

Assessment of Genetic Diversity of Cowpea Accessions Based on Agro-morphological Traits for Selection in Breeding Programs

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Abstract: The lack of morphological characterization of cowpea varieties significantly hinders the effective utilization of the genetic diversity present within this crop for its development and viable agricultural productivity. This also impedes the development of superior cowpea varieties that are resistant to climatic problems and environmental stresses which have led to a great task for plant breeders and farmers. As a result of this, the current research was conducted to assess the diversity present in eight cowpea accessions using morphological characters so as to select the best accession for further breeding work. The research was conducted at the botanical garden of the department Plant Science and Biotechnology, Federal University Oye-Ekiti. Two seeds of each accession were planted in a 3m plot of inter-row spacing of 1m and intra-row spacing of 50cm and replicated thrice in a randomized complete block design (RCBD). Data was collected on ten morphological characters at maturity and analyzed using ANOVA, principal component analysis (PCA), and cluster analysis. The first three principal component axes accounted for 88.66% of total variation as shown by PCA, with days to flowering, plant height, and yield-related traits having the highest contribution to diversity. Cluster analysis clustered the accessions into four clusters, isolating accessions 14k-2132-1 and 10k-843-3 as morphologically distinct, suggesting that they possess distinctive morphological traits that varied significantly from others, making it selection material for further breeding programs. The findings highlight the significance of morphological traits in assessing genetic diversity, guiding selection for developing cowpea varieties with high yield, disease-resistant, and stress-tolerant.

Keywords: Cowpea accessions, morphological traits, genetic diversity, cluster analysis and principal component analysis

Received for publication on September 03, 2025

1. Introduction

Cowpea (*Vigna unguiculata* (L.) Walp) is an important crop which acts as a good source of protein, vitamins, fodder for animals and source of income for farmers (Kamara, and Ajeigbe, 2009). It is an autogamous dicotyledonous crop plant with narrow genetic base present in the Fabaceae family (Aboki and Yuguda, 2013). It is an herbaceous crop which grows and matures within one growing season, it is grown for its edible seeds or forage. They are generally cultivated for grain while a small fraction is grown as green leafy vegetables and silage in Africa or as fresh pods in eastern Asia (Boukar *et al.*, 2015). It is an essential nutrient and is the main source of protein for millions of people in sub-Saharan Africa.

The knowledge of diverse and related genotypes of cowpea is highly significant in the production and breeding of the crop. This helps in the selection process for hybridization program in the development of improved cowpea (Mafakheri *et al.*, 2017), remove repetitions of genotypes and select cowpea crops with good quality and high yielding for cultivation and preservation in gene banks (Mafakheri *et al.*, 2017). The study helps plant breeders to evaluate the extent and degree of genetic variability that exist within and between crop varieties, identifying how related and divergent germplasms of crops are so as to allow them to select divergent parental combinations which will be able to generate heterotic hybrid in the first filial generation and transgressive segregants in the segregating population (Singh *et al.*, 2022). Evaluating genetic diversity through phenotyping and genotyping is vital for increasing the efficacy and precision of breeding programs, leading to development of high yield and stress-resilient crops (Kumar *et al.*, 2024). Morphological, biochemical and molecular analyses can be used to assess genetic diversity in cowpea and many other crops (Gbadevi *et al.*, 2021; Bhandari *et al.*, 2017). Germplasm assemblage, assessment and conservation are the initial breeding activities before any other breeding program can be undertaken in Sub-Sahara Africa (Boukar *et al.*, 2018).

Preliminary characterization and selection of germplasm on the field can be achieved by using phenotypic traits to evaluate genetic variability present in the crop (Komolafe *et al.*, 2021). Also, characterization using morphological data is important for estimating and correlating degrees of diversity which exist among populations of crops (Komolafe *et al.*, 2021).

Genetic diversity studies using phenotypic traits and agro-morphological data entail detailed examination and documentation of the germination, vegetative, reproductive stages and morphological traits of the plants (Komolafe *et al.*, 2021). This helps in grouping diverse cowpea genotypes into different sub-groups based on their similarities or differences, which can be used for choosing varieties with desirable traits such as improved quality, stress tolerance and high yield potential. The effective estimation of phenotypic traits provides significant knowledge of the genetic variability of cowpea, which are essential for selection and the production of desirable varieties.

Absence of extensive characterization of cowpea using morphological markers deters the effective application of the genetic variability that exists among this crop for its improvement. The lack of morphological characterization of cowpea varieties significantly hinders the effective utilization of the genetic diversity present within this crop for its development and viable agricultural productivity (Rajesh *et al.*, 2022). This also impedes the development of superior cowpea varieties that are resistant to climatic problems and environmental stresses which have led to a great task for plant breeders and farmers. As a result of this, the current research was conducted to assess the

diversity present in eight cowpea accessions using morphological characters so as to select the best accession for further breeding work.

2. Materials and Methods

The seeds employed in this study were acquired from the International Institute of Tropical Agriculture (IITA) located in Ibadan, Oyo State, Nigeria. The study was conducted at the botanical garden of the Department of Plant Science and Biotechnology, Federal University Oye-Ekiti, Ekiti State, Nigeria. Two seeds of each accession were planted in a 3m plot of inter-row spacing of 1m and intra-row spacing of 50cm and replicated thrice in a randomized complete block design (RCBD). Weeding and other agronomic practices were carried out throughout the period of growth of the plants till maturity. Data were collected on ten morphological characters at maturity and analyzed.

2.1 Data analysis

Data collected including growth parameters, flowering, fruiting and yield data were subjected to analysis of variance (ANOVA) and PCA techniques using Library (CAR), (FactoMineR), (Factoextra), and (GGplot2) tools were employed to assess significant variability within and between cowpea accessions for various agronomic traits. Mean separation tests, such as Tukey's Honestly Significant Difference (HSD) and Clustering analysis using Library (hclust) at a significance level were applied to identify superior-performing accessions.

3. Results (or Results and Discussion)

3.1 Analysis of variance (ANOVA) for morphological traits of cowpea accessions

The analysis of variance (ANOVA) for morphological traits of cowpea accessions in Table 1 demonstrated significant genetic variability among the accessions for most traits. For the trait number of days to germination (NDG), accessions exhibited highly significant differences ($p < 0.001$) with a mean square of 54.36, indicating considerable genetic variability among the cowpea accessions for this trait. There was no significant difference among the accessions for all the traits studied except for pod length for replication and error mean squares. This shows that the variation displayed among these accessions for these traits was as a result of genetic factors rather than the effect of the environment.

There were also highly significant differences among the accessions for Days to flowering (DFT) at ($p < 0.001$) with a mean square of 50.61. Plant height at flowering (PHF) and maximum plant height (MPH) also exhibited highly significant differences ($p < 0.001$) among accessions with mean squares of 34.12 and 108.63 respectively. The replication means squares for PHF and MPH together with their error mean squares were non-significant, which further shows that the variability among the accessions was due to genetic influence on this trait. For node depth from the main stem (NDFM), the differences among accessions were non-significant with a mean square of 142.41, indicating that this trait was more influenced by environmental conditions than by genetic factors. The replication mean square for NDFM was 29.51, suggesting some environmental variation, while the error mean square was 25.52, emphasizing the environmental impact on this trait.

Table 1: Mean square for morphological traits of cowpea accessions

SOV	Df	NDG	DTF	PHF	NDFM	NBR	PL	LA	NSPP	NPPP	MPH
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Accessions	7	54.36** *	50.61** *	34.12** *	142.41 ns	68.34* *	89.65* *	30.58* *	29.52**	88.54* *	108.63** *
Replication	2	0.86ns	0.88ns	2.01ns	29.51	0.10ns	5.84*	1.90ns	2.45ns	0.05ns	14.58
Error	14	1.81	0.99	1.62	25.52	1.07	1.05	1.48	0.60	0.60	4.36

SOV= Source of variation, Df= degree of freedom, ns= non-significant, *** $p < 0.001$; ** $p < 0.01$; * $p < 0.05$, PHF=Plant height at flowering, NDG= Number of days to germination; DTF= days to flowering, NDFM= node depth from the main stem, LA= leaf area, NPPP= Number of pod/plants, NSPP= Number of seed/pods; PL=pod length; NBR= number of branches, MPH=maximum plant height

Other traits such as number of branches (NBR), pod length (PL), leaf area per plant (LA), number of seeds per pod (NSPP), number of pods per plant (NPPP), and maximum plant height (MPH) exhibited highly significant differences among accessions at $p < 0.01$ for NBr, PL, LA, NSPP, NPPP and MPH with mean squares of 68.34, 89.65, 30.58, 29.52, 88.54, and 108.63, respectively. This shows that there is great variability among the accessions for these traits under study.

3.2 Mean separation

The result of the morphological characterization of eight cowpea accessions is presented in Table 2. The result showed significant variances in the number of days to germination (NDG) among the accessions. Accession 14k-2132-1 germinated earlier with an average of 4.6 ± 0.29 days, followed by 16-234-3 and 14k-1903-1, which both had relatively low germination times of 5.3 ± 0.35 and 5.3 ± 0.15 days, respectively, while accession 14k-1814-1 had longest germination period of 8.2 ± 0.35 days on average. Accession 15k-2244-3, 16-2573-6 and 14k-1903-1 flowered earlier at 41.3 ± 0.35 , 42.2 ± 0.14^c and 42.6 ± 0.31^c days respectively and these values are not significantly different from one another at $p \leq 0.05$. But it took longest time of 47.0 ± 1.24^a days for accession 14k-2132-1 to flower.

Plant heights also vary considerably among the accessions. 14k-2132-1 had the highest height of 18.6 ± 0.12^a , followed by 10k-843-3 and 16-234-3 with heights of 17.5 ± 0.15^b and 17.0 ± 0.69^b respectively, accessions 14k-1903-1 and 15k-2244-3 had moderate average heights of 15.3 ± 0.34^c and 14.5 ± 0.41^c respectively while accession 16-2573-6 had the shortest average height of 9.6 ± 0.14^c .

Accessions 16-2573-6 and 16k-1984-3 had the highest number of branches per plant with average of 77.7 ± 0.35 and 76.3 ± 0.35 respectively, while 10k-843-3 had the fewest branches with an average of 57.7 ± 0.35 . Pod length (PL), leaf area (LA), number of seeds per pod (NSPP), number of pods per plant (NPPP), and maximum plant height (MPH) also showed significant differences among the accessions. For instance, 14k-1903-1 had the longest pods with an average of 21.5 ± 0.32 cm and the largest leaf area of 14.3 ± 0.11 cm, while 14k-2132-1 had the highest number of seeds per pod (20.9 ± 0.55) with highest number of pods per plant (42.3 ± 0.02) and also the tallest accession with an average heights of 92.3 ± 0.45 cm.

Table 2: Mean separation of eight accessions of cowpea for ten characters

Values are presented in the mean. Values with the same superscript across the column are not significantly

Accession	NDG	DTF	PH	NDFM	NBR	PL	LA	NSPP	NPPP	MPH
16-2573-6	5.6±0.35 ^c	42.2±0.14 ^c	9.6±0.14 ^e	60.7±0.14 ^a	77.7±0.35 ^a	17.73±0.23 ^b	10.3±0.44 ^b	12.2±0.35	25.2±0.35 ^d _e	60.2±0.44 ^c _d
16k-1984-3	6.6±0.21 ^b	43.6±0.28 ^b _c	12.2±0.32 ^d	58.7±0.36 ^a	76.3±0.35 ^a	15.8±0.12 ^{bc}	7.7±0.34 ^c	15.3±0.78 ^c	32.3±0.45 ^c	72.3±0.08 ^b _c
14k-1814-1	8.2±0.35 ^a	43.3±0.45 ^b _c	10.1±0.78 ^d _e	63.3±0.39 ^a	68.3±0.35 ^b	20.43±0.36 ^a	12.3±0.35 ^a _b	11.3±0.18 ^d	20.7±0.11 ^e	52.3±0.35 ^d
10k-843-3	6.3±0.31 ^b	44.6±1.54 ^b	17.5±0.15 ^b	62.7±0.32 ^a	57.7±0.35 ^c	13.2±0.64 ^d	5.7±0.30 ^d	14.6±0.75 ^c _d	27.7±0.03 ^d	65.3±0.63 ^c
16-234-3	5.3±0.35 ^c	44.2±0.37 ^b	17.0±0.69 ^b	65.3±0.35 ^a	70.3±0.34 ^a _b	18.87±0.71 ^a _b	10.6±0.38 ^b	18.6±0.65 ^b	37.7±0.35 ^b	82.3±0.34 ^b
15k-2244-3	7.0±0.34 ^a _b	41.3±0.35 ^c	14.5±0.41 ^c	58.7±0.44	67.6±0.31 ^b	16.23±0.03 ^b _c	8.6±0.35 ^c	13.9±0.25 ^c _d	23.3±0.44 ^d _e	57.7±0.32 ^d
14k-1903-1	5.3±0.15 ^c	42.6±0.31 ^c	15.3±0.34 ^c	61.3±0.46 ^a	63.7±0.33 ^b	21.5±0.32 ^a	14.3±0.11 ^a	16.4±0.15 ^b _c	32.3±0.78 ^c	70.3±0.31 ^b _c
14k-2132-1	4.6±0.29 ^d	47.0±1.24 ^a	18.6±0.12 ^a	64.7±0.35 ^a	73.3±0.02 ^a _b	14.07±0.37 ^d	6.3±0.14 ^d	20.9±0.55 ^a	42.3±0.02 ^a	92.3±0.45 ^a

different at p≤0.05 DMRT

Table 3: Principal component analysis

Traits	Component 1	Component 2	Component 3
NDG	-0.790	-0.357	0.137
DTF	0.872	-0.141	0.043
PH	0.8195	-0.176	0.454
NDFM	0.5921	0.268	0.393
NBr	0.025	0.240	-0.942
PL	-0.457	0.865	0.177

LA	-0.489	0.836	0.211
NSP	0.948	0.224	-0.317
NPPP	0.941	0.251	-0.146
MPH	0.946	0.183	-0.163
Eigenvalue	5.57	1.90	1.39
Variance percentage	55.67	19.03	13.95
Cumulative variance	55.67	674.70	88.66

Bolded: traits with significant contribution to the total variation

3.3 Principal Component Analysis of cowpea accession

The percentage cumulative variance and the eigenvalues of the first three principal component (PC) axes of ten agronomic characters are presented in table 3. The first three PC axes had eigenvalues of 5.57, 1.90 and 1.39 respectively, which jointly accounted for 88.66% of the total variation among the eight accessions of cowpea. The first principal component axes (PCA1) which accounted for largest proportion of variation (55.67%) was mostly loaded by days to flowering (DTF), plant height (PH), number of seeds per pod (NSP), number of pods per plant (NPPP), and maximum plant height (MPH). These traits made a significant contribution to component 1. But number of days of germination exhibited very high negative loading (-0.790) to component 1. These traits significantly contributed to Component 1, suggesting that they were strongly correlated and played a major role in distinguishing between the cowpea accessions. Conversely, the number of days to germination (NDG) had a high negative loading, indicating an inverse relationship with the other traits in this component.

The second principal component axes (PCA 2) were positively and mostly loaded by pod length (PL) and leaf area (LA), while number of days to germination, days to flowering and plant height exhibited minimum negative loading to the component. Component 2, explaining 19.03% of the variance, was predominantly influenced by pod length (PL) and leaf area (LA), both showing strong positive loadings. This component highlighted the traits related to the physical size and development of the plant parts. The traits NDG, DTF, and PH had negative loadings on this component, indicating they were less influential here compared to Component 1. The positive loadings of PL and LA in Component 2 suggested that accessions with larger pods and greater leaf area were distinct along this dimension.

The third principal component axis (PCA 3) which accounted for 13.95% of the variance was mostly loaded by plant height at flowering and node depth from the main stem (NDFM). It was highly

negatively loaded by number of branches (NBr), which makes it different from the other components. The highest eigenvalue (5.57) occurred at the first principal component axis, which shows that this axis plays a principal role in showing the variability among the accessions, followed by component 2 (1.90) and component 3 (1.39). This indicated that accessions with fewer branches significantly contributed to this component. Plant height (PH) and node depth from the main stem (NDFM) had moderate positive loadings, suggesting a secondary influence. The combination of these traits in Component 3 provided a nuanced view of the structural attributes of the accessions, particularly highlighting variations in branching patterns.

3.4 Principal component analysis biplot

The relationship among the ten morphological characters of cowpea accessions is shown by the principal component analysis (PCA) biplot in Figure 1. The first two dimensions (Dim1 and Dim2) had biplot values of 55.7% and 19% respectively and jointly accounted for 74.7% of the total variation. The longer arrows showed the effect of the traits on the individual dimensions and the relationship between the traits is represented by angle between the arrows. Traits such as days to flowering (DTF), plant height (PH), number of seeds per pod (NSP), number of pods per plant (NPPP), and maximum plant height (MPH) were grouped together with long arrows in a positive direction in dimension 1. This indicated the strong correlation between these traits that these traits were highly correlated with each other and highly imparted dimension 1 and the traits with higher values were related with the accessions placed along the positive side of this dimension.

The number of days to germination (NDG) showed by its long arrow facing the opposite direction indicated a strong negative correlation with other traits in Dimension 1. This indicated that accessions which germinated earlier inclined to have greater values for days to flowering, plant height at flowering, number of seeds per pod, number of pods per plant and maximum plant height. The opposite direction of NDG to the other traits suggested that it was a key differentiator among the accessions, contrasting the other major traits in Dimension 1. The prominent arrows facing upward in dimension 2 showed a positive influence of pod length and leaf area on this dimension. This specified that accessions which have longer pod lengths and larger leaf area were distinct in Dim2. This shows their unique contributing role in differentiating accessions as a result structural size and vegetative characteristics. The distinctive pattern of the arrow shown by the number of branches nearly perpendicular to most other traits showed that it was less related with them. Number of branches helped in differentiating between accessions in this dimension, mostly those accessions which have higher branching patterns.

The arrangements of eight accessions of cowpea along the first two principal component axes are illustrated in Figures 2. The distribution of accessions on axes 1 and 2, which accounted for 55.68% and 19.03% of the variance respectively showed that accession 14k-2132-1 which was positioned far to the right along Dim 1, is the most distant accession showing its strong correlation

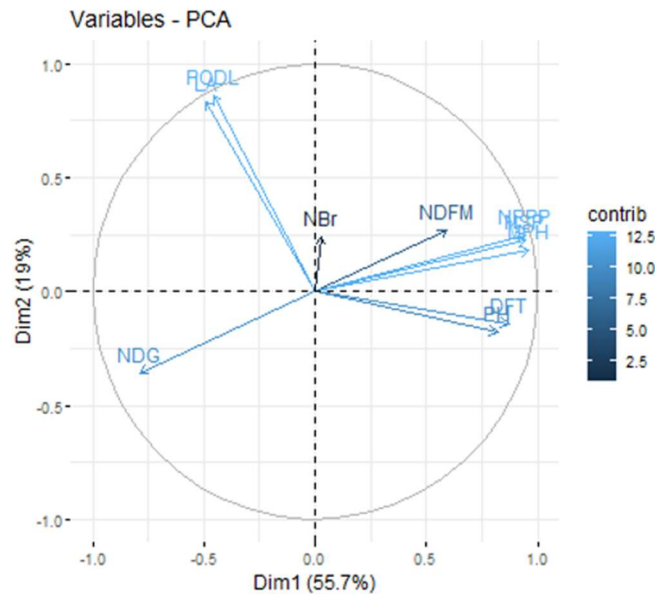


Figure 1: Principal component analysis among the morphological traits in eight accessions of cowpea

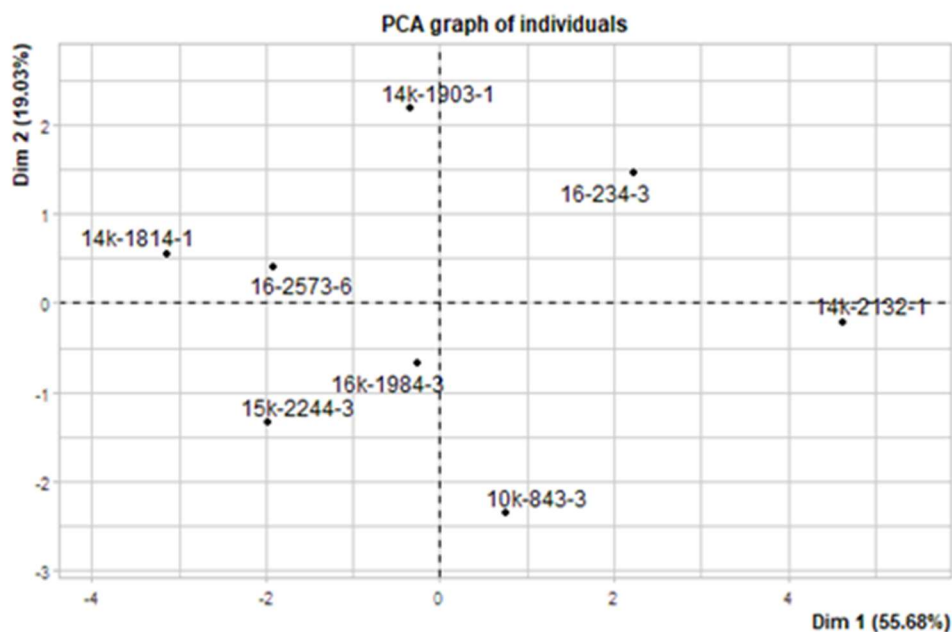


Figure 2: Individual PCA graphs

with days to flowering, plant height at flowering, number of seeds per pod, number of pods per plant, and maximum plant height, that are heavily loaded in dimension 1. This accession was different in these traits compared to the others. At the upper part toward the north side of the plot was located accession 14k-1903-1 showing it as correlating positively with dimension 2. This implied that the pod length and leaf area of this accession are larger, pod length and leaf area being the traits that loaded significantly on Dim2. In the lower quadrant accessions were found 15k-2244-3 and 10k-843-3, showing that they are negatively correlated with dimensions 1 and 2. This suggested that these accessions had traits differing from those which have high positive loadings on these dimensions. This means that accessions 15k-2244-3 and 10k-843-3 had shorter days to flowering, shorter plant height, fewer seeds per pod, and smaller pod length and leaf area. The manner in which they are

distinctly positioned to others highlights their variance from the accessions found in the positive regions of the dimensions.

Grouped around the middle of the plot are accessions 16-2573-6 and 16k-1984-3, signifying them as possessing average values for many traits. The way they are located centrally showed that all the traits measured are balanced with no extremity in any direction. This indicated adequate performance of the accessions across different environments.

Finally, the location of accession 16-234-3 at the upper right side of the biplot suggested that it has a solid positive relationship with Dim1 traits together with moderate positive association with Dim2 traits. This means that its flowering, plant height, and maximum plant height are high while its pod length and leaf area have moderate values. This makes it potential accession with high performance in terms of growth and yield related traits.

3.5 Clustering analysis of cowpea accessions

The genetic relationship among the eight accessions of cowpea, based on ten morphological traits, is presented in Figure 3. The height of the branches indicates the level of similarity between the clusters. If the branch height is high, it means it has greater dissimilarity between the clusters, but a lower height indicates higher similarity within the cluster. At 0.0 level of similarity, all the accessions were distinct from one another while at 1.5 level of similarity, all the accessions were grouped into four clusters, with cluster 1 comprising of four accessions, namely 14k-1814-1, 15k-2244-3, 16-2573-6 and 16k-1984-3 and cluster 2 also had a one accession 14k-2132-1, cluster three also had 10k-843-3 as the only accessions, while cluster four contain two accessions, 14k-1903-1 and 16-234-3. The accessions which clustered together in cluster 1 suggested them have related morphological traits. This shows that there is high level of similarities among these four accessions, which makes them have similar characteristics in terms of vegetative, growth performance and yield. Cluster 2 with 14k-2132-1 as the only accession distinguished itself distinctly from the rest. This suggested that accession 14k-2132-1 possess distinctive morphological traits that varied significantly from others. Cluster 3 was also a one cluster in the sense that it had 10k-843-3 as the only accession which also makes it distinct from others too but its slight proximity to the last two accessions; 14k-1903-1 and 16-234-3 reflected its connection with them. Accessions 14k-1903-1 and 16-234-3 are found in cluster 4, their clustering together shows how similarly related they are. This indicated similar morphological traits between these two accessions, which makes them more identical in comparison with others.

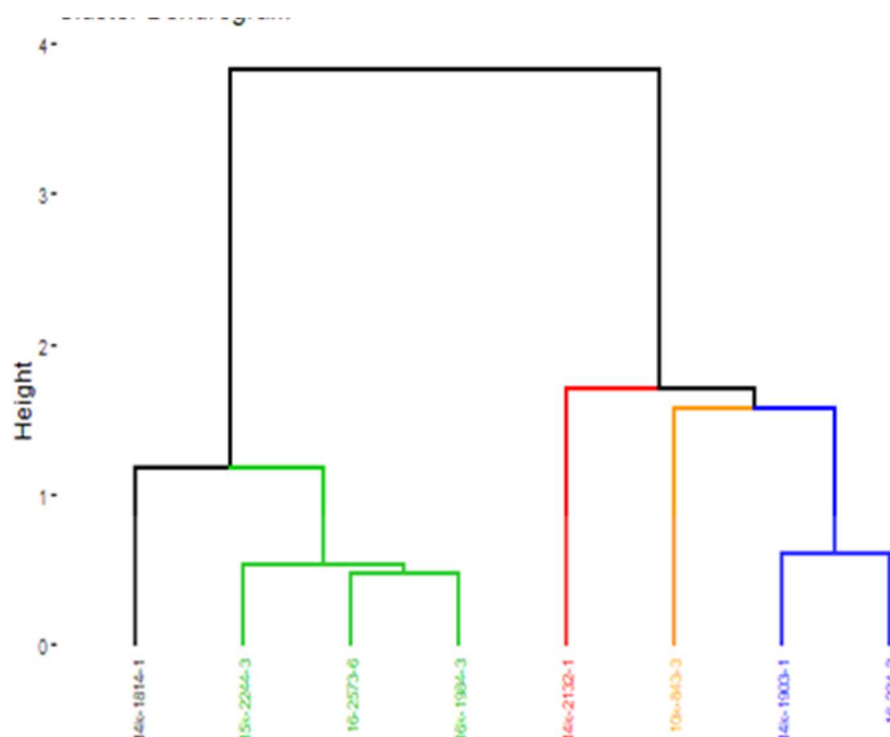


Figure 3: Cluster dendrogram of eight accessions

4. Discussion

Analysis carried out based on morphological traits showed highly significant differences for most of the traits which indicated presence of great variability in all the accessions studied. This may be as a result of the differences in the genetic component of the various accessions as reported by Komolafe *et al.* (2021); Priyanka *et al.* (2018). Substantial genetic variation exists in most traits except for node depth (NDFM) as revealed by analysis of variance (ANOVA). Node depth (NDFM) as a trait is non-significant which shows that it is predominantly influenced by environmental factors. Traits such as maximum plant height, pod length, number of pods per plant, and number of seeds per pod were highly significant, which suggests high heritability and shows that these traits are highly heritable. This significant variability in traits highlights the possibility of choosing accessions with higher plant heights, pods per plant, and number of seeds per pod to increase biomass and probably improve yield through wide vegetative growth, reproductive and fruiting process. The greater proportion (88.66%) of the total variation accounted for by the first three principal component axes shows the efficiency of the selected traits in distinguishing among accessions. This is in line with the findings of Ahiakpa *et al.* (2013) and Doku, (2011) who also obtained high percentage of 82.97% and 91.87% respectively of the total variability, but in disparity with the reports of Komolafe *et al.* (2021) and Torres-Moran *et al.*, (2011) who reported 76.30% and 75.77% respectively of the total variation.

The eight accessions were grouped into four clusters based on their morphological traits by clustering analysis. Clusters 1 and 4 have four and two accessions respectively which were morphologically related, while clusters 2 and 3 have one accession each which are unique and distinct from each other and the rest. The accessions in cluster 1 are divergent from accessions in cluster 2, 3 and 4. The accessions in different clusters may possess high potential for breeding which is pivotal to selection purposes and these accessions from different clusters may be used as parents in

hybridization program to produce heterotic hybrid. This corroborates the findings of Ahiakpa *et al.* (2013) and Doku (2011) who stated that accessions in single clusters which are different from others may serve as prospective parents for breeding programme. This is in line with the report of Boukar *et al.* (2015) who found that cluster analysis based on agro-morphological traits helps identify accessions for targeted crosses.

Cluster analysis showed divergent clusters that reveal resemblances and variances in morphological traits which are essential for plant breeding and crop improvement. Accession 14k-2132-1 found in cluster 2 is different from others due to its distinctive morphological traits such as most tall, pods per plant, highest seeds per pod, this makes it a potential material to select for further breeding work which will produce heterotic hybrid with high yield, stress tolerant and nutritional quality. Accession 10k-843-3 in cluster 3 is also distinct and unique in the sense that it has some correlation with accessions in cluster 4. This could make crossing between accessions in these two clusters, a process referred to as hybridization which is a great prospect for improving genetic diversity in cowpea breeding. The similar morphological traits and genetic interactions between the accessions in cluster 4 (14k-1903-1 and 16-234-3) suggested that these could be used as parent in hybridization program to develop improved varieties.

5. Conclusions

The study concludes that there is significant genetic variability in many of the traits in the genetic diversity studies of eight accessions of cowpea, which indicates high breeding potential through selection. There is highly significant difference for traits such as plant height at flowering, pod length, number of pods per plant, and number of seeds per pod, which shows that these traits are not controlled by the environment but by genetic factors, which forms the basis for their selection. Principal component analysis (PCA) successfully clustered the traits as a result of their influence on the total variability. The first three PC axes jointly accounted for 88.66% of the total variation among the eight accessions of cowpea. The traits such as plant height at flowering, pod length, number of pods per plant, and number of seeds per pod significantly contributed to principal component axes 1, showing them as strongly correlated and played important role in differentiating between the accessions of cowpea. Number of days to germination was highly negatively loaded in this component, which indicated inverse correlation with other traits in the component. Cluster analysis grouped the accessions into four clusters, showing the distinct and related accessions. Accession 14k-2132-1 distinguished itself distinctly from the rest because it possesses distinctive morphological traits that varied significantly from others. 14k-2132-1 as the only accession distinguished itself distinctly from the rest. This suggested that accession 14k-2132-1 possess distinctive morphological traits that varied significantly from others, making it selection material for further breeding programs. The findings highlight the significance of morphological traits in assessing genetic diversity, guiding selection for developing cowpea varieties with high yield, disease-resistant, and stress-tolerant.

Authors' Contributions

All authors contributed to the study conception, Ronke Justina Komolafe designed the research, wrote and reviewed the manuscript, Iyanu Oluwatobi Opatola collected and analysed the data, Oyinade Aderoju David, Modupe Doris Ajiboye reviewed the manuscript.

Funding

No funding was received before, during and after the research.

Acknowledgments

The authors acknowledged the support of International Institute of Tropical Agriculture (IITA) located in Ibadan, for providing the cowpea accessions used for this research.

Conflict of Interest:

The authors declare no conflict of interest.

Data availability statement: The data that associated, and/or supporting findings in the current study are available from the corresponding author upon reasonable request.

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