

Communication

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Preliminary study on character associations, phenotypic and genotypic divergence for yield and related quantitative traits among cowpea landraces (*Vigna unguiculata*) from the Western Highland Region of Cameroon

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Abstract: Cowpea (*Vigna unguiculata*) is an important tropical legume crop contributing significantly to food security in tropical regions. The present study was carried out to determine the extent of genetic variation, to estimate character associations, heritability and genetic advance of 25 quantitative traits in 30 genotypes of cultivated *Vigna unguiculata* from the western highland region of Cameroon. These quantitative traits were selected among cowpea descriptor lists. For all these traits, the analysis of variance showed significant difference among genotypes, highlighting the existence of important genetic divergence among the studied accessions. The highest phenotypic and genotypic coefficient of variation was observed in grain yield, pod yield and 100 seed weight. Genetic advance of these three characters was also the highest. Broad sense heritability was high in general, with 20 traits out of 25 having heritability values greater than 70%. This high heritability indicates little influence of the environment on these characters in cowpea. The highest heritability was recorded for 100 seed weight (98.15%) and

the lowest for shoot weight (41.38%). At 0.05 probability level, grain yield correlated significantly with 21 out of the 24 other quantitative traits. Among others, grain yield correlated positively and significantly with 100 seed weight, number of pods per plant, number of branches per plant, number of nodes per plant, plant height, plant width, pod length, pod width, seed length, seed width and number of seeds per pod. These positive correlations between grain yield and many other traits indicate that a selection program based on any of these traits will result in increasing yield. Cluster analysis using UPGMA method revealed five distinct clusters. Genotypes named KEB-CP025, KEB-CP006, KEB-CP098, KEB-CP070, and more importantly KEB-CP054 and KEB-CP004, were grouped in a single cluster and were characterized by a significantly higher grain yield, pod yield, number of pods per plant, number of seed per pod, plant height, pod length and pod width compared to other clusters. Accessions KEB-CP036 and KEB-CP031 produced significantly more important fresh biomass. These genotypes could be used as parents in genetic improvement programs aiming to increase yield and fresh biomass in cowpea.

Keywords: Morphometric analysis, Genetic Advance, Genetic divergence, Coefficient of variation, Grain yield, Heritability

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1 Introduction

Cowpea (*Vigna unguiculata*) is one of the most important tropical grain legumes, responsible for feeding people, their livestock and the next crop because of its nitrogen fixing characteristics (Singh et al. 1997). Due to its high

protein content (20-25%), cowpea can efficiently substitute meat for people who can't afford because of poverty (Diouf and Hilu 2005; Sharmar et al. 2013). In 2010, the world's cowpea production was estimated to be about 5.3 million tons, with Sub-Saharan Africa accounting for the majority (4.9 million tons), harvested on a cultivated area of 10 million hectares (Nedumaran et al. 2015). In Cameroon, the northern and western regions are the largest contributors to the national production that is estimated to be about 110000 tons, from a planted area of 105 000 hectares (Dudje et al. 2009; Bidima 2012). The major constraints to the production of this grain legume are the lack of high-yielding cultivars, resistant to abiotic and biotic stresses, among which diseases and insect pests are the most prevalent (Nkamleu et al. 2000).

Farmers are continuing to use introduced genotypes, described as high-yielding. This has resulted in the loss of a huge number of well-adapted local landraces, narrowing down the gene pool of the crop. As we narrow the gene pool of a crop species, this crop become vulnerable to diseases, pests and adverse climatic changes (Aremu 2012; Frankel et al. 1995). Broadening the gene pool is therefore required for crop selection and development of new cultivars (Subudhi et al. 2006). It is then pertinent to capture and conserve the genetic diversity existing in farmers' land. Genetic improvement approaches including selection, DNA-recombinant technology, hybridization and heterosis have been practiced to increase the yield of many crop species, and breaking the yield ceiling has been the challenge of many researchers in the field of plant breeding. For plant improvement, genotype identification using agro-morphological traits is a key step. Agro-morphological properties of crop varieties help to determine their potential yield, their agronomic fitness and their aptitude to tolerate biotic and abiotic stress. For example, a local common bean genotype from Cameroon, designated KEB-CB049, was revealed to be tolerant to salinity (NaCl) stress (Kouam et al. 2017)

For a crop species, acquiring estimates of genetic parameters, such as heritability and phenotypic correlation between traits, is of great importance in genetic improvement programs. They help in decision-making related to the choice of the most appropriate traits that should be selected across the different stages of a program, as well as the weight that should be assigned to each trait, separately or combined (Kang 2002). In cowpea, heritability and correlation between phenotypic traits have been studied. Heritability measures the influence of the environment on a trait, while correlation measures the degree of association between two variables (Gerrano et al. 2015; Srinival et al. 2016). High heritability indicates

little influence of the environment and assures high reproduction of a trait in several distinct environments. Significant association, or high correlation, between two characters allows selection of a trait of interest through another correlated trait which is easier to be measured, especially when the former is of complex inheritance like grain yield (Ceballos 2004). With the main objective of a plant breeding program being the improvement of food quality and yield, using significant associations between characters would allow direct selection and optimize gains in genetic improvement programs (Odjugo 2008; Xie et al. 2015). For effective selection in cowpea, breeders should make an effort to know the genetic variability, estimate character association and heritability of important agronomic traits. The aim of this study was to estimate the morphological diversity among *V. unguiculata* genotypes, estimate broad sense heritability and Genetic Advance, and assess the significance of the association between different characters. These estimates will assist in the design of selection strategies for cowpea breeding programs.

2 Material and methods

2.1 Plant material and study site

Cowpea accessions were collected from the Western Region of Cameroon. They were collected from market places, farmers' fields and the Institute of Agricultural Research for Development (IRAD). A total of 30 accessions were used for the study (Table 1). The study was carried out at the Research and Teaching Farm of the Faculty of Agronomy and Agricultural Sciences of the University of Dschang, located in the West Region of Cameroon, at a latitude of 5°20' North and a longitude of 10°05' East, and 1407 m altitude above sea level. The annual rainfall of the study site ranges from 1800 to 2000 mm, with an average annual temperature of around 20.50°C and a relative humidity of about 76.8%.

2.2 Experimental design

The 30 accessions were sown in the field under rain-fed conditions from August to December 2016, in a randomized complete block design (RCBD) with three replicates, on a total area of 2000 cm × 1980 cm. The blocks of 600 cm × 2000 cm each were distanced 90 cm from each other. Each block consisted of 30 experimental units of 200 cm × 200 cm, for each of the 30 accessions. Each experimental

Table 1: Codes and origins of the studied cowpea genotypes from the western region of Cameroon

No	Genotypes/ Variety	Village / District	Division
1	KEB-CP040	Fongotongo/Dschang	Menoua
2	KEB-CP071	Babou / Bangangté	Ndé
3	KEB-CP044	Bandjoun	Koung-Khi
4	KEB-CP048	Ntcho/Bafoussam	Mifi
5	KEB-CP045	Balembo	Haut-kam
6	KEB-CP069	Bazou	Ndé
7	KEB-CP018	Bafoussam	Mifi
8	KEB-CP060	Bangou	haut-plateaux
9	KEB-CP009	Bandjoun	Nkouh-khi
10	KEB-CP059	Bangou	Haut-plateaux
11	KEB-CP067	Bangangte	Ndé
12	MTA-22	IRAD	Foumbot
13	KEB-CP010	Bandjoun	Koung-Khi
14	KEB-CP025	Foto	Menoua
15	KEB-CP006	Bafoussam	Mifi
16	KEB-CP049	Bafoussam	Mifi
17	KEB-CP036	Makaka	Noun
18	KEB-CP051	Bandjoun	Koung-Khi
19	KEB-CP054	Bandjoun	Koung-Khi
20	KEB-CP046	Balembo	Haut-kam
21	KEB-CP004	Bafoussam	Mifi
22	KEB-CP098	Santchou	Menoua
23	KEB-CP038	Foumbot	Noun
24	KEB-CP039	Fondenera/Dschang	Menoua
25	KEB-CP020	Bafoussam	Mifi
26	KEB-CP070	Bantoum	Ndé
27	KEB-CP029	Dschang	Menoua
28	KEB-CP057	Bangou	Haut-plateaux
29	KEB-CP068	Bazou	Ndé
30	KEB-CP033	Kouoptamo	Noun

unit comprised 16 plants, separated by 50cm within rows and 50cm between rows. This was done to avoid competition among neighboring plants and to ensure a sound establishment of accessions. For quantitative analysis, four plants were sampled from the center of each experimental unit populated with sixteen individuals. A total of 12 plants per accessions were analyzed. Agronomic and plant protection practices were applied to provide plants with adequate growing conditions.

2.3 Data collection and analysis

In this study, data were recorded from four plants in each accession and in each replicate. Plants were evaluated for 25 quantitative traits that are described according to International Board for Plant Genetic Resources descriptors for cowpea (IBPGR 1983). Table 2 presents the 25 quantitative traits and their descriptions used in the analysis. For each trait, the data collected was subjected to

Table 2: List of quantitative traits and their descriptions

No.	Quantitative trait	Description
1	Petiole Length (cm)	Mean length of four randomly selected petioles of plants in each replicate
2	50% Flowering (days)	Number of days from sowing to flower appearance in 50% of plant in each replicate
3	TL. Length (cm)	Mean length of four randomly selected terminal leaves in each replicate
4	TL. Width (cm)	Mean width of four randomly selected terminal leaves in each replicate
5	Nb. Node	Mean number of nodes per plant of four selected plants in each replicate
6	Nb. Branches	Mean number of branches per plant of four selected plants in each replicate
7	Plant Height (cm)	Mean height of four selected plants at four weeks from sowing
8	Plant Width (cm)	Mean width of four selected plants at four weeks from sowing
9	Seed Length (cm)	Mean length of four randomly selected seeds in each replicate at harvest
10	Seed Width (cm)	Mean width of four randomly selected seeds in each replicate at harvest
11	Pod Width (cm)	Mean width of four randomly selected pods in each replicate at harvest
12	Pod Length (cm)	Mean length of four randomly selected pods in each replicate at harvest
13	Ovule/pod	Mean number of ovules of four randomly selected pods in each replicate at harvest
14	Seed/pod	Mean number of seeds of four randomly selected pods in each replicate at harvest
15	100 SW (g)	Weight of 100 seeds of each of four selected plant in each replicate at harvest
16	Pod/plant	Total number of pods per plant counted at the time of harvest
17	Shoot Weight (g)	Total weight of shoots of four randomly selected plants in each replicate
18	Germination (%)	Ration germinated seeds / number of seeds planted in each replicate
19	50% Poding (days)	Number of days from sowing to appearance of pods in 50% of plants in each replicate
20	Peduncle Length (cm)	Mean length of four randomly selected peduncles in each replicate
21	Pod/peduncle	Mean number of pods in four selected peduncles in each replicate
22	50% Maturity (days)	Number of days from sowing to physiological maturity of pods in 50% of plants in each replicate
23	Seed set (%)	Ratio number of seeds / number of ovules of four randomly selected pods in each replicate at the time of harvest
24	Pod yield (g)	Total weight of all the pods per plant of four selected plants in each replicate at harvest
25	Grain yield (g)	Total weight of all the seeds per plant of four selected plants in each replicate at harvest

Analysis of Variance (ANOVA) to test the variation among blocks and genotypes. The ANOVA was performed using XLSTAT version 2014 and Prism 6.0 computer software programs. Genetic parameters were calculated to assess the genetic variability among genotypes and to determine the genetic and environmental effects on the studied traits. Hence, the following parameters were measured for each trait: (1) mean of the trait: $\bar{X} = \sum xi / n$, where xi = value of an observation and n = number of observations, (2) genotypic variance: $\sigma_G^2 = (MS_G - MS_E) / r$, where MS_G = mean square of genotypes, MS_E = mean square of error, r = number of replicates, (3) environmental variance: $\sigma_E^2 = MS_E$, (4) phenotypic variance: $\sigma_P^2 = \sigma_G^2 + \sigma_E^2$, (5) broad sense heritability: $h_B^2 = \sigma_G^2 / \sigma_P^2$, (6) genotypic coefficient of variation: $GCV = 100 \times \sqrt{\sigma_G^2} / \bar{X}$, (7) phenotypic coefficient of variation: $PCV = 100 \times \sqrt{\sigma_P^2} / \bar{X}$, (8) genetic advance as

percentage of mean: $GA = k \times h^2B \times 100 \times \sqrt{\sigma_P^2} / \bar{X}$ where k is a constant = 2.06 at 5% selection pressure. The above formulas are from Singh and Chaudhary (1977) and Fehr (1987). Correlation coefficients were used to assess the relationship among different phenotypic traits. These coefficients were computed using XLSTAT computer program. Quantitative data were further analyzed using Euclidian distance coefficients. Hierarchical cluster analyses were then carried out from these coefficients, using the same XLSTAT program that produced a dendrogram via UPGMA method. For the different clusters obtained, ANOVA and comparison of means were performed using XLSTAT program. Quantitative data were exposed to principal component analysis (PCA) with the eigenvectors and eigenvalues determined using the same XLSTAT program.

Ethical approval: The conducted research is not related to either human or animals use.

3 Results

3.1 Genetic variation of quantitative traits

The coefficients of variation for the different measured quantitative traits are presented in Table 3. High coefficients of variation imply a wide range, while low coefficients of variation indicate a small range of the measured trait. The highest coefficient of variation values were observed for pod yield (28.62%), grain yield (28.22%), 100 seed weight (25.96%) and shoot weight (25.41%). The lowest coefficients of variation were found with seed set (4.35%) and time to 50% maturity (5.93%). The mean squares of the 25 quantitative traits from the 30 studied genotypes of cowpea are displayed in Table 4. The ANOVA showed a highly significant variation between cowpea genotypes for all the studied traits. Significant differences were also found between blocks for a number of the studied traits. Phenotypic (PCV) and genotypic coefficients of variation (GCV) for the different quantitative traits are presented in Table 5. The highest values of these coefficients were recorded for grain yield, pod yield, 100 seed weight and shoot weight, while the lowest values were noted for time to 50% maturity, time to 50% podding, time to 50% flowering and seed set (Table 5). Accessions KEB-CP054 and KEB-CP004 were the most productive, with pod yields of 221.00 and 215.33 g/plant, respectively, and grain yields of 149.29 and 146.42 g/plant, respectively. The least productive genotype was KEB-CP060, with a pod yield of 62.17 g/plant and a grain yield of 38.83 g/plant (Table 3).

3.2 Genotypic variance, phenotypic variance and heritability estimates

The phenotypic variance of a trait under study is composed of heritable (genotypic variance) and non-heritable (environmental variance) values, which are related as follows: phenotypic variance = genotypic variance + environmental variance. Phenotypic and genotypic variances of the 25 studied traits are presented in Table 5. Genotypic variance was the main contributor to the phenotypic variance (total variance) for 23 of the 25 studied traits. Germination percentage and shoot weight were the two characters most influenced by the environment. Broad sense heritability values in cultivated

V. unguiculata ranged from 41.38% to 98.15%. Broad sense heritability was higher in general and exceeded 70% in 20 of the 25 studied traits. 100 seed weight and time to 50% podding exhibited the highest broad sense heritability of more than 98%, followed by time to 50% flowering (96.53%), pod length (96.28%), pod width (96.04%) and seed length (95.94%). The lowest heritability values were found in shoot weight (41.38%), germination percentage (45.32%), number of pods per plant (56.21%) and seeds set (56.94%). Genetic Advance (GA) as percentage of mean ranged from 11.73% (time to 50% maturity) to 105.61% (100 seed weight) (Table 5).

3.3 Character associations

Using the 25 quantitative characters, 300 associations with correlation coefficients were generated and are presented in Table 6. Among these 300 associations, 124 associations were found to be not correlated, 144 associations were found to be positively correlated, while 32 associations were negatively correlated. Grain yield was positively and significantly correlated with 19 other traits. This included plant height, plant width, number of nodes, number of branches, peduncle length, pod yield, seed length, seed width, 100 seed weight, number of seeds per pod, number of pods per plant, pod length and pod width (Table 6). Grain yield was negatively and significantly correlated with the number of pods per peduncle and seed set (Table 6).

3.4 Cluster and principal component analysis

Using the 25 quantitative traits, Euclidian distances between *V. unguiculata* genotypes were calculated and the UPGMA dendrogram was constructed (Figure 1). This dendrogram grouped the 30 *V. unguiculata* genotypes in five distinct clusters. Clusters 1, 2, 3, 4 and 5 had 9, 3, 10, 6 and 2 adherents, respectively. The mean values of the different clusters for the 25 quantitative traits are presented in Table 7. The highest values of important yield components, including grain yield, pod yield, plant height, number of pods per plant, pod length and pod width were observed in Cluster 5. The lowest values of these same traits were observed in Cluster 2. Cluster 5 contained accessions with the highest shoot weight (350.70 g/plant), peduncle length (41.00 cm), seed length (0.96 cm), seed width (0.69 cm) and 100 seed weight (18.50 g) (Table 7). Principal component analysis (PCA) was carried out for all of the 25 quantitative traits. The first four components

Table 3: Quantitative trait estimates for 30 cultivated *V. unguiculata* genotypes

Accession	Pet. Length	50%F TL	TL	Nb. Node	Nb. Branch	P. Height	P. Width	Shoot Weight	% germ50%	Pod Length	Pod peduncle	50%M Seed set	Pod yield	Grain yield	Seed Length	Seed Width	Pod Width	Pod Length	Pod Ovule / Seed/ pod	100SWPod/ plant					
KEB-CP040	2.08	76.00	8.96	4.67	4.17	17.50	15.58	203.56	0.75	78.00	38.17	2.92	101.00	82.87	165.42	107.55	0.94	0.59	1.00	19.42	18.17	15.00	13.50	82.00	
KEB-CP071	2.03	76.00	7.17	3.17	4.00	13.08	12.50	112.78	0.58	77.00	34.67	4.92	101.00	96.53	106.83	67.63	0.64	0.47	0.61	16.00	16.67	16.08	9.17	71.50	
KEB-CP044	2.18	68.00	9.08	5.50	4.33	4.27	16.42	167.33	0.52	74.00	35.42	2.50	95.33	91.03	150.33	95.18	0.98	0.72	0.97	19.63	18.25	16.58	15.53	60.75	
KEB-CP048	2.02	68.00	9.08	4.17	4.67	14.92	15.92	187.11	0.56	74.00	35.17	2.58	94.00	93.34	176.17	111.45	0.71	0.55	0.73	18.63	17.25	16.08	11.33	88.83	
KEB-CP045	2.08	63.67	9.96	5.13	4.42	19.33	18.92	249.89	0.58	68.00	31.50	2.33	94.00	88.07	135.17	87.37	0.99	0.68	0.88	21.21	16.83	14.83	18.33	61.08	
KEB-CP069	1.93	74.00	8.08	3.75	3.83	15.17	14.42	176.67	0.71	77.00	33.67	3.92	96.67	99.04	107.92	72.16	0.73	0.54	0.73	16.50	16.17	16.00	8.77	69.92	
KEB-CP018	2.12	65.00	9.25	5.17	4.50	18.33	19.67	239.56	0.83	67.67	38.25	2.42	92.67	92.36	129.08	90.70	0.90	0.58	0.93	19.92	17.08	15.75	13.93	61.33	
KEB-CP060	2.13	60.00	7.58	3.63	4.33	14.92	15.33	120.33	0.73	64.00	29.25	2.50	85.00	98.99	62.17	38.83	0.58	0.45	0.78	15.92	16.00	15.83	8.93	41.00	
KEB-CP009	1.90	68.00	7.25	3.33	4.67	14.83	13.25	246.89	0.60	72.00	27.58	3.58	94.00	96.45	101.83	74.92	0.55	0.44	0.70	14.29	16.50	15.92	9.57	86.75	
KEB-CP059	1.98	63.00	9.25	3.58	5.00	18.25	18.17	225.44	0.77	66.00	29.58	2.83	85.00	94.84	99.58	66.42	0.59	0.45	0.61	15.33	16.08	15.25	9.73	66.50	
KEB-CP067	2.05	76.00	9.08	6.25	5.00	17.83	18.33	187.67	0.54	79.00	39.42	2.83	104.00	91.32	198.84	138.81	0.98	0.64	0.95	25.79	20.75	19.00	15.83	82.00	
MTA-22	2.18	64.00	12.92	2.50	4.75	21.08	18.67	184.44	0.79	67.00	21.92	2.75	96.00	91.54	96.25	73.68	0.81	0.62	1.04	17.71	17.42	15.92	17.27	45.17	
KEB-CP010	2.37	74.00	8.58	4.38	4.75	16.58	14.75	185.11	0.77	77.00	39.50	3.33	102.00	90.48	181.75	118.45	0.86	0.59	0.87	19.33	17.58	15.92	12.67	87.50	
KEB-CP025	2.13	73.00	9.08	5.33	4.92	17.17	16.08	260.78	0.85	77.00	41.08	3.00	102.00	93.87	175.58	108.86	0.80	0.58	0.98	18.75	17.17	16.08	13.70	85.50	
KEB-CP006	2.27	61.00	10.92	5.67	5.25	20.58	23.08	275.22	0.58	64.33	37.25	2.50	90.00	90.35	207.33	138.18	1.05	0.65	0.97	21.25	17.08	15.42	18.50	89.42	
KEB-CP049	2.28	63.67	10.67	5.25	4.92	17.08	19.17	214.33	0.44	65.67	44.25	2.92	94.00	90.62	182.23	112.92	0.93	0.73	0.95	20.92	18.42	16.67	16.23	74.33	
KEB-CP036	2.05	68.00	10.83	5.08	5.08	17.75	19.58	357.56	0.75	71.00	41.00	2.67	94.00	96.34	177.50	119.25	0.88	0.65	0.93	20.17	18.67	18.00	16.30	64.25	
KEB-CP051	2.08	62.33	11.00	5.67	5.33	18.00	21.25	343.89	0.44	65.33	41.00	2.42	94.00	80.72	174.58	127.13	1.04	0.73	0.98	20.96	16.58	13.42	20.70	67.50	
KEB-CP054	2.87	69.33	9.75	5.42	5.00	19.33	16.17	218.33	0.58	72.67	37.00	2.75	99.67	93.81	221.00	149.29	0.88	0.63	0.98	21.42	18.58	17.42	15.07	85.33	
KEB-CP046	2.34	63.00	10.50	5.58	5.17	18.50	20.33	253.56	0.88	66.00	33.33	2.50	92.67	89.94	131.42	89.45	0.93	0.63	0.89	21.67	18.42	16.58	14.80	64.33	
KEB-CP004	2.17	75.00	10.50	5.17	5.00	21.08	18.00	248.44	0.67	79.00	41.08	2.25	104.00	95.19	215.33	146.42	0.97	0.77	1.39	27.67	19.08	18.33	18.93	62.92	
KEB-CP098	2.00	71.00	9.67	5.17	4.92	17.75	23.42	280.22	0.83	73.33	39.75	2.42	102.33	91.25	204.33	112.73	0.89	0.62	0.92	27.58	21.83	19.92	12.43	74.00	
KEB-CP038	2.16	64.00	9.75	4.67	5.25	18.17	22.33	257.11	0.79	68.00	48.25	2.75	90.33	90.80	145.01	124.51	1.01	0.64	0.99	22.33	17.75	16.08	19.60	58.92	
KEB-CP039	2.29	74.00	7.50	4.25	4.42	17.25	12.58	236.56	0.48	77.00	34.50	2.75	101.00	92.57	123.75	81.38	0.78	0.59	0.93	19.58	19.00	17.58	12.80	55.83	
KEB-CP020	2.18	74.00	10.33	4.67	5.00	21.25	17.50	206.11	0.73	79.00	32.67	2.58	103.00	90.23	186.92	123.41	1.09	0.70	1.06	24.83	19.50	17.58	18.77	57.08	
KEB-CP070	1.86	69.33	10.83	5.50	4.92	20.33	20.42	265.22	0.71	73.67	37.33	3.25	97.00	93.78	203.25	130.94	0.78	0.61	0.88	19.42	17.33	16.25	13.00	99.17	
KEB-CP029	1.98	77.00	9.08	4.54	5.00	15.75	17.67	219.78	0.54	79.00	42.75	2.67	101.67	88.95	193.33	127.17	0.88	0.60	1.00	19.71	18.17	16.17	14.40	90.92	
KEB-CP057	2.03	68.00	8.33	3.75	5.00	18.33	16.58	189.33	0.73	72.00	31.50	3.92	90.00	95.33	93.50	66.43	0.52	0.41	0.68	13.75	15.92	15.17	8.33	88.50	
KEB-CP068	1.88	76.00	7.83	3.00	4.67	14.25	9.92	121.78	0.42	80.67	27.00	3.25	106.00	96.18	97.92	58.58	0.77	0.60	0.78	18.58	17.33	16.67	10.43	65.75	
KEB-CP033	2.46	72.67	11.92	5.75	5.00	20.58	21.42	214.33	0.54	75.33	36.25	2.50	105.00	91.65	189.00	125.75	0.88	0.72	1.03	24.25	17.92	16.42	20.10	67.50	
Mean	2.13	69.23	9.49	4.66	4.78	17.76	17.58	221.64	0.66	72.66	36.00	2.88	96.91	92.28	154.44	102.85	0.84	0.60	0.90	20.08	17.78	16.40	14.29	71.85	
Min	1.86	60.00	7.17	2.50	3.83	13.08	9.92	112.78	0.42	64.00	21.92	2.25	85.00	80.72	62.17	38.83	0.52	0.41	0.61	13.75	15.92	13.42	8.33	41.00	
Max	2.87	77.00	12.92	6.25	5.33	21.25	23.42	357.56	0.88	80.67	48.25	4.92	106.00	99.04	221.00	149.29	1.09	0.77	1.39	27.67	21.83	19.92	20.70	99.17	
Std. Dev	0.20	5.31	1.39	0.95	0.38	2.16	3.27	56.32	0.13	5.25	5.64	0.58	5.75	4.02	44.20	29.03	0.15	0.09	0.16	3.51	1.36	1.30	3.71	14.38	
CV (%)	9.43	7.67	14.68	20.47	7.89	8.01	12.18	18.61	25.41	20.49	7.23	15.67	20.06	5.94	4.35	28.61	28.22	18.30	15.27	17.32	17.46	7.65	7.90	25.96	20.01

Table 4: Means squares of variance for 25 quantitative traits in cultivated *V. unguiculata*

Source of Variation	df	Mean squares	Pet. Length	50%.F	TL. Length	TL. Width	Nb. Node	Nb. Branches	P. Height	P. Width	
Block	2	1.805**	2.700 ^{NS}	4.375 ^{NS}	16.155**	11.325**	11.585**	32.269*	7.411**		
Accession	29	0.487**	84.555**	23.225**	10.904**	1.703**	1.725**	56.143**	128.428**		
Error	270	0.036	1.000	1.797	0.795	0.136	0.127	9.641	15.164		
Source of Variation	df	Mean squares	Seed Length	Seed Width	Pod Width	Pod Length	Ovule/pod	Seed/pod	100 SW	Pod/plant	
Block	2	0.030**	0.006 ^{NS}	0.001 ^{NS}	0.827 ^{NS}	3.608 ^{NS}	1.658 ^{NS}	1.798 ^{NS}	9990.253**		
Accession	29	0.288**	0.101**	0.295**	147.589**	22.222**	21.238**	165.049**	2479.774**		
Error	270	0.004	0.004	0.004	1.873	1.385	1.973	1.03	511.112		
Source of Variation	df	Mean squares	Shoot Weight	% Germination	50%.Pod	Ped. Length	Pod/peduncle	50%.M	Seed set	Pod yield	Grain yield
Block	2	130898.211**	762.200 ^{NS}	0.744*	4.869 ^{NS}	0.108 ^{NS}	2.878 ^{NS}	8.501 ^{NS}	70220.828**	29147.325**	
Accession	29	28550.385**	544.840**	82.701**	382.204**	4.009**	99.309**	193.474**	22799.720**	10412.906**	
Error	270	9156.204	156.250	0.533	25.475	0.324	2.089	38.944	2392.715	1025.96	

*: Significantly different at 0.050 probability level; **: Significantly different at 0.010 probability level; ^{NS}: Not significant

Table 5: Estimates of genotypic and phenotypic variance components, broad sense heritability and Genetic Advance for 25 quantitative traits in cultivated *Vigna unguiculata*

Quantitative trait	Mean	σ^2_G	σ^2_P	GCV (%)	PCV (%)	h^2_B (%)	GA (%)
Petiole Length	2.134	0.150	0.186	18.168	20.226	80.680	33.616
50% Flowering	69.233	27.852	28.852	7.623	7.758	96.534	15.428
TL. Length	9.492	7.143	8.940	28.157	31.501	79.899	51.847
TL. Width	4.656	3.370	4.165	39.430	43.835	80.911	73.062
Nb. Node	4.775	0.522	0.658	15.136	16.992	79.342	27.773
Nb. Branches	4.762	0.533	0.660	15.327	17.056	80.748	28.372
Plant height	17.756	15.501	25.142	22.174	28.240	61.653	35.866
Plant Width	17.581	37.755	52.919	34.950	41.378	71.345	60.814
Seed Length	0.844	0.095	0.099	36.448	37.210	95.946	73.545
Seed Width	0.605	0.032	0.036	29.735	31.521	88.991	57.784
Pod Width	0.904	0.097	0.101	34.435	35.138	96.040	69.518
Pod Length	20.083	48.572	50.445	34.702	35.365	96.287	70.147
Ovule/pod	17.783	6.946	8.331	14.820	16.230	83.375	27.876
Seed/pod	16.397	6.422	8.395	15.454	17.670	76.497	27.845
100 SW	14.289	54.673	55.703	51.748	52.233	98.151	105.610
Pod/plant	71.853	656.221	1167.333	35.652	47.550	56.215	55.065
Shoot Weight	221.644	6464.727	15620.931	36.276	56.389	41.385	48.074
% Germination	0.657	129.530	285.780	17.326	25.735	45.325	24.028
50% Poding	72.656	27.389	27.922	7.203	7.273	98.091	14.696
Peduncle Length	36.003	118.910	144.385	30.288	33.375	82.356	56.622
Pod/peduncle	2.883	1.228	1.552	38.438	43.211	79.128	70.436
50% Maturity	96.911	32.407	34.496	5.874	6.061	93.944	11.729
Seed set	92.281	51.510	90.454	7.777	10.306	56.946	12.090
Pod yield	154.444	6802.335	9195.050	53.402	62.088	73.978	94.618
Grain yield	102.851	3128.982	4154.942	54.387	62.672	75.307	97.226

σ^2_G = Genotypic variance; σ^2_P = Phenotypic variance; GCV = Genotypic coefficient of variation; PCV = Phenotypic coefficient of variation; h^2_B = Broad sense heritability; GA = Genetic Advance

of the PCA explained 75.90 % of the total variation (Table 8). The first component accounted for 41.99 % of the total variation, and was attributed to most of the yield traits (grain yield, pod yield, 100 seed weight, seed length, seed width, pod length, pod width). The second component accounted for 18.10% of the total variation, mostly due to time to 50% flowering, time to 50% poding and time to 50% maturity. The third component accounted for 8.55% of the total variation, dominated by the number of pods per plant. The fourth component included the percentage of germination, seed set and the number of seeds per pod and accounted for 6.95% of the total variation.

4 Discussion

The genetic analysis of quantitative traits is a requirement for genetic improvement programs of crops. Therefore, understanding the magnitude of genetic variability, estimating heritability and character associations in crop species is essential, and provides the foundation for selection and genetic improvement programs (Idahosa et al. 2010). Significant differences were observed among genotypes for all quantitative traits. This occurrence of significant variability among *V. unguiculata* accessions was expected, since the study was carried out on

Table 6: Pearson's correlation coefficients between 25 quantitative traits in cultivated *Vigna unguiculata*

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	
Pet. Length (1)	1																									
50%.F (2)	-0.12	1																								
TL. Length (3)	0.30	-0.35	1																							
TL. Width (4)	0.36	-0.06	0.42	1																						
Nb. Node (5)	0.24	-0.29	0.58	0.45	1																					
Nb. Branch (6)	0.24	-0.26	0.57	0.44	1.00	1																				
P. Height (7)	0.39	-0.23	0.79	0.47	0.52	0.52	1																			
P. Width (8)	0.15	-0.49	0.75	0.62	0.63	0.61	0.65	1																		
Shoot Weight (9)	0.03	-0.30	0.49	0.54	0.60	0.60	0.44	0.65	1																	
% Germ (10)	-0.05	-0.15	0.11	-0.07	0.05	0.05	0.23	0.28	0.17	1																
50%.Pod (11)	-0.14	0.98	-0.35	-0.06	-0.27	-0.26	-0.20	-0.52	-0.32	-0.17	1															
Ped. Length (12)	0.16	0.14	0.15	0.66	0.35	0.35	0.07	0.44	0.46	-0.01	0.09	1														
Pod/pod (13)	-0.30	0.36	-0.54	-0.53	-0.45	-0.44	-0.54	-0.56	-0.45	-0.03	0.31	-0.21	1													
50%.M (14)	0.11	0.87	-0.01	0.15	-0.08	-0.06	0.02	-0.26	-0.14	-0.24	0.85	0.17	0.09	1												
Seed set (15)	-0.17	0.09	-0.41	-0.46	-0.29	-0.29	-0.33	-0.42	-0.38	0.15	0.13	-0.35	0.43	-0.12	1											
Pod yield (16)	0.35	0.27	0.47	0.76	0.50	0.49	0.45	0.48	0.47	-0.12	0.26	0.67	-0.40	0.46	-0.40	1										
Grain yield (17)	0.38	0.19	0.52	0.75	0.58	0.57	0.52	0.53	0.52	-0.11	0.19	0.71	-0.41	0.38	-0.44	0.96	1									
Seed Length (18)	0.34	0.00	0.57	0.69	0.36	0.35	0.54	0.54	0.42	-0.10	0.00	0.52	-0.60	0.30	-0.67	0.65	0.70	1								
Seed Width (19)	0.36	0.04	0.66	0.66	0.37	0.36	0.56	0.47	0.39	-0.28	0.06	0.46	-0.61	0.39	-0.52	0.66	0.68	0.89	1							
Pod Width (20)	0.38	0.14	0.59	0.52	0.37	0.38	0.65	0.40	0.36	0.00	0.15	0.43	-0.63	0.41	-0.40	0.62	0.67	0.74	0.81	1						
Pod Length (21)	0.31	0.20	0.49	0.68	0.42	0.42	0.53	0.54	0.35	-0.03	0.20	0.50	-0.60	0.50	-0.37	0.74	0.72	0.78	0.79	0.75	1					
Ovule/pod (22)	0.22	0.38	0.23	0.48	0.27	0.27	0.28	0.29	0.21	0.01	0.36	0.38	-0.39	0.57	-0.23	0.61	0.54	0.53	0.53	0.82	1					
Seed/pod (23)	0.13	0.42	0.02	0.23	0.12	0.13	0.11	0.06	0.02	0.07	0.42	0.19	-0.17	0.49	0.32	0.40	0.32	0.18	0.26	0.32	0.62	0.85	1			
100 SW (24)	0.40	-0.18	0.77	0.61	0.54	0.54	0.70	0.64	0.51	-0.14	-0.17	0.42	-0.64	0.17	-0.60	0.57	0.68	0.86	0.87	0.79	0.70	0.36	0.05	1		
Pod/plant (25)	-0.09	0.30	-0.12	0.25	0.20	0.19	-0.12	0.00	0.14	-0.10	0.29	0.31	0.31	0.19	-0.09	0.49	0.43	-0.11	-0.17	-0.18	-0.09	-0.01	-0.05	-0.21	1	

Values in bold are significantly different from 0 at the p = 0.050 probability level

Table 7: Mean values of 25 quantitative traits for five groups revealed by cluster analysis on 30 cultivated *Vigna unguiculata* accessions

Quantitative trait	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5
Petiole Length (cm)	2.18 ± 0.05 ^a	2.01 ± 0.05 ^a	2.10 ± 0.046 ^a	2.22 ± 0.14 ^a	2.06 ± 0.01 ^a
50% Flowering (Days)	72.15 ± 1.52 ^a	70.67 ± 3.37 ^a	66.67 ± 1.35 ^a	69.78 ± 1.97 ^a	65.17 ± 1.27 ^a
TL. Length (cm)	9.64 ± 0.36 ^{ab}	7.53 ± 0.12 ^c	9.28 ± 0.53 ^b	10.13 ± 0.30 ^{ab}	10.92 ± 0.04 ^a
TL. Width (cm)	5.02 ± 0.23 ^{ab}	3.27 ± 0.12 ^c	4.17 ± 0.30 ^{bc}	5.38 ± 0.08 ^a	5.38 ± 0.13 ^a
Nb. Node	4.76 ± 0.11 ^{abc}	4.33 ± 0.13 ^c	4.70 ± 0.14 ^{bc}	5.00 ± 0.05 ^{ab}	5.21 ± 0.06 ^a
Nb. Branches	4.74 ± 0.11 ^{abc}	4.33 ± 0.12 ^c	4.68 ± 0.14 ^{bc}	4.99 ± 0.04 ^{ab}	5.20 ± 0.06 ^a
Plant Height (cm)	17.68 ± 0.69 ^a	14.08 ± 0.34 ^b	17.92 ± 0.58 ^a	19.37 ± 0.65 ^a	17.88 ± 0.07 ^a
Plant Width (cm)	17.42 ± 0.68 ^a	12.58 ± 0.99 ^b	17.49 ± 1.01 ^a	19.53 ± 1.34 ^a	20.42 ± 0.37 ^a
Shoot Weight (g)	198.40 ± 5.82 ^c	118.30 ± 1.76 ^d	225.90 ± 9.74 ^c	258.00 ± 9.16 ^b	350.70 ± 3.06 ^a
% Germination (%)	59.89 ± 3.96 ^a	57.67 ± 5.66 ^a	71.60 ± 3.97 ^a	70.33 ± 4.80 ^a	59.50 ± 6.93 ^a
50%.Pod (Days)	75.67 ± 1.43 ^a	73.89 ± 3.19 ^a	70.07 ± 1.34 ^a	73.33 ± 2.06 ^a	68.17 ± 1.27 ^a
Peduncle Length (cm)	38.18 ± 1.25 ^{ab}	30.31 ± 1.44 ^c	33.01 ± 2.19 ^{bc}	38.92 ± 0.79 ^{ab}	41.00 ± 0.01 ^a
Pod/peduncle	2.76 ± 0.09 ^{ab}	3.56 ± 0.45 ^a	2.97 ± 0.19 ^{ab}	2.69 ± 0.15 ^{ab}	2.55 ± 0.06 ^b
50% Maturity (Days)	100.00 ± 1.45 ^a	97.33 ± 4.01 ^a	93.23 ± 1.37 ^a	99.17 ± 2.08 ^a	94.00 ± 0.01 ^a
Seed set (%)	90.05 ± 0.98 ^b	97.23 ± 0.56 ^a	93.09 ± 1.05 ^{ab}	93.04 ± 0.75 ^{ab}	88.53 ± 3.49 ^b
Pod yield (g/plant)	180.40 ± 4.97 ^{ab}	88.97 ± 8.63 ^d	116.40 ± 5.88 ^c	204.50 ± 6.42 ^a	176.00 ± 0.65 ^b
Grain yield (g/plant)	117.90 ± 4.26 ^a	55.01 ± 5.38 ^c	82.70 ± 5.44 ^b	131.10 ± 6.95 ^a	123.20 ± 1.76 ^a
Seed Length (cm)	0.92 ± 0.03 ^a	0.66 ± 0.04 ^b	0.78 ± 0.06 ^{ab}	0.89 ± 0.04 ^a	0.96 ± 0.04 ^a
Seed Width (cm)	0.65 ± 0.02 ^{ab}	0.51 ± 0.03 ^c	0.56 ± 0.03 ^{bc}	0.64 ± 0.03 ^{ab}	0.69 ± 0.02 ^a
Pod Width (cm)	0.95 ± 0.03 ^a	0.72 ± 0.04 ^b	0.84 ± 0.05 ^{ab}	1.02 ± 0.07 ^a	0.96 ± 0.01 ^a
Pod Length (cm)	21.39 ± 0.92 ^{ab}	16.83 ± 0.55 ^c	18.23 ± 0.99 ^{bc}	22.68 ± 1.62 ^a	20.57 ± 0.17 ^{abc}
Ovule/pod	18.45 ± 0.35 ^a	16.67 ± 0.24 ^a	17.12 ± 0.33 ^a	18.51 ± 0.74 ^a	17.63 ± 0.47 ^a
Seed/pod	16.60 ± 0.38 ^a	16.19 ± 0.16 ^a	15.91 ± 0.25 ^a	17.24 ± 0.68 ^a	15.71 ± 1.02 ^a
100 SW (g)	15.37 ± 0.94 ^{ab}	9.51 ± 0.29 ^c	13.31 ± 1.32 ^{bc}	15.27 ± 1.15 ^{ab}	18.50 ± 0.98 ^a
Pod/plant	76.77 ± 4.17 ^{ab}	59.42 ± 5.92 ^b	65.83 ± 4.20 ^{ab}	82.72 ± 5.16 ^a	65.88 ± 0.73 ^{abc}

Values with different letters in the same row indicate a significant difference at the 0.050 probability level

genotypes from different locations. Using quantitative descriptors, Gerrano et al. (2015), Srinivas et al. (2016), Suganthi and Murugan (2008), Withanage (2005) and Malarvizhi et al. (2005) reported the existence of important genetic variation among *V. unguiculata* genotypes. The same observation was reported for *V. mungo* (Veeramani et al. 2005), another crop from the same genus. Other crop species showed significant genetic variation among genotypes with the help of quantitative markers: *Oryza sativa* (Roy et al. 2014; Tuhina-Khatun et al. 2015), *Triticum durum* (Wolde et al. 2016), *Cucumis sativus* (Ene et al. 2016) and *Jatropha curcas* (Shabanmofrad et al. 2013)

The coefficient of variation compares the relative amount of variability between morphological traits (Sharma 1988). According to Deshmukh et al. (1986), PCV and GCV values are considered high when greater

than 20%. Values between 10% and 20% are considered moderate and values less than 10% are considered low. High GCV indicates the presence of exploitable genetic variability for the traits, which can facilitate selection (Yadav et al. 2009). In this study, 15 out of the 25 quantitative traits showed high PCV and GCV values. The highest GCV were recorded for grain yield (54.38%), pod yield (53.40%), 100 seed weight (51.74%), terminal leaf width (39.43%), number of pods per peduncle (38.43%) and number of pods per plant (35.62%) (Table 5). These results imply that there is a high amount of exploitable genetic variability among the studied cowpea accessions. These traits therefore present greater potential than seed set, time to 50% flowering, time to 50% podding or time to 50% maturity, with low genotypic coefficients of variation of 7.77, 7.62, 7.20 and 5.87%, respectively. The PCV and GCV

Table 8: Eigenvectors and eigenvalues of the first four principle components for 25 quantitative traits of 30 accessions of cowpea (*Vigna unguiculata*)

Variable	eigenvectors			
	PC1	PC2	PC3	PC4
Pet.Length	0.130	-0.014	-0.139	-0.041
50%.F	-0.017	0.445	0.038	-0.013
TL.Length	0.227	-0.177	-0.103	0.025
TL.Width	0.248	0.018	0.143	-0.070
Nb. Node	0.207	-0.148	0.246	0.182
Nb. Branches	0.205	-0.141	0.242	0.186
P.Heigh	0.220	-0.130	-0.136	0.124
P.Width	0.226	-0.228	0.095	0.142
Shoot Weight	0.192	-0.159	0.231	0.077
% Germination	-0.007	-0.122	0.016	0.464
50%.Pod	-0.018	0.442	0.020	-0.011
Ped.Length	0.185	0.091	0.288	-0.083
Pod/peduncle	-0.214	0.134	0.217	-0.044
50%.M	0.083	0.411	-0.076	-0.049
Seed set	-0.177	0.060	-0.017	0.423
Pod yield	0.255	0.162	0.220	-0.024
Grain yield	0.267	0.113	0.219	-0.055
Seed Length	0.265	0.034	-0.147	-0.208
Seed Width	0.265	0.061	-0.207	-0.192
Pod Width	0.251	0.080	-0.217	-0.021
Pod Length	0.264	0.147	-0.136	0.132
Ovule/pod	0.192	0.242	-0.101	0.285
Seed/pod	0.098	0.268	-0.107	0.503
100 SW	0.272	-0.075	-0.157	-0.185
Pod/plant	0.016	0.133	0.582	-0.091
Eigenvalue	10.498	4.526	2.214	1.738
Variability (%)	41.992	18.104	8.855	6.951
Cumulative variance (%)	41.992	60.096	68.950	75.902

PC1: First principle component; PC2: Second principle component; PC3: Third principle component; and PC4: Fourth principle component.

values of the morphological traits observed in this study are consistent with previous results for cowpea (Suganthi and Murugan 2008; Gerrano et al. 2015; Withanage 2005)

Heritability helps to indicate the level of environmental influence on the expression of a phenotypic trait. According to Robinson et al. (1949), heritability values help the breeder to know the possibility and degree to which the improvement of a trait is possible through selection. Heritability values greater than 80% are considered very high, values between 60 and 79% are considered moderately high, values between 40 and

59% are considered medium while values less than 40% are considered low (Singh 2001). Heritability estimates of grain yield in the present study were therefore classed as moderately high, as was reported in a previous study on cowpea (Gerrano et al. 2015). Besides grain yield, quantitative traits, including 100 seed weight, number of seeds per pod, number of pods per plant, number of branches per plant and plant height, presented high heritability values. Similar results were reported on cowpea by Suganthi and Murugan (2008), Srinivas et al. (2016) and Gerrano et al. (2015). High heritability values

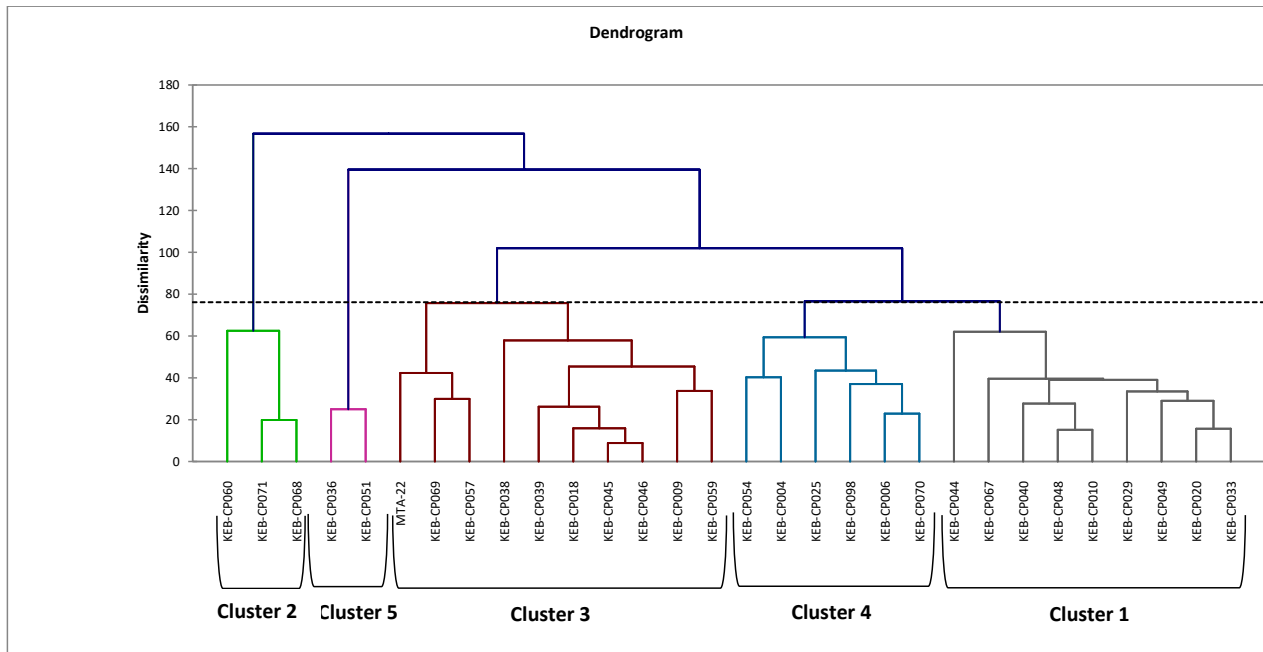


Figure 1: Dendrogram using the UPGMA method based on Euclidian distance, grouping 30 *V. unguiculata* accessions

for a trait indicate a relative small contribution of the environment to the expression of the phenotype, making selection of the trait easier. Genetic Advance is important in predicting the expected genetic gain from one cycle of selection (Hamdi et al. 2003). Genetic Advance as percent of the mean, according to Johnson et al. (1955), is classified as high when exceeding 20%, moderate when between 10 and 20% and is considered as low when below 10%. Genetic Advance was moderate for four traits: seed set, time to 50% flowering, time to 50% podding and time to 50% maturity. However, GA was high for all the other 21 traits. In accessing a more effective selection of a trait, heritability complemented with GA is more useful compared to heritability taken alone (Panse 1957). This study shows that the high heritability estimates recorded for most of the studied traits were associated with high GA. However, time to 50% flowering, time to 50% podding and time to 50% maturity had a high estimation of heritability associated with a lower percentage of GA. This is an indication of the presence of non-additive gene effects for these traits. High heritability coupled with high GA for a given trait is an indication that the trait is directed by additive gene action and selection based on this trait would be more effective and efficient (Eid 2009).

For any crop, it is important to know the correlation between characters, as it is useful in designing a proper and effective plant improvement program. Because yield is a complex trait, direct selection may be difficult. The identification of highly correlated characters appears

appropriate. This study revealed strong correlations between seed length and grain yield, 100 seed weight and grain yield, between 100 seed weight and seed length, between number of seeds per pod and pod length, between number of branches per plant and plant biomass and between grain yield and leaf width. Some of these characters, like seed length or 100 seed weight, can therefore be considered in early selection when improving yield. These are important traits that can be enhanced in the cowpea improvement program. Similar positive correlations between these traits were found when analyzing cowpea accessions from South Africa (Gerrano et al. 2015). In the present study, using 25 quantitative traits, the 30 analyzed genotypes were ranged in five distinct clusters using dissimilarity coefficients. This high number of clusters indicates a high level of diversity in the studied genotypes, which was confirmed by principal component analysis. The first four principal components explained 75.90 % of the total variation. Likewise, Gerrano et al. (2015) classified 25 genotypes of cowpea in four distinct clusters using 16 quantitative traits with the first four principal components explaining 72.69% of the total variation.

5 Conclusion

Phenotypic evaluation of plant genetic resource is important for the identification of potential parents and traits of interest to be used in crop improvement programs.

This study, using 25 quantitative traits, revealed important genetic variability among 30 cowpea genotypes from Western Cameroon. This important genetic variability was confirmed by cluster and principal component analysis. Many significant character associations were found. Grain yield correlated significantly with many other quantitative traits. Genotypes with desired characteristics should be properly conserved as raw materials for genetic improvement programs. KEB-CP036 and KEB-CP031 were identified as genotypes with important fresh biomass production. These two genotypes could be used as parents when undertaking genetic improvement for fodder production. As well, KEB-CP054 and KEB-CP004 were identified as genotypes associated with high grain yield and should be considered when breeding for yield.

Conflict of interest: Authors state no conflict of interest.

Authors' contributions: Eric Bertrand Kouam and Toscani Ngompe-Deffo collected the plant material. Toscani Ngompe-Deffo performed the experimental trial. Eric Bertrand Kouam conceived the study, analyzed data, interpreted results and wrote the paper. Remy Stéphane Pasquet, Mariette Anoumaa reviewed the manuscript and contributed to the interpretation and presentation of results. All authors read and approved the final manuscript.

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