.59k	12.05hij	310.92mn	10.26k	263.76i
Cwp5	68a	132abcd	14.08efghi	4.31de	7.20cdefg	13.93cde	11.49gh	1.41bcdedgh	44.90bc	18.09ab	1000.90cd	61.90c	1723.58efg
GM	64.73	117.28	14.61	3.92	7.1	12.51	11.97	1.34	32.55	15.29	1025.9	45.03	1387.568
CV%	5.18	6.5	9.74	16.16	11.91	7.95	10.53	21.09	14.34	11.91	14	13.39	17.96
LSD	4.58	10.4	1.95	0.09	1.16	1.36	1.72	0.39	6.38	2.49	235.17	8.24	340.619
MS _e	11.24	57	2.03	0.4	0.72	0.99	1.59	0.08	21.78	3.32	20639	36.35	62136.166
MS _e	75.78**	465.18**	25.57**	1.58**	7.69**	19.47**	4.41**	0.41**	437.57**	10.67**	825745.00**	1256.24**	1829331.36**

** Significant at P≤0.01; GM = grand mean; LSD = least significant difference; CV = coefficient of variation; MSE = mean square for error; MSG = mean square for genotype;

D50 = days to 50% flowering; D95 = days to 95% maturity; HSWt = hundred seed weight; LAI = leaf area index; NB = number of primary branches; NIP = number of internodes per plant;

NSPP = number of seeds per pod; PH = plant height; NPP = number of pods per plant; PL = pod length; PWT = dry biomass weight per plant; GYP = grain yield per plant; GY = grain yield per hectare.

number of pods per plant (NPP), pod length (PL), dry biomass weight per plant (PWT), grain yield per plant (GYP) and grain yield per hectare (GY). Leaf area index (LAI) was measured using Ceptometer AccuPAR model LP-80[®] at 50% flowering on five randomly selected plants in a plot. Data were subjected to analysis of variance (ANOVA) in Agrobases Generation II (2008) (Agronomix Software Inc., Winnipeg, Canada) with means separated with least significant difference. The genotypic effect was considered as fixed factor. Principal component analysis (PCA) was done using accession means. The procedure of Uguru (1995) was used to compare genetic variability and heritability effects among traits.

RESULTS AND DISCUSSION

Genetic variation: The ANOVA showed a highly significant ($p \leq 0.01$) differences among the accessions for all the traits studied (Table 1). Glenda and Acc5352 were the earliest to flower in 48 and 53 days, respectively. These accessions also matured early and were relatively short in height. Plant height ranged from 0.3 m for Glenda to 1.82 m for Cwp2. Accessions Cwp4 and L-cwp3 gave the highest yield of 2624 and 2528 kg ha⁻¹, respectively. In this study, the highest values for grain yield per plant was found in Acc2355 (85 g). The highest mean value for dry biomass weight per plant (PWT) was recorded in Cwp1 (2383 g), hence, this accession can be recommended for animal feed during the dry season. Gerrano *et al.* (2015) reported that the genotypes with high dry biomass weight can be useful as livestock feeds during the dry season when fodder is scarce. Mean values for hundred seed weight (HSWt) ranged from 10.25 g for Acc1998 to 24.08 g for L-cwp3. The longest pod was recorded in Cwp2 followed by Cwp5. Despite having the lowest mean of HSWt, Acc1998 outperformed other accessions in number of pods per plant (NPP): 50 versus the lowest value of 12 recorded for Acc2024.

Genetic parameters: Estimates of genotypic components are presented in Table 2. The phenotypic and genotypic variances was portioned into phenotypic coefficient of variations (PCV) and genotypic coefficient of variations (GCV). The highest broad-sense heritability was recorded for grain yield per plant (GYP) (98.57%) and number of seeds per pod had the lowest heritability of 84.24%.

Traits association: Significant and positive correlation was observed between grain yield per plant and number of pods per plant, dry biomass weight per plant, number of seeds per plant, pod length or plant height (Table 3). Total grain yield correlated significantly with grain yield per plant and number of pods per plant. Pod length significantly correlated with hundred seed weight and plant height. Number of pods per plant exhibited a highly significant and positive association with number of seeds per plant, grain yield per hectare, grain yield per plant and dry biomass weight per plant. The results showed that days to 50% flowering correlated positively and highly significantly with days to 95% maturity, plant height and leaf area index.

Principal component analysis (PCA) and principal component (PC) biplot: The results of PCA are presented in Table 4 and Fig 1. The first two PCs explained more than 50% of the total variation. The traits that were highly associated in PC1 were HSWt, NSPP, PL and GYP. Traits associated with PC2 were D95, PH and NPP. Grain yield per plant contributed more variation for this component. The PC3 was mainly dominated by D50, LAI, NB and NIP.

Accessions in the top right quadrant were highly associated and characterized by NPP, GYP, GY, PWT and NSPP (Fig 1). The longest pods, heaviest seeds, tallest plants, and late maturity traits characterized accessions that were found in the right bottom quadrant. The accessions grouped

Table 2: Genetic and heritability estimates for 13 agronomic traits of cowpea.

Traits	σ^2_g	σ^2_p	GCV	PCV	h^2_{bs} (%)
D50	72.03	83.27	13.11	14.10	93.01
D95	446.18	503.18	18.01	19.13	94.17
HSWt	24.90	26.92	34.15	35.51	96.16
LAI	1.45	1.85	30.76	34.75	88.54
NB	7.45	8.16	38.43	40.23	95.52
NIP	19.14	20.13	34.99	35.88	97.51
NSPP	3.88	5.47	16.46	19.54	84.24
PH	0.39	0.47	46.39	50.98	91.00
NPP	430.31	452.09	63.73	65.33	97.56
PL	9.57	12.88	20.23	23.48	86.18
PWT	818865.33	846384.00	88.21	89.69	96.75
GYP	1244.12	1280.47	78.33	79.46	98.57
GY	1808619.30	1870755.47	130344.55	134822.62	96.68

D50 = days to 50% flowering; D95 = days to 95% maturity; HSWt = hundred seed weight; LAI = leaf area index; NB = number of primary branches; NIP = number of internode per plant; NSPP = number of seed per pod; PH = plant height; NPP = number of pod per plant; PL = pod length; PWT = dry biomass weight per plant; GYP = grain yield per plant; GY = total grain yield; σ^2_g = genotypic variance; σ^2_p = phenotypic variance; GCV = genotypic coefficient of variation; PCV = phenotypic coefficient of variation; h^2_{bs} (%) = broad sense heritability.

Table 3: Pearson correlation coefficients among 13 quantitative traits of tested cowpea accessions.

Trait	D50	D95	HSWt	LAI	NB	NIP	NSPP	PH	NPP	PL	PWT	GYP
D95	0.72**											
HSWt	0.09ns	0.29ns										
LAI	0.46*	0.12ns	-0.30ns									
NB	0.18ns	0.01ns	-0.54**	0.47*								
NIP	0.09ns	-0.07ns	-0.43**	0.42*	0.89*							
NSPP	0.28ns	0.13ns	0.06ns	0.24ns	0.15ns	-0.07ns						
PH	0.50**	0.59**	0.33ns	0.17ns	-0.08ns	-0.06ns	0.28ns					
NPP	-0.12ns	-0.22ns	0.05ns	0.00ns	0.17ns	0.14ns	0.54**	-0.12ns				
PL	0.11ns	0.24ns	0.53*	-0.12ns	-0.21ns	-0.05ns	0.26ns	0.49*	0.32ns			
PWT	-0.13ns	-0.20ns	0.15ns	-0.02ns	-0.28ns	-0.26ns	0.55**	0.15	0.64**	0.51**		
GYP	-0.09ns	-0.07ns	0.21ns	-0.02ns	0.07ns	0.06ns	0.66**	0.13*	0.85**	0.53**	0.70**	
GY	-0.09ns	0.10ns	0.34ns	-0.23ns	-0.02ns	-0.13ns	0.39ns	0.01	0.60**	0.21ns	0.17ns	0.64*

ns, *, ** not significant, significant at $P \leq 0.05$ or significant at $P \leq 0.01$, respectively. D50 = days to 50% flowering; D95 = days to 95% maturity; HSWt = hundred seed weight; LAI = leaf area index; NB = number of primary branches; NIP = number of internode per plant; NSPP = number of seed per pod; PH = plant height; NPP = number of pod per plant; PL = pod length; PWT = dry biomass weight per plant; GYP = grain yield per plant; GY = grain yield per hectare.

Table 4: Principal component (PC) analysis showing the eigenvector, eigenvalue and cumulative percentage of the first 4 principal component axes.

Traits	Eigenvector			
	PC1	PC2	PC3	PC4
D50	0.099	-0.292	0.423	-0.03
D95	0.157	-0.390	0.279	0.261
HSWt	0.301	-0.235	-0.189	0.242
LAI	-0.077	0.048	0.45	-0.345
NB	-0.164	0.243	0.46	0.232
NIP	-0.166	0.216	0.407	0.211
NSPP	0.307	0.188	0.223	-0.186
PH	0.247	-0.304	0.246	-0.117
NPP	0.283	0.423	0.049	0.085
PL	0.365	-0.049	0.023	-0.042
PWT	0.343	0.219	-0.079	-0.501
GYP	0.379	0.333	0.061	0.059
GY	0.271	0.202	-0.049	0.586
Eigenvalue	4.139	2.968	2.705	1.136
Variability (%)	29.567	21.201	19.319	8.113
Cumulative (%)	29.567	50.768	70.087	78.20

D50 = days to 50% flowering; D95 = days to 95% maturity; HSWt = hundred seed weight; LAI = leaf area index; NB = number of primary branches; NIP = number of internode per plant; NSPP = number of seed per pod; PH = plant height; NPP = number of pod per plant; PL = pod length; PWT = dry biomass weight per plant; GYP = grain yield per plant; GY = total grain yield.

in the left top quadrant were characterized by high NB, NIP and had highest values for LAI. The lowest values for all the traits were associated with accessions located in the left bottom quadrant.

The tested germplasm accessions were scattered in the biplot (Fig 1) indicating that the accessions are genetically diverse for the agronomic traits evaluated and can be used for development of breeding population. Accessions L-cwp3,

Glenda, Acc2024 and acc2355 were distinct accessions and found far away from the origin indicating that this accessions had some peculiar genes that can be used in the improvement programme.

The significant and positive associations between GY with NPP and GYP (Table 3) implies that selection for these traits may lead to higher yield and simultaneous improvement of these traits. In this study, highly significant ($P < 0.01$) variations were observed among the tested cowpea accessions for all agronomic traits, showing a high level of phenotypic differences among them (Table 1). The current study confirmed the previous reports in cowpea (Nwosu *et al.*, 2013; Gerrano *et al.*, 2015; 2019b). Kamara *et al.* (2017) observed significant variations in the agronomic characteristics of the cultivars in Nigeria. Phenotypic traits are controlled by many genes and influenced by environmental conditions. The existence of genetic variation in the current study among tested accessions could allow improvement of yield and related traits of cowpea in South Africa. In the current study, Glenda (local check) and Acc5352 flowered early as compared to the rest of tested cowpea accessions and could be selected for earliness and early maturity traits and short stature genes. Similarly, (Gerrano *et al.*, 2015) selected cowpea genotypes for earliness genes. The accessions L-cwp3 and Cwp2 exhibited larger seeds size and longer pods, respectively. Gerrano *et al.* (2017) similarly reported that cowpea seed size is an important quantitative trait for consumer acceptability and commercialization in South Africa. Moreover, Kamara *et al.* (2012) previously reported that fodder yield, total dry matter, harvest index and 100-seed weight were significantly correlated with grain yield. Thus, cultivation of unimproved cowpea varieties limit the small-holder farmers from exploiting the genetic gain that accumulate with continuous cowpea breeding.

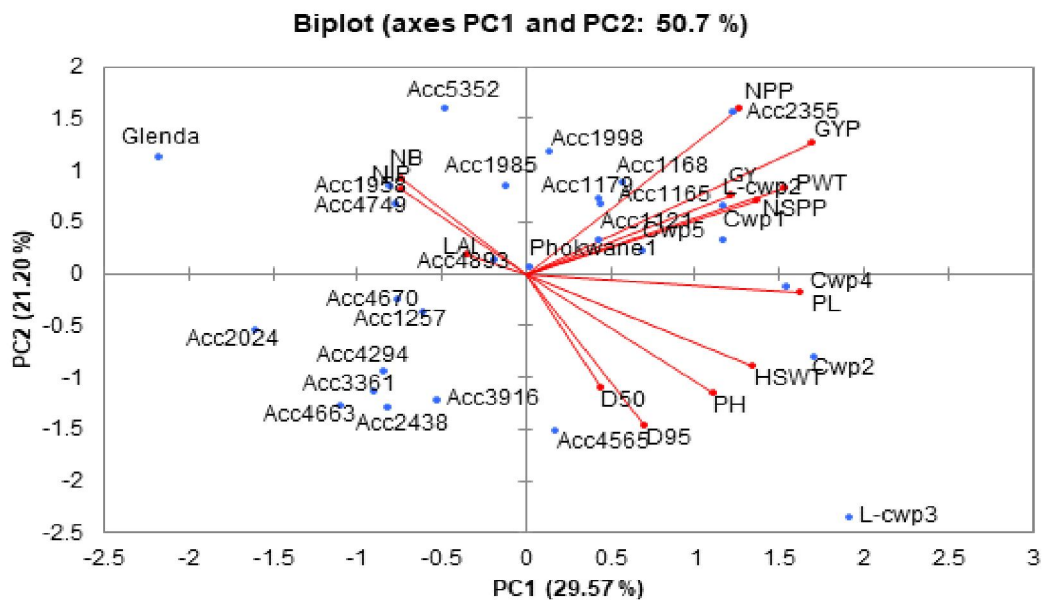


Fig 1: Principal component score plot of PC1 and PC2 describing the variation among cowpea accessions estimated using the data set of agronomic traits; D50 = days to 50% flowering; D95 = days to 95% maturity; HSWt = hundred seed weight; LAI = leaf area index; NB = number of primary branches; NIP = number of internode per plant, NSPP = number of seed per pod; PH = plant height; NPP = number of pod per plant; PL = pod length; PWT = dry biomass weight per plant, GYP = grain yield per plant, GY = total grain yield; blue dots=accessions; red dots=agronomic traits.

In the present study, high h^2 s estimates were recorded for all agronomic traits evaluated (Table 2), suggesting that a considerable amount of variance is heritable to the progenies for the improvement of these traits. Similarly, Aliyu and Makinde (2016) reported the low variance due to environmental factors in Nigeria. Moreover, Nwosu *et al.* (2013) reported that additive gene action dominated expression of traits due to high heritability in broad sense. They found higher heritability values in most phenotypic traits in cultivated and a wild relative cowpea. Gerrano *et al.* (2015) reported high heritability and genetic parameters for most of the agronomic traits in South Africa.

The PC biplot indicated that cowpea accessions were scattered randomly across the entire quadrant, indicating the existence of wide range of genetic variability among them. The accessions grouped into clusters based on their agronomic trait associations. Accessions Acc4893, Phokwane1, Cwp5 and Cwp4 were grouped close to the origin, indicating that these accessions had a similar genetic relationship for most of the traits; Accessions Glenda, Acc2024, Acc4565, Acc5352, L-cwp3 and Acc2355 were positioned far from the origin, indicating that these accessions had unique genes/alleles compared to the rest of the accessions evaluated. The biplot indicated relative

association of accessions to traits based on their closeness, indicating they had relatively similar values for those specific traits.

Accessions Acc2024, Acc5352, Acc2355, Acc4565, Glenda and L-cwp3 appear to be the most genetically distinct based on the traits evaluated and can serve as potential and candidate parental lines for hybridization for the traits of interest in future cowpea breeding.

CONCLUSION

The study affirmed that collection, characterization, and evaluation of 28 accessions of cowpea for agronomic traits are important in discerning genetic variability that can be exploited in plant breeding to improve cowpea value chain. The experiment was conducted at one site and therefore, we would recommend that further researches be done under different environmental conditions in order to validate their usefulness in future cowpea breeding efforts and recommendation for cultivation by small-scale farmers in the country.

ACKNOWLEDGEMENT

The first author acknowledges the Agricultural Research Council, Professional Development Program for providing funding for research.

REFERENCES

- Aliyu, M.O. and Makinde, B.O. (2016). Phenotypic analysis of seed yield and yield components in cowpea [*Vigna unguiculata* (L.) Walp]. *Plant Breeding and Biotechnology*. **4**: 252-261.
- Anonymous. (1983). International biodiversity for plant genetic resources, Cowpea descriptors. International Board for Plant Genetic Resources, Rome, Italy.

- Asiwe, J.A.N. (2009). Needs assessment of cowpea production practices, constraints and utilization in South Africa. *African Journal of Biotechnology*. **8**: 5383-5388.
- Gerrano, A.S., Adebola, P.O., van Rensburg, W.S. and Laurie, S.M. (2015). Genetic variability in cowpea [*Vigna unguiculata* (L.) Walp.] genotypes. *South African Journal of Plant and Soil*. **32**: 165-174.
- Gerrano, A.S., van Rensburg, W.S. and Adebola, P.O. (2017). Preliminary evaluation of seed and germination traits in cowpea (*Vigna unguiculata*) genotypes. *South African Journal of Plant and Soil*. **34**: 399-402.
- Gerrano, A.S., Jansen van Rensburg, W.S., Venter, S.L., Shargie, N.G., Amelework, B.A., Shimelis, H.A. and Labuschagne, M.T. (2019a). Selection of cowpea genotypes based on grain mineral and total protein content, *Acta Agriculturae Scandinavica, Section B - Soil & Plant Science*. **69**:155-166. DOI: 10.1080/09064710.2018.1520290.
- Gerrano, A.S., Jansen van Rensburg, W.S., Kutu, F.R. (2019b). Agronomic evaluation and identification of potential cowpea [*Vigna unguiculata* (L.) Walp] genotypes in South Africa. *Acta Agriculturae Scandinavica, Section B. Soil and Plant Science*. **69**(4): 295-303. DOI: 10.1080/09064710.2018.1562564.
- Kamara, A.Y., Ewansiha, S.U., Ajeigbe, H.A., Okechukwu, R., Tefera, H., Boukar, O. and L.O. Omoigui. (2012). Improvements in grain and fodder yield of cowpea (*Vigna unguiculata*) varieties developed in the Sudan savannas of Nigeria over the past four decades. Proceedings of the Fifth World Cowpea Conference, 171-188.
- Kamara, A.Y., Ewansiha, S., Ajeigbe, H., Omoigui, L., Tofa, A.I. and Karim, K.Y. (2017). Agronomic evaluation of cowpea cultivars developed for the West African Savannas. *Legume Research*. **40**: 669-676.
- Molosiwa, O.O., Gwafila, C., Makore, J. and Chite, M.S. (2016). Phenotypic variation in cowpea [*Vigna unguiculata* (L.) Walp.] germplasm collection from Botswana. *International Journal of Horticulture and Floriculture*. **3**: 168-178.
- Nwosu, D.J., Aladele, S., Adeosun, J.O., Nwadike, C. and Awa, E.N. (2013). Cross compatibility and F1 reproductive potential of cultivated cowpea varieties and a wild relative (subsp. *unguiculata* var. *spontenea*). *Greener Journal of Agricultural Sciences*. **3**: 391-395.
- Singh, B.B. (2005). Cowpea [*Vigna unguiculata* (L.) Walp.]. *Genetic Resources, Chromosome Engineering and Crop Improvement*. **1**: 117-162.
- Timko, M.P. and Singh, B.B. (2008). Cowpea, a multifunctional legume. *Genomics of Tropical Crop Plants*. Springer, New York.
- Uguru, M.I. (1995). Heritable relationships and variability of yield and yield components in vegetable cowpea. *African Journal of Crop Science*. **3**: 23-28.