Heliyon 8 (2022) e08855

Contents lists available at ScienceDirect

Heliyon

journal homepage: www.cell.com/heliyon

Research article

CellPress

Phenotypic description of elite cowpea (*Vigna ungiculata L*. Walp) genotypes grown in drought-prone environments using agronomic traits



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ARTICLE INFO

Keywords: Agronomic traits Cowpea Cluster analysis Pearson's correlation Principal components

ABSTRACT

Identification and selection of cowpea genotypes possessing suitable agronomic attributes is key for cultivar development to increase production. The objective of this study was to evaluate cowpea genotypes using agronomic traits to aid selection and identification of best genotypes for adoption and breeding to develop highyielding cultivars. Agronomic traits of 20 cowpea genotypes were evaluated under Tompi Seleka and Polokwane environments using a completely randomised block design. Significant ($P \le 0.01$) genotype effect was identified for a gronomic traits, whereas environment effect was significant ($P \le 0.05$) for number of productive branches (NB), leaf width (LW), leaf length (LL), hundred-seed weight (HSW) and grain yield (GY). Significant genotype-by-environment interaction effect was observed for pod length (PL), pod width (PW) and number of seeds per pod (SPP). Correlation analysis revealed positive and significant associations between NB with LW (r = $0.58; P \le 0.01$, LL ($r = 0.67; P \le 0.01$), number of pods per plant (PPP) ($r = 0.56; P \le 0.01$) and HSW (r = 0.47; P \leq 0.05). LW was positively and significantly correlated with LL (r = 0.71; $P \leq 0.00$), PPP (r = 0.56; $P \leq 0.01$) and SPP (r = 0.58; $P \le 0.01$). Positive and significant correlation was observed between LL with chlorophyll content index (CCI) (r = 0.54; $P \le 0.05$), PPP (r = 0.68; $P \le 0.01$) and pod length (PL) (r = 0.52; $P \le 0.05$). PW was positively and significantly associated with PL (r = 0.68; $P \le 0.01$) and SPP (r = 0.61; $P \le 0.01$), whereas PL was positively associated with SPP (r = 0.82; $P \le 0.01$). Cowpea genotypes CH14, Embo buff, IT89D-349, IT96D-602, Veg cowpea 1, Veg cowpea 2, Veg cowpea 3 and Veg cowpea dakama red recorded high NB, plant height (PH), LL, LW, chlorophyll content index (CCI), number of pods per plant (PPP), HSW and GY. Also, genotypes 2460, IT96D-748, Oukawa, Ukaluleni, Veg cowpea dakama cream and Vigna Onb were associated with PL, SPP and PW. The identified genotypes possessing suitable agronomic traits are recommended for farmer-adoption and inclusion in breeding programs for cultivar development.

1. Introduction

Cowpea (*Vigna unguiculata* (L.) Walp.; 2n = 2x = 22) which is referred to as black-eyed pea is a widely cultivated legume, vegetable and fodder crop of African origin (Langyintuo et al., 2003; Kabas et al., 2007; Gonçalves et al., 2016; da Silva et al., 2018; Gomes et al., 2019). Globally, 12.5 million hectares of land are cultivated under cowpea production to yield seven million tons of grain produced per annum (FAOSTAT, 2020). Cowpea is cultivated for its fresh leaves, green pods and grain which are rich sources of macro and micro-nutrients (i.e, carbohydrate, protein, vitamins and minerals) (Gonçalves et al., 2016; Carvalho et al., 2019; Bai et al., 2020; ElMasry et al., 2021; Silva et al., 2021). These renders cowpea a key crop for food, nutrition and health security. Despite the role of cowpea as a food and nutrition security crop, the development of improved cultivars to increase production remains unsatisfactory, partially attributable to limited breeding efforts to identify and select suitable genotypes possessing superior performance in major production regions.

The production of the crop is hampered by biotic stresses including weeds (e.g., *Striga gesnerioides* (Willd.), etc.) (Tchiagam et al., 2010; Horn et al., 2015), insects (e.g., aphids, flower thrips, etc.) (Karungi et al., 2000; Agele et al., 2006; Abudulai et al., 2017), bacterial diseases (e.g., bacterial blight, bacterial pustule, etc.) (Viswanatha et al., 2011), fungi (e.g., leaf smut, anthracnose, etc.) (Adejumo et al., 2001; Fery and Dukes, 2011) and viruses (e.g., yellow mosaic, aphid borne mosaic, southern bean mosaic, etc.) (Mbeyagala et al., 2014). Abiotic environmental stress such as drought and heat, poor soil fertility and salinity also affect

https://doi.org/10.1016/j.heliyon.2022.e08855

Received 15 November 2021; Received in revised form 6 January 2022; Accepted 25 January 2022

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cowpea production (Osakabe et al., 2014; Ravelombola et al., 2018; Gomes et al., 2019, 2020). Though cowpea is generally tolerant to most environmental stresses (Tankari et al., 2021), continuous effort to deploy high-yielding cultivars possessing desirable agronomic attributes is crucial to enhance cowpea production.

Agronomic traits that are selected to improve cowpea yield potential include number of days to flowering and maturity, number of productive branches, leaf length and width, pod length and width, number of pods per plant, number of seeds per pod, grain yield and hundred-seed weight. Cowpea possess significant genetic variation for these agronomic traits which are important for genetic improvement (Shimelis and Shiringani, 2010; Menssen et al., 2017; Odeseye et al., 2018; Gerrano et al., 2019; Nkoana et al., 2019). Evaluation and selection of these agronomic traits is important to aid identification and selection of high-yielding candidate genotypes.

In order to aid the release of high-yielding cowpea genotypes for adoption and breeding, 20 genetically diverse cowpea genotypes were sourced from the International Institute for Tropical Agriculture (IITA) and Agricultural Research Council (ARC) pre-breeding nurseries for screening. Therefore, the objective of this study was to evaluate cowpea genotypes using agronomic traits to aid selection and identification of best genotypes for adoption and breeding to develop high-yielding cultivars.

Table 1. List of cowpea genotypes evaluated in the present study.

Genotype (G) code	Genotype name	Origin	Growth habit	Reference
G1	2460	South Africa	Prostate	Gerrano et al., 2015
G2	5431	South Africa	Upright	Gerrano et al., 2015
G3	CH14	South Africa	Prostrate	NA
G4	Embo Buff	South Africa	Semi-erect	Gerrano et al., 2015
G5	IT89D-349	Nigeria	Upright	NA
G6	IT93K 129-4	Nigeria	Upright	NA
G7	IT96D-602	Nigeria	Upright	Gerrano et al., 2015
G8	IT96D-748	Nigeria	Erect	NA
G9	Kisumu mix	Kenya	Prostate	Gerrano et al., 2015
G10	Meter long bean piet	South Africa	Prostrate	Gerrano et al., 2015
G11	Oukawa	South Africa	Prostate	Gerrano et al., 2015
G12	Tatro mix	Kenya	Prostate	Gerrano et al., 2015
G13	TVU7778	Nigeria	Upright	Gerrano et al., 2015
G14	Ukaluleni	South Africa	Prostate	Gerrano et al., 2015
G15	Veg cowpea 1	South Africa	Semi-upright	Gerrano et al., 2015
G16	Veg cowpea 2	South Africa	Semi-upright	Gerrano et al., 2015
G17	Veg cowpea 3	South Africa	Upright	Gerrano et al., 2015
G18	Veg cowpea dakama cream	South Africa	Upright	Gerrano et al., 2015
G19	Veg cowpea dakama red	South Africa	Upright	Gerrano et al., 2015
G20	Vigna Onb	South Africa	Prostate	Gerrano et al., 2015

NA, not available.

2. Materials and methods

2.1. Plant materials and study environments

Twenty genetically diverse cowpea genotypes obtained from the Agricultural Research Council - Vegetables, Industrial and Medicinal Plants (ARC-VIMP) genebank collections were used in the present study. These genotypes were selected based on their origin and varied growth habits (Table 1). The experiments were conducted at Polokwane $(25.8560^\circ$ S, 25.6403° E, 1369 m above sea level) and Tompi Seleka (25.6740° S, 28.3395° E, 1168 m above sea level) in South Africa during the 2018/2019 summer cropping season. Polokwane is characterised by sandy and acidic (pH \sim 4.5–5.2) soils, annual precipitation of \sim 443 mm and average air temperature of 27.51 °C. The soils in Tompi Seleka are generally sandy loams with pH of 6.5, annual rainfall of 480 mm and average air temperature of 22.75 °C. The test sites represented unique environmental conditions for cowpea production in South Africa in terms of geographical condition, soil characteristics including fertility, soil pH. soil temperature, and climate including rain, relative humidity, heat units as well as evapotranspiration. Both sites are characterized as being drought-prone areas in the Northern part of the country.

2.2. Experimental design and trial establishment

The cowpea genotypes were evaluated using a completely randomised block design with three replications. Four rows of 4-m length were used, with inter and intra-row spacings of 1 m and 0.40 m, respectively. Two seeds were sown per hole and seedlings were later thinned to one plant two weeks after emergence. These resulted in a total of 40 plants per plot. The plants were planted under rainfed conditions and irrigation was provided sparingly during crop establishment to avoid wilting. Agronomic management practices including insect, weed and diseasecontrol were carried out using chemical and cultural measures recommended for cowpea production.

2.3. Data collection

Data was collected on 11 agronomic traits following the International Board for Plant Genetic Resources descriptor list (IBPGR, 1983). To avoid border effect, data was collected from the two middle rows from five randomly selected and tagged plants. The following agronomic traits were recorded: number of productive branches per plant (NB) were counted at physiological maturity when maximum growth has occurred and when the plants appeared brown in colour; plant height (PH) in mm; leaf width (LW) in cm; leaf length (LL) in cm; chlorophyll content index (CCI) was recorded during the vegetative growth stage from the adaxial surface of healthy leaf using chlorophyll meter (CCM 200 plus Opti-Sciences, Hudson, New York, USA); pod length (PD) in cm; pod width (PW) in mm; number of pods per plant (PPP) were counted at physiological maturity; grain yield (GY) was recorded in g plant⁻¹ and converted to t ha^{-1} (i.e. the area per plant was 0.4 m²); hundred-seed weight (HSW) was calculated in grams from 100 randomly sampled seeds; and number of seeds per pod (SPP) were counted after harvest. Grain moisture content was determined at harvesting, and 14% is standard constant moisture content for legumes (Parker and Namuth-Covert, 2017) including cowpea.

2.4. Data analysis

Data collected at Tompi Seleka and Polokwane environments were subjected to analysis of variance (ANOVA) using Genstat 18.2^{th} edition (VSN International, Hempstead, UK) to determine genotype, environment, and genotype-by-environment interaction effects on the assessed agronomic traits. Mean separation was performed using the least significant difference (LSD) test at 5% probability level. Pearson correlation coefficients (*r*) were estimated using RStudio Version 3.2.1 (R Development

Table 2. A	Analysis of variance	showing mean	squares and sign	nificant tests f	or agronomic	traits of 20	cowpea ger	notypes eva	aluated across	Tompi Sele	eka and Po	olokwane
environme	ents of South Africa.											

Source of variance	d.f.	NB	PH	LW	LL	CCI	PPP	PW	PL	SPP	HSW	GY
Replication	2	10.59 **	2835.00 **	8.40**	3.95**	111.40**	286.50**	5.03**	0.49**	13.21**	134.49**	0.03**
Genotype (G)	19	8.33**	9688.00**	8.91**	16.05**	1463.90**	1413.00 **	20.66**	67.45 **	71.95 **	267.62**	0.79**
Environment (E)	1	31.35**	929.00 ^{ns}	12.83*	28.45*	46.40 ^{ns}	294.4 ns	7.04 ns	2.40 ns	0.84 ns	1238.29**	0.62**
G.E	19	3.73 ^{ns}	3057.00 ^{ns}	3.74 ^{ns}	7.29 ^{ns}	187.8 ^{ns}	0.40 ns	5.16 **	26.38 **	15.71 **	51.29 ^{ns}	0.03 ns
Error	78	3.10	2571.00	3.34	6.75	116.10	107.70	2.30	6.81	6.65	71.21	0.25

d.f., degrees of freedom; NB, number of productive branches; PH, plant height; LW, leaf width; LL, leaf length; CCI, chlorophyll content index; PPP, number of pods per plant; PW, pod width; PL, pod length; SPP, number of seeds per pod; HSW, hundred-seed weight; GY, grain yield; **, significant at $P \le 0.01$; *, significant at $P \le 0.05$; ns, not significant.

Core Team, 2008). Based on the correlation matrix, principal component analysis (PCA) was conducted to identify influential traits using RStudio Version 3.2.1 (R Development Core Team, 2008). Principal component (PC) biplots were constructed using RStudio Version 3.2.1 (R Development Core Team, 2008) to visualize inter-relationships between test genotypes and the evaluated traits. The hierarchical cluster analysis was conducted using the Single Linkage and Euclidean distance method using SPSS version 25 (SPSS Inc., Chicago, IL, USA 2008).

3. Results and discussion

3.1. Genotype, environment, and genotype-by-environment interaction effects on agronomic traits

ANOVA depicting genotype, environment and genotype-byenvironment interaction effects for assessed traits is presented in Table 2. Genotype main effect was significant ($P \le 0.05$) for all evaluated traits, suggesting presence of genetic variation among the evaluated genotypes. For example, genotypes G19, G2, G15 and G7 recorded high GY of >1.00 t ha⁻¹ (i.e., 2.02, 1.09, 1.06 and 1.03 t ha⁻¹, in that order), whereas genotypes G13, G4, G12 and G11 recorded low GY values of ≤ 0.40 t ha⁻¹ (Table 3). Significant ($P \le 0.05$) environment effect was observed for NB, LW, LL, HSW and GY, signifying differential environmental conditions among test locations. Further, genotype-by-environment interaction effect was significant ($P \le 0.01$) for PD, PW and SPP. Significant genotype-by-environment effects in cowpea for various agronomic traits were reported elsewhere (Horn et al., 2018; Owusu et al., 2021).

3.2. Mean performance of cowpea genotypes for agronomic traits

Selection of agronomic traits is key to speed up genetic improvement to increase cowpea yield output (Romanus et al., 2008; Patel and Jain,

Table 3.	Mean v	alues of	agronomic	traits among	t 20 w	heat gen	otypes	evaluated	across	Tompi	Seleka	and	Polokwane e	nvironments.
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Genotype	NB	PH	LW	LL	CCI	PPP	PW	PL	SPP	HSW	GY
G1	7.33	107.78	6.80	10.66	6.23	14.50	10.59	19.92	16.44	30.50	0.50
G2	7.78	116.78	6.50	10.50	32.53	37.11	7.82	17.48	13.44	15.73	1.09
G3	7.78	87.22	7.13	11.74	54.13	49.00	6.97	15.52	11.56	22.73	0.72
G4	7.67	168.67	7.66	12.67	28.00	32.56	7.89	15.59	15.00	23.91	0.32
G5	9.11	134.67	6.23	11.01	31.80	51.33	6.80	17.66	13.33	11.90	0.85
G6	7.44	244.11	5.54	10.90	50.53	42.33	6.81	11.78	8.22	15.56	0.47
G7	7.44	97.56	6.11	13.18	84.97	44.22	9.23	19.12	12.78	13.48	1.03
G8	7.89	137.56	9.01	12.60	44.93	31.11	10.72	19.66	16.33	15.00	0.59
G9	7.56	153.67	7.21	13.10	37.83	19.34	11.66	18.35	15.33	12.40	0.70
G10	5.44	134.89	5.32	7.92	24.70	8.78	4.73	9.11	7.22	7.44	0.75
G11	6.22	126.33	6.56	10.77	62.73	47.67	7.20	18.82	15.56	14.32	0.36
G12	6.33	103.44	4.67	10.59	34.37	20.33	7.17	14.42	13.57	33.38	0.35
G13	8.67	158.89	7.68	13.42	49.03	52.22	6.72	17.44	13.11	29.20	0.32
G14	7.11	76.56	6.46	10.76	37.77	39.00	9.23	17.63	18.11	34.81	0.52
G15	7.33	212.00	9.41	12.07	41.87	45.89	7.75	17.13	17.35	16.90	1.06
G16	8.89	189.22	4.50	11.86	23.77	66.00	8.05	17.38	15.67	16.41	0.83
G17	8.33	146.11	7.33	12.19	45.60	34.33	7.80	16.97	16.67	23.08	0.98
G18	7.33	154.44	6.93	11.78	41.60	39.89	9.46	22.02	19.00	16.26	0.48
G19	8.22	13.22	7.33	11.31	47.60	51.44	7.26	19.80	16.78	39.33	2.02
G20	8.00	205.00	8.90	12.60	24.63	66.00	8.81	18.48	17.22	14.54	0.41
Mean	7.59	138.41	6.86	11.58	40.23	39.65	8.13	17.21	14.63	20.34	0.72
Minimum	5.44	13.22	4.50	7.92	6.23	8.78	4.73	9.11	7.22	7.44	0.32
Maximum	9.11	244.11	9.41	13.42	84.97	66.00	11.66	22.02	19.00	39.33	2.02
SED	1.44	41.40	1.49	2.12	8.80	8.47	1.24	2.13	2.11	6.89	0.20
LSD	2.86	82.42	2.97	4.22	17.52	16.87	2.47	4.24	4.19	13.72	0.41
CV (%)	7.30	5.90	6.90	2.80	3.90	7.00	4.20	0.60	3.90	10.70	1.40

See genotype (G) codes in Table 1.

Note: NB, number of productive branches; PH, plant height; LW, leaf width; LL, leaf length; CCI, chlorophyll content index; PPP, number of pods per plant; PW, pod width; PL, pod length; SPP, number of seeds per pod; HSW, hundred-seed weight; GY, grain yield; SED, Standard error of difference; LSD, least significant difference; CV, coefficient of variation.

Table 4. Pearson's correlation coefficients (*r*) matrix showing associations between agronomic traits among cowpea genotypes across Tompi Seleka and Polokwane environments.

Traits	NB	PH	LW	LL	CCI	PPP	PW	PL	SPP	HSW	GY
NB											
PH	0.29 ^{ns}										
LW	0.58**	0.41 ^{ns}									
LL	0.67**	0.36 ^{ns}	0.71**								
CCI	0.21 ^{ns}	-0.05 ^{ns}	0.23 ^{ns}	0.54*							
PPP	0.56**	0.36 ^{ns}	0.56**	0.68**	0.30 ^{ns}						
PW	-0.04 ^{ns}	0.02 ^{ns}	0.07 ^{ns}	0.12 ^{ns}	-0.08 ^{ns}	-0.16 ^{ns}					
PL	0.28 ^{ns}	-0.01 ^{ns}	0.49 ^{ns}	0.52*	0.23 ^{ns}	0.32 ^{ns}	0.68**				
SPP	0.30 ^{ns}	0.08 ^{ns}	0.58**	0.43 ^{ns}	-0.07 ^{ns}	0.24 ^{ns}	0.61**	0.82**			
HSW	0.47*	-0.32 ^{ns}	0.28 ^{ns}	0.35 ^{ns}	0.17 ^{ns}	0.08 ^{ns}	-0.05 ^{ns}	0.16 ^{ns}	0.34 ^{ns}		
GY	0.36 ^{ns}	-0.13 ^{ns}	0.27 ^{ns}	0.09 ^{ns}	0.09 ^{ns}	0.26 ^{ns}	-0.18 ^{ns}	0.16 ^{ns}	0.10 ^{ns}	0.13 ^{ns}	

Note: NB, number of productive branches; PH, plant height; LW, leaf width; LL, leaf length; CCI, chlorophyll content index; PPP, number of pods per plant; PW, pod width; PL, pod length; SPP, number of seeds per pod; HSW, hundred-seed weight; GY, grain yield; **, significant at $P \le 0.01$; *, significant at $P \le 0.05$; ns, not significant.

2012; Aliyu and Makinde, 2016; Mofokeng et al., 2020). Mean values of the studied agronomic traits among cowpea genotypes across the two test environments are shown in Table 3. Selection of NB is key in breeding programs targeting genetic improvement to enhance cowpea yield potential. In the present study, high NB of >8 was observed for genotypes G5 (9.11), G16 (8.89), G13 (8.67), G17 (8.33) and G19 (8.22). Anjeela et al. (2021) reported mean number of productive branches of 17.31 among cowpea varieties Aakash and Prakash, which is higher than values observed in the present study. PH affect light interception and photosynthesis. High PH was observed for genotypes G6, G15 and G20 (i.e., 244.11, 212.00 and 205.00 mm, respectively), whereas G9 recorded the lowest low PH value of 13.22 mm. High average PH of 408.90 mm was reported in cultivar SARI-3-11-100 (Owusu et al., 2021), which is higher than values recorded in the present study. This cultivar (i.e., SARI-3-11-100) was a biparental cross of Padi-Tuya × Sanzio and could have been subjected to advanced genetic improvement for PH. The cowpea genotypes identified with high PH (i.e., G6, G15 and G20) are potential genetic resources for breeding.

Selection of plant leaf traits such as LW and LL is important in cowpea improvement programs. In the present study, LW and LL ranged between 4.50-9.41 cm and 7.92-13.43 cm, in that order. Average LW and LL values ranging between 4.78-22.02 cm and 12.36-67.72 cm, were reported in cowpea by Gerrano et al. (2019). Genotypes G15 and G16 recorded the highest and lowest LW values of 9.41 cm and 4.5 cm, respectively. High LL values of >13 cm were recorded for G13, G7 and G9, whereas G10 recorded the lowest value of 7.92 cm. Selection of genotypes possessing desirable leaf traits could improve cowpea performance. The chlorophyll pigment is responsible for capturing sunlight to drive photosynthesis. In the present study, high CCI values were observed for genotypes G7 (84.97), G11 (62.73), G3 (54.13) and G9 (50.53) and G13 (82.37). Barro et al. (2018) reported that CCI in cowpea ranges from 42.20-62.00 with a general mean of 51.38. Selection of genotypes identified with high CCI (i.e., G3, G7, G9, G11 and G13) could be important to enhance genetic improvement for enhanced yield potential in cowpea.

PPP is a major agronomic trait associated with cowpea yield potential. Genotypes such as G20 and G16 were identified with high PPP (i.e., 66.00), whereas G10 recorded the lowest PPP of 8.78. Average PPP ranging between 4.80 and 15.6 was reported in cowpea accessions (Menssen et al., 2017), which is lower than the range of values observed in the present study. PW determines seed size and yield in cowpea. High PW values of 11.66, 10.72 and 10.59 mm were recorded for genotypes G9, G8 and G1, whereas genotypes such as G10 recorded the lowest PW of 7.73 mm. PW of 7.44 mm was reported in cowpea (Anjeela et al., 2021), which is lower than values observed for the selected genotypes (i.e., G1, G8 and G9). PL is an important agronomic trait affecting seed yield in cowpea. The current study identified genotypes such as G18, G1, G19, G8 and G7 with long pods of >19 cm, whereas G10 recorded the lowest PL of 9.11 cm. The mean PL of 16.10 cm was reported in cowpea genotype *ANKCP2* (Jayasingha and Fernando, 2020), which is comparable to values observed in the current study. SPP determines yield potential in cowpea. In the present study, genotypes G18, G14, G15 and G20 were identified with high SPP of >17, whereas G10 and G6 recorded low SPP of \leq 9. Gerrano et al. (2019) reported average SPP of 27.37 in cowpea much higher than current observations. Contrastingly, Jayasingha and Fernando (2020) reported average number of seeds per pod of 12.12 among cowpea genotypes. The genotypes identified that possess yield-contributing traits (i.e., PPP, PW, PL and SPP) could be important genetic resources for breeding high-yielding cowpea cultivars.

HSW is an important agronomic trait that is selected to enhance genetic improvement for increased yield potential in cowpea. The present study identified genotypes such as G19, G14, G12 and G1 with high HSW values of >30 g, whereas G10, G5 and G9 were identified with low HSW of <13 g. The high HSW observed for genotype G1 (i.e., 30.50) could be due to high PW of 10.59 mm recorded for this genotype, which could have resulted in increased seed size. HSW of 38 g was recorded in cowpea genotype Drum elsewhere (Odeseye et al., 2018), which is comparable to the value of 39.33 g recorded for G19 in the current study. High mean HSW of 69.81 g was reported in cowpea genotype ARC018 (Mbuma et al., 2021). The higher values of hundred-seed weight in this genotype could be due to favorable environmental conditions in the test locations (i.e., Roodeplaat, Rustenburg and Potchefstroom). The genotypes identified with high hundred-seed weight (i.e., G19, G14, G12 and G1) could be selected for inclusion in subsequent breeding activities targeting genetic improvement to enhance cowpea productivity.

Selection of high GY is pivotal in cowpea breeding. In the present study, genotypes such as G19, G2, G15 and G7 recorded high GY of >1.00 t h⁻¹, whereas G13, G4, G12 and G11 recorded low GY of ≤ 0.4 t h⁻¹. The high GY observed for genotype G7 could be due to high PL (19.12 cm) and SPP (17.35) recorded for this genotype. Also, high GY in genotype G15 could have resulted from high SPP of 17.35 observed for this genotype. Significant and positive phenotypic correlations were observed between GY with PL and SPP (Romanus et al., 2008). GY of ≤ 2 t ha⁻¹ was reported by Iseki et al. (2021) and Owusu et al. (2021), which is comparable to the findings of the current study. The cowpea genotypes identified with high GY (i.e., G2, G7, G15 and G19) could be selected for adoption and for incorporation in breeding activities to develop breeding populations with superior yield potential.

Table 5. Rotated principal component loading scores, explained and cumulative variances of agronomic traits among 20 cowpea genotypes across Tompi Seleka and Polokwane environments.

Traits	PC1	PC2	PC3	PC4
NB	0.37	0.24	0.09	0.20
РН	0.15	0.16	-0.68	0.12
LW	0.42	0.07	-0.11	0.15
LL	0.44	0.13	-0.07	-0.28
CCI	0.19	0.22	0.17	-0.73
PPP	0.34	-0.43	0.03	0.19
PW	0.34	0.29	-0.17	0.01
PL	0.13	-0.61	-0.11	-0.11
SPP	0.15	0.19	0.32	0.51
HSW	0.20	0.03	0.58	0.01
GY	0.35	-0.41	0.04	-0.09
Explained variance (Eigenvalue)	4.14	2.03	1.50	1.07
Percentage of variance	37.64	18.49	13.59	9.75
Cumulative variance	29.58	56.13	69.72	79.47

Note: NB, number of productive branches; PH, plant height; LW, leaf width; LL, leaf length; CCI, chlorophyll content index; PPP, number of pods per plant; PW, pod width; PL, pod length; SPP, number of seeds per pod; HSW, hundred-seed weight; GY, grain yield.

3.3. Pearson correlations among agronomic traits

Yield improvement can be increased through (in) direct selection of yield-related agronomic traits (Oladejo et al., 2011; Kamara et al., 2011). Pearson correlation (*r*) matrix showing associations among the studied agronomic traits across test environments is presented in Table 4. Positive and significant correlations were observed between NB with LW (r = 0.58; $P \le 0.01$), LL (r = 0.67; $P \le 0.01$), PPP (r = 0.56; $P \le 0.01$) and HSW (r = 0.47; $P \le 0.05$). This implies that selection of high NB could be important to breed cowpea genotypes possessing high PPP and HSW. LW was positively and significantly correlated with LL (r = 0.71; $P \le 0.01$),

PPP (r = 0.56; $P \le 0.01$) and SPP (r = 0.58; $P \le 0.01$). Selection of high LW could result in cowpea genotypes with high LL, PPP, PL and SPP. Positive and significant correlation was observed between LL with CCI (r = 0.54; $P \le 0.05$), PPP (r = 0.68; $P \le 0.01$) and PL (r = 0.52; $P \le 0.05$). Further, PW was positively and significantly associated with PL (r = 0.68; $P \le 0.01$) and SPP (r = 0.61; $P \le 0.01$), whereas PL was positively associated with SPP (r = 0.82; $P \le 0.01$). Selection for one of the positively correlated traits could result in indirect improvement of the other trait. Positive association between agronomic traits in cowpea were reported by several authors (Suganthi and Murugan, 2008; Edematie et al., 2021; Shanko et al., 2014; Mbuma et al., 2021).

3.4. Principal components analysis of studied agronomic traits

Explained and cumulative variances of the studied agronomic traits among the 20 cowpea genotypes evaluated across Tompi Seleka and Polokwane environments are presented in Table 5. PCA identified four principal components (PCs) of which PC1, PC2, PC3 and PC4 explained 37.64, 18.49, 13.59 and 9.75 % of total variation, respectively. High PC loadings were observed for NB, LW, LL, PW and GY in PC1, indicating ability for these traits to explain most phenotypic variation that is present among the studied cowpea genotypes. High loadings were recorded for PL and PPP in PC2. PH and HSW recorded high loadings in PC3, whereas CCI and SPP correlated with PC4.

Principal component biplot displaying the inter-relationship between studied cowpea genotypes and agronomic traits evaluated across Tompi Seleka and Polokwane is presented in Figure 1. Angles below 45° between vector lines of variables reveal association among traits. Genotypes that are superior performers in particular trait are plotted furthest to the vector line and those inferior performance plotted closest to the vector line. As a result, genotypes such as G3, G4, G5, G7, G15, G16, G17 and G19 were superior performers for the following traits namely: NB, PH, LL, LW, CCI, PPP, HSW and GY. Further, genotypes such as G1, G8, G11, G14, G18 and G20 showed excellent performance for PL, SPP and PW. The identified genotypes could be important genetic resources for breeding to improve genetic gains for agronomic traits.



Figure 1. Biplot showing grouping of 20 cowpea genotypes superimposed with agronomic traits across Tompi Seleka and Polokwane environments. Note: NB, number of productive branches; PH, plant height; LW, leaf width; LL, leaf length; CCI, chlorophyll content index; PPP, number of pods per plant; PW, pod width; PL, pod length; SPP, number of seeds per pod; HSW, hundred-seed weight; GY, grain yield. See genotype (G) codes in Table 1.



Figure 2. Cluster analysis of 20 cowpea genotypes based on agronomic traits using single linkage and Euclidean distance methods. See genotype (G) codes in Table 1.

3.5. Cluster analysis

Dendrogram showing relationships among the studied cowpea genotypes for assessed traits across Tompi Seleka and Polokwane is presented in Figure 2. The genotypes were grouped into three clusters (i.e. A, B and C). Cluster A comprised of thirteen genotypes (i.e. G2, G3, G4, G5, G6, G7, G8, G11, G13, G15, G17, G19 and G20). Cluster B comprised of five genotypes (i.e. G1, G12, G14, G16 and G18), whereas Cluster C consisted of two genotypes (i.e. G9 and G10), signifying the uniqueness of test genotypes for agronomic traits. Among these genotypes, G19 was identified with high grain yield values of 2.02 and 1.68 t ha⁻¹ under Tompi Seleka and Polokwane environments, respectively (Table 3). These genotypes (i.e., G13, G15, G16 and G19) could be subjected to further screening for stability using multi-location trials and recommended for cultivar design and adoption in South Africa.

4. Conclusion

This study evaluated agronomic traits among selected cowpea genotypes to aid in the identification of suitable genotypes for cultivation and cultivar design. Cowpea genotypes CH14, Embo buff, IT89D-349, IT96D- 602, Veg cowpea 1, Veg cowpea 2, Veg cowpea 3 and Veg cowpea dakama red possessing high number of productive branches, plant height, leaf length, leaf width, chlorophyll content index, number of pods per plant, hundred-seed weight and grain yield were identified and selected. Genotypes 2460, IT96D-748, Oukawa, Ukaluleni, Veg cowpea dakama cream and Vigna Onb were recommended for breeding possessing high PL, SPP and PW. The selected genotypes are useful genetic resources for cultivation and for incorporation in subsequent breeding activities to enhance cultivar design and development.

Declarations

Author contribution statement

Abe Shegro Gerrano: Conceived and designed the experiments; Performed the experiments; Contributed reagents, materials, analysis tools or data.

Zamalotshwa Goodness Thungo: Analyzed and interpreted the data; Wrote the paper.

Sydney Mavengahama: Conceived and designed the experiments; Analyzed and interpreted the data.

Funding statement

This work was supported by Department of Agriculture, Land, Rural and Development (DALRD).

Data availability statement

Data will be made available on request.

Declaration of interests statement

The authors declare no conflict of interest.

Additional information

No additional information is available for this paper.

Acknowledgements

The Agricultural Research Council (ARC) in South Africa is acknowledged for provision of elite cowpea genotypes.

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