

## EVALUATION OF AGRO-MORPHOLOGICAL DIVERSITY IN SOME SEGREGATING LINES OF COWPEA (*VIGNA UNGUICULATA* L. WALP)

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### ABSTRACT

A study was conducted to evaluate agro-morphological characteristics of some segregating lines of eight accessions of cowpea (*Vigna unguiculata* L. Walp.) using seeds from a first cycle generation progenies. Eight cowpea accessions [GH3684<sub>1</sub> (red), GH3684B<sub>4</sub> (mottle brown), GH3684B<sub>5</sub> (mottle brown), GH3684A<sub>2</sub> (red), GH3684C<sub>2</sub> (red), GHUCO1<sub>BL</sub> (black), GH3684<sub>BL</sub> (black) and GH7184<sub>BL</sub> (black with spots)] and an out group IT97K-499-35 (white) were cultivated under field conditions. Twenty three agro-morphological traits were assessed for thirty three lines of cowpea. A dendrogram generated using 23 agro-morphological characters distinguished the cowpea accessions into two lineages, with the out-group being the most diverse. Generally, morphological polymorphism revealed discriminations among the cowpea accessions studied. Seed weight, plant height, number of branches, length of branches, number of leaves, number of peduncles, length of peduncles and number of seeds per pod as well as number of pods per plant differed significantly ( $p \leq 0.05$ ) among the cowpea accessions. The evidence showed that there were variations in morphological characteristics expressed by the cowpea accessions and these were segregations in one trait or the other. The cowpea accession GHUCO1<sub>BL</sub> is possibly a cross between IT97K-499-35 x SARC-LO2. The segregation lines of GH3684 had the greatest diversity probably due to genotype environment interactions.

### INTRODUCTION

Provision of food security is a challenge, especially in many developing countries like Ghana. Cowpea production may be one of the most promising solutions that can be exploited to meet this challenge, because the value of cowpea lies in its high protein content (23-29%) and drought tolerance. It has the ability to fix atmospheric nitrogen, which allows it to survive on poor soils (Steele, 1972). In Africa, it is estimated that over 200 million people consume

cowpea daily (Obembe, 2009). Worldwide, cowpea is cultivated, over 10.5 million hectares, with a total production of 3.9 million tons (Obembe, 2009). Despite the benefits of cowpea as a food legume in farming systems and its importance to curb food crisis, abiotic and biotic factors remain the major constraints to cowpea production and storage.

Cowpea production in Ghana is constrained by low and variable grain yields, grain quality and susceptibility to diseases and pests. Genetic

improvements are limited by the lack of knowledge of genetic diversity of the indigenous and cultivated germplasm (Moalafi *et al.*, 2010). The varietal requirements of cowpea in terms of plant type, maturity date, seed type (colour preference), and use pattern are extremely diverse from region to region, thus making cowpea breeding programmes more complex as compared to other crops (Tian and Xu, 1993). Since no single variety is suitable for all conditions, there is a need to develop varieties with multiple traits, to suit the specific needs of different environments and cropping systems.

Study of segregating traits in cowpea progenies derived by hybridization of domesticated types may provide improved cultivars that would be of importance to breeding programmes. Genetic diversity in the available gene pool is the foundation of all crop improvement programmes. Diversity is essential to offset crop vulnerability due to abiotic and biotic stresses, ensure long-term selection gain in genetic improvement and promote rational use of genetic resources (Barrett *et al.*, 1998). Assessment of genetic diversity in cowpea genotypes would facilitate development of cultivars for specific production constraints by providing an index of parental lines to be used in breeding programmes. Identification of parental lines to exploit heterosis and to introduce valuable characters into the cowpea breeding programmes will require more reliable information about the existing level of diversity among breeding lines.

The crucial issue in cowpea breeding is to explore agro-morphological characters of the crop to identify breeding lines and select desirable traits for improvement of the crop geared towards release of new varieties. The objective of this study was to evaluate agro-morphological characters of some segregating lines of cowpea and to predict their genetic relatedness that could be used to improve cowpea.

#### MATERIALS AND METHODS

The study was carried out at the Teaching and Research Farm of the School of Agriculture in

the University of Cape Coast, located at 5° 6' 0" N latitude and 1° 15' 0" W longitude. The cowpea that were used in this study comprised 33 progenies sampled from eight cowpea accessions; GH3684<sub>1</sub> (red); GH3684A<sub>2</sub> (red); GH3684B<sub>4</sub> (mottle brown); GH 3684B<sub>5</sub> (mottle brown); GH3684C<sub>2</sub> (red); GH3684<sub>BL</sub> (black); GH7184<sub>BL</sub> (black with spots); GHUCO1<sub>BL</sub> (black) and IT97K-499-35 (white) used as an outgroup. These were first cycle generation progenies obtained from a stock of the previous year cultivated germplasm that were selected based on seed coat colour, size and response to *Striga gesnerioides* infection. All the cowpea used in this study, were observed to have no *Striga gesnerioides* attachment when tested for resistance, based on pot culture experiment except GH7184<sub>BL</sub>. The GH3684 germplasm was obtained from the Plant Genetic Resources Research Institute (PGRRI), Bunso, Ghana. The GHUCO1<sub>BL</sub> were black seeds obtained from breeding population descendants from crosses between IT97k-499-35 x SARC-LO2 or IT97k-499-35 x Apagbaala which were white seeded plants obtained through an open field cultivation system. However, the exact lineage of GHUCO1 and GH7184<sub>BL</sub> were not known. IT97k-499-35 is an IITA material known to be resistant to *Striga gesnerioides*, races 1 and 3.

Three seeds were sown with four replicates in RCB design at a spacing of 1 m x 1 m between and within rows during the main crop season (June, 2009). The seedlings were thinned out to one plant per stand. The weeds were controlled manually. Data were collected on 23 agro-morphological characters (Table 1). In all fourteen qualitative and nine quantitative parameters were assessed based on the International Board for Plant Genetic Resources cowpea descriptors (IBPGR, 1983). The quantitative data collected were subjected to analysis of variance (ANOVA) using "MINITAB 15" statistical software. Both the quantitative and qualitative data comprising 23 characters were ranked and subjected to cluster analysis using the "Power Maker V3.25" software for Windows. In the process of hierarchical clustering, the unweighted pair group method of arithmetic

**Table 1: Agro-morphological characters evaluated and the methods used**

Serial No.	Characters	Method of Measurement	Rating scale	Nature of character
1	Growth Habit	Visual estimation	Prostrate= 0, Semi Prostrate=1, Semi Erect= 2, Erect= 3	Qualitative
2	Twinning Tendency	Visual estimation	Non Twinning= 0, Slight= 2, Intermediate= 4, Pronounced= 6	Qualitative
3	Plant hairiness	Feeling with hand	Glabrescent= 1, Short Appressed hairs = 2, Pubescent to hirsute= 3	Qualitative
4	Plant Pigmentation	Visual estimation	Non Pigmented= 0, Slight= 1 Moderately at the Base and Tip= 2, Intermediate= 3, Extensive= 4, Solid= 5	Qualitative
5	Raceme position	Visual estimation	Throughout Canopy= 0, In Upper Canopy= 2, Mostly Above canopy= 4	Qualitative
6	Pod attachment to peduncle	Visual estimation	Pendant= 0, 30° - 90°= 2, Erect= 4	Qualitative
7	Immature pod pigmentation	Visual estimation	None= 0, Pigmented Tip= 1, Pigmented Tip and Suture= 2, Pigmented suture= 3	Qualitative
8	Colour of matured Pods	Visual estimation	Pale Green= 0, Intermediate Green= 3, Dark Green= 6	Qualitative
9	Plant Vigor	Visual estimation	Non Vigorous= 0, Intermediate= 2, Vigorous= 4, Very Vigorous= 6	Qualitative
11	Leaf colour	Visual estimation	Pale Green= 0, Intermediate= 3, Dark Green= 6	Qualitative
12	Flower pigmentation	Visual estimation	Non Pigmented= 0, Wing Pigmented= 1, Pigmented Margin= 2, Wing with Pigmented Margin= 3, completely pigmented= 4	Qualitative
13	Seed coat colour	Visual estimation	Cream= 0, Red= 1, White= 2, Black with spots,= 3, Brown= 4, Mottle brown= 5, Brown and Black= 6, Cream and Black= 7, Brown with spots= 8, Reddish Mottled Brown= 9	Qualitative
14	Eye Colour	Visual estimation	Normal Eye (blend with seed coat colour)= 0, Black Eye= 1, Pinkish Eye= 2, yellowish Eye= 3, Purplish eye= 4	Qualitative
15	Plant Height	Measured (cm)	-	Quantitative
16	Number of main Branches	Counted	-	Quantitative
17	Length of main Branches	Measured (cm)	-	Quantitative
18	Number of leaves	Counted	-	Quantitative
19	Number of peduncles per plant	Counted	-	Quantitative
20	Length of peduncle	Measured (cm)	-	Quantitative
21	Number of pods per plant	Counted	-	Quantitative
22	Number of seeds per pod	Counted	-	Quantitative
23	Seed weight	Measured (g)	-	Quantitative

average (UPGMA) was used. The generated tree was viewed with the software program "MEGA (Molecular Evolutionary Genetic Analysis) version 4.0" for Windows (Tamura *et al.*, 2007).

## RESULTS

### Evaluation of qualitative traits

Table 2 shows the fourteen qualitative characters of the 33 samples of eight cowpea accessions and the outgroup (IT97K-499-35).

### Growth habit

Varied growth habits were observed in the cowpea accessions which included prostrate (5.9%), semi-prostrate (14.7%) semi erect (35.3%) and erect (44.1%). Accession GHUCO1<sub>BL</sub> was observed to exhibit prostrate, semi-prostrate and semi-erect forms of growth habits. The rest of the cowpea accessions exhibited single growth habit. The growth habit of GH3684<sub>1</sub>, GH3684B<sub>4</sub> and GH3684A<sub>2</sub> were semi erect while GH3684C<sub>2</sub>, GH368B<sub>5</sub>, GH3684<sub>BL</sub>, GH7184BL and IT97K-499-35 were erect.

### Twinning tendency

The out-group IT97K-499-35 consisting of 3% of the population exhibited non-twinning tendency. Accessions GH3684<sub>1</sub> and GH3684B<sub>4</sub> were slight. GH3684<sub>BL</sub>, GH3684B<sub>5</sub> and GHUCO1 were intermediate while GH3684C<sub>2</sub> and GH7184<sub>BL</sub> were pronounced. However, GH3684A<sub>2</sub> was observed to exhibit both slight and intermediate twinning tendencies.

### Colour of flowers and pods

Most of the cowpea accessions produced mauve or purple flower colours. Nevertheless, GH3684 C<sub>2</sub>L<sub>4</sub>P<sub>8</sub>, GH7185<sub>BLK</sub> L<sub>4</sub> P<sub>1</sub>, and IT97K-499-35 had white flower. Most of the pods of the cowpea accessions (53 %) at maturity were purplish green in colour including GH3684A<sub>2</sub>, GH3684B<sub>4</sub> and GH3684B<sub>5</sub>. Thirty eight percent of the accessions were pale green including GHUCO1<sub>BL</sub>. Accessions GH7184<sub>BL</sub>, GH3684<sub>BL</sub> and the outgroup IT97K-499-35 had green matured pods (8.8 %). Plants from acces-

sion GH 3684C<sub>2</sub> had both purplish and pale green colour pods and that of GH 3684<sub>BL</sub> exhibited both pale green and green colours.

### Pod pigmentation and other traits

Almost all the accessions of cowpea (83.3%) had immature pods with pigmented tips which were found in the following accessions; GH3484<sub>1</sub>, GH3484C<sub>2</sub>, GH3484A<sub>2</sub>, GH3484B<sub>5</sub> and GH7284<sub>BL</sub>. However, pods of accessions GHUCO1<sub>BL</sub> and GH3484<sub>BL</sub> exhibited both pigmented tip with pigmented tip and suture (14%) whereas the out-group was observed to be non-pigmented (2.7%). Despite variations in most of the qualitative parameters assessed, plant vigor, flower pigmentation and raceme position, with exception of the out-group the rest were observed to have similar hairiness.

### Evaluation of quantitative traits

All quantitative morphological data collected were subjected to analysis of variance (ANOVA) using the MINITAB 15 software for Microsoft windows. Nine quantitative morphological characters measured for samples from eight accessions of cowpea and the out-group are presented in Table 3. There were significant variations ( $p < 0.05$ ) in the quantitative traits among the cowpea accessions for all the parameters that were evaluated. Hundred seed weight, plant height, number of main branches, length of branches, number of leaves, number of peduncles, length of peduncles, number of seeds per pod and number of pods per plant differed significantly ( $p < 0.5$ ) among and within the various cowpea accessions studied (Table 3). The hundred seed weight of all the cowpea accessions ranged from 10.4g to 19.7g. GHUCO1<sub>BL</sub>L<sub>4</sub>P<sub>8</sub> had the highest seed weight (19.7g) and the lowest, 10.4g in GH3684L<sub>1</sub>P<sub>4</sub>. The out-group, IT97K-499-35 produced a seed weight of 17.1g. There were significant differences ( $p < 0.05$ ) in the mean plant height among and within the various cowpea accessions. The plant height ranged from 18.3 cm in accession GH3684A<sub>2</sub>L<sub>1</sub>P<sub>6</sub> to 62.0 cm in GH3684C<sub>2</sub>L<sub>3</sub>P<sub>6</sub>. However the out-group had an average plant height of 27.5 cm. The number of main

**Table 2: Qualitative characters of various cowpea accessions studied**

Accession No.	GH	TT	PH	RP	IMP	CMP	FC	LC	PP	PV	FP	PAP	SCC	EC
GH3684 <sub>1</sub> L <sub>1</sub> P <sub>4</sub>	1	2	2	4	1	0	3	0	2	4	0	1	1	0
GH3684 <sub>1</sub> L <sub>2</sub> P <sub>7</sub>	1	2	2	4	1	0	3	0	2	4	0	1	5	0
GH3684 <sub>1</sub> L <sub>2</sub> P <sub>8</sub>	1	2	2	4	1	0	3	0	2	4	0	1	7	0
GH3684C <sub>2</sub> L <sub>1</sub> P <sub>7</sub>	3	6	2	4	1	0	3	3	2	4	0	1	0	3
GH3684C <sub>2</sub> L <sub>2</sub> P <sub>2</sub>	3	6	2	4	1	0	3	3	2	4	0	1	1	0
GH3684C <sub>2</sub> L <sub>3</sub> P <sub>6</sub>	3	6	2	4	1	3	3	3	3	4	0	3	4	0
GH3684C <sub>2</sub> L <sub>4</sub> P <sub>8</sub>	3	6	2	4	1	0	1	3	2	4	0	1	9	0
GH7184 <sub>BL</sub> L <sub>4</sub> P <sub>1</sub>	3	6	2	4	1	6	1	3	2	4	0	1	3	0
GH3684A <sub>2</sub> L <sub>1</sub> P <sub>6</sub>	2	2	2	4	1	0	3	0	2	4	0	1	4	0
GH3684A <sub>2</sub> L <sub>2</sub> P <sub>1</sub>	2	2	2	4	1	0	3	0	2	4	0	1	8	2
GH3684A <sub>2</sub> L <sub>3</sub> P <sub>4</sub>	2	4	2	4	1	0	3	0	2	4	0	1	4	0
GH3684 <sub>BL</sub> L <sub>1</sub> P <sub>1</sub>	3	4	2	4	1	3	3	3	2	4	0	2	9	0
GH3684 <sub>BL</sub> L <sub>1</sub> P <sub>5</sub>	3	4	2	4	1	3	3	3	2	4	0	2	0	1
GH3684 <sub>BL</sub> L <sub>2</sub> P <sub>1</sub>	3	4	2	4	2	3	3	3	3	4	0	2	3	0
GH3684 <sub>BL</sub> L <sub>2</sub> P <sub>3</sub>	3	4	2	4	2	3	3	3	3	4	0	2	5	0
GH3684 <sub>BL</sub> L <sub>2</sub> P <sub>7</sub>	3	4	2	4	2	3	3	3	3	4	0	2	9	1
GH3684 <sub>BL</sub> L <sub>4</sub> P <sub>6</sub>	2	4	2	4	1	6	3	3	4	4	0	3	0	1
GHUCO1 <sub>BL</sub> L <sub>1</sub> P <sub>3</sub>	2	4	2	4	1	3	3	3	3	4	0	3	0	1
GHUCO1 <sub>BL</sub> L <sub>1</sub> P <sub>6</sub>	2	4	2	4	1	3	3	3	3	4	0	3	4	0
GHUCO1 <sub>BL</sub> L <sub>1</sub> P <sub>8</sub>	2	4	2	4	1	3	3	3	3	4	0	3	2	1
GHUCO1 <sub>BL</sub> L <sub>2</sub> P <sub>2</sub>	1	4	2	4	2	3	3	3	2	4	0	3	8	0
GHUCO1 <sub>BL</sub> L <sub>2</sub> P <sub>5</sub>	1	4	2	4	2	3	3	3	2	4	0	3	0	1
GHUCO1 <sub>BL</sub> L <sub>4</sub> P <sub>1</sub>	0	4	2	4	1	3	3	3	2	4	0	3	4	0
GHUCO1 <sub>BL</sub> L <sub>4</sub> P <sub>8</sub>	0	4	2	4	1	3	3	3	2	4	0	3	8	0
GH3684B <sub>5</sub> L <sub>1</sub> P <sub>2</sub>	3	4	2	4	1	0	3	0	2	4	0	1	4	0
GH3684B <sub>5</sub> L <sub>2</sub> P <sub>2</sub>	3	4	2	4	1	0	3	0	2	4	0	1	4	0
GH3684B <sub>5</sub> L <sub>3</sub> P <sub>2</sub>	3	4	2	4	1	0	3	0	2	4	0	1	1	0
GH3684B <sub>5</sub> L <sub>4</sub> P <sub>8</sub>	3	4	2	4	1	0	3	0	2	4	0	1	1	0
GH3684B <sub>4</sub> L <sub>1</sub> P <sub>1</sub>	2	2	2	4	1	0	3	0	2	4	0	1	5	0
GH3684B <sub>4</sub> L <sub>2</sub> P <sub>5</sub>	2	2	2	4	1	0	3	0	2	4	0	1	5	0
GH3684B <sub>4</sub> L <sub>2</sub> P <sub>7</sub>	2	2	2	4	1	0	3	0	2	4	0	1	4	0
GH3684B <sub>4</sub> L <sub>4</sub> P <sub>1</sub>	2	2	2	4	1	0	3	0	2	4	0	1	4	0
GH3684B <sub>4</sub> L <sub>4</sub> P <sub>3</sub>	2	2	2	4	1	0	3	0	2	4	0	1	4	0
IT97K-499-35	3	0	1	4	1	6	1	6	1	4	0	2	2	1

GH= growth habit, TT= twinning tendency, PH= plant hairiness, RP= raceme position, IPP= immature pod pigmentation, FC= flower colour, LC= leaf colour, PP= plant pigmentation, PV= plant vigor, FP= flower pigmentation, PAP= pod attachment to peduncle, SCC= seed coat colour, EC= eye colour

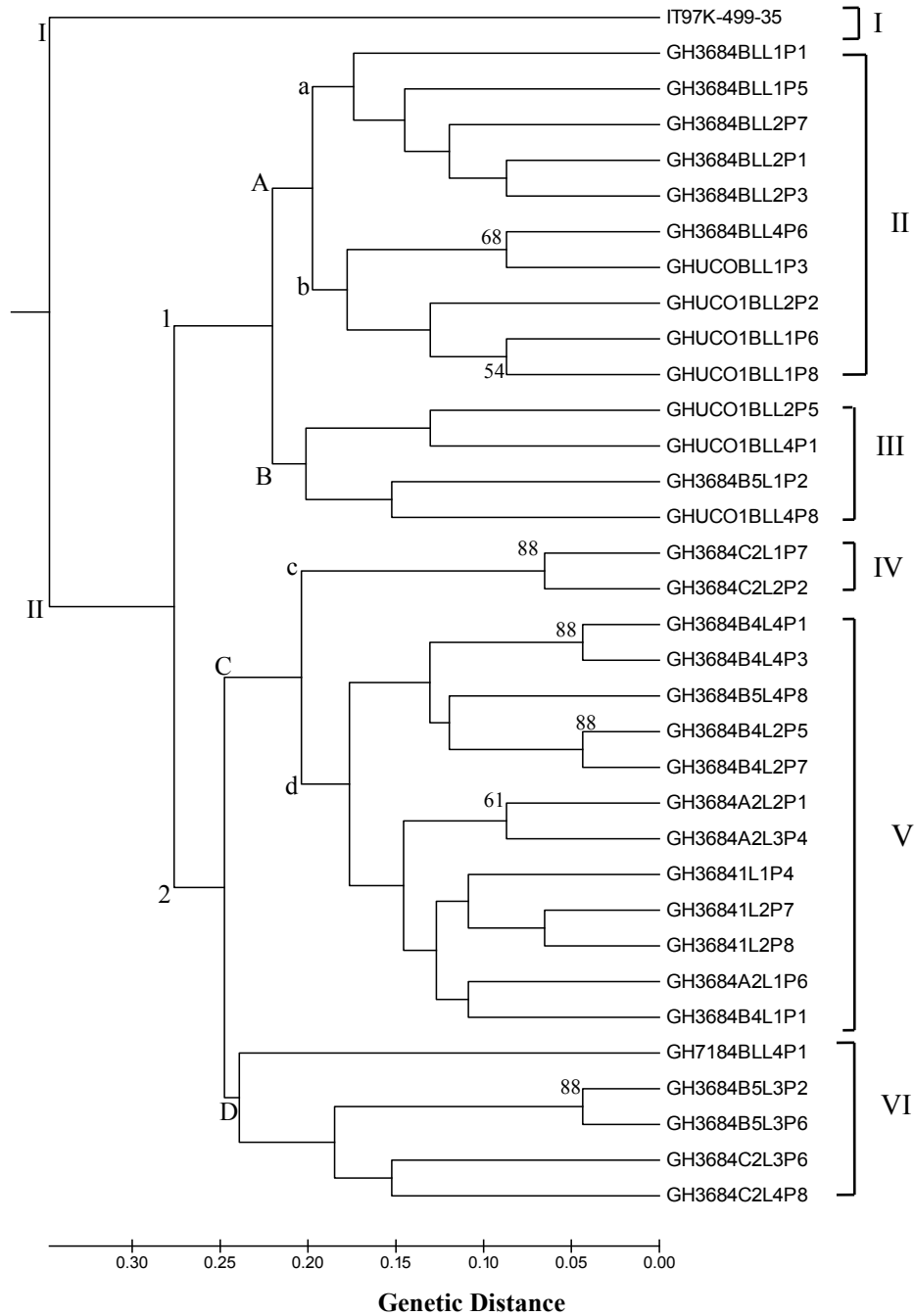
branches ranged from 5 to 9 per plant with the out-group, IT97K-499-35 and accession GH7184<sub>BL</sub> having the least number of branches per plant. (Table 3). The mean number of leaves differed significantly ( $p < 0.05$ ) among the eight cowpea accessions. The mean number of leaves per plant was lowest in accession GHUCO1<sub>BL</sub>L<sub>1</sub>P<sub>6</sub> (47) and highest in accession GHUCO1<sub>BL</sub>L<sub>4</sub>P<sub>8</sub> (298). The out-group IT97K-

499-35 had an average of 54 leaves per plant. The mean peduncle length also differed significantly ( $p < 0.05$ ) among the eight cowpea accessions. The minimum mean peduncle length recorded was 5.0 cm for GH3684A<sub>2</sub>L<sub>2</sub>P<sub>1</sub> and the maximum was 54.0 cm for GHUCO1<sub>BL</sub>L<sub>2</sub>P<sub>5</sub>. The out-group, IT97K-499-35 recorded mean peduncle length of 32.2 cm.

**Table 3: Mean scores of nine quantitative traits of cowpea**

Accession	100SW(g)	VSH(cm)	MB	LB(cm)	NL	NP	LP(cm)	NSP	NPP
GH3684I1L1P4	10.41	22.8	8	85.2	109	5	8.2	13	20
GH3684I1L2P7	13.53	30.3	9	84.1	134	5	17.2	17	23
GH3684I1L2P8	12.36	24.8	6	99.3	124	4	12.7	16	19
GH3684C2L1P7	12.09	42.6	6	185.2	133	23	30.9	18	18
GH3684C2L2P2	11.11	51.8	7	182.7	124	28	39.4	16	16
GH3684C2L3P6	15.47	62.0	6	215.5	165	36	30.1	19	40
GH3684C2L4P8	12.31	48.9	8	213.1	155	46	30.5	18	28
GH7184BLL4P1	13.35	31.4	5	156.5	77	19	23.9	14	15
GH3684A2L1P6	15.83	18.3	6	77.2	82	8	16.7	12	8
GH3684A2L2P1	16.00	23.4	6	178.6	67	11	5.0	17	26
GH3684A2L3P4	15.26	39.4	8	128.1	127	8	8.1	16	14
GH3684BLL1P1	11.37	50.9	7	203.9	109	30	28.3	16	32
GH3684BLL1P5	12.65	44.5	9	215.5	129	21	32.4	18	36
GH3684BLL2P1	11.15	57.5	8	182.7	125	42	37.9	18	59
GH3684BLL2P3	14.18	53.9	7	139.6	143	67	41.7	13	38
GH3684BLL2P7	16.83	55.6	9	165.3	179	24	39.2	14	11
GH3684BLL4P6	14.48	54.3	8	239.3	151	48	40.2	13	9
GHUCO1BL1P3	17.99	55.1	9	276.0	149	20	21.2	16	49
GHUCO1BL1P6	16.88	50.6	7	233.4	47	33	23.9	15	50
GHUCO1BL1P8	17.3	53.9	9	228.4	177	23	33.6	10	50
GHUCO1BL2P2	16.06	46.1	6	234.2	101	9	53.8	7	24
GHUCO1BL2P5	16.28	47.9	7	211.8	184	21	54.1	12	64
GHUCO1BL4P1	18.65	38.6	6	254.5	115	16	27.6	14	14
GHUCO1BL4P8	19.72	52.1	6	247.2	298	13	30.9	18	11
GH3684B5L1P2	15.03	29.7	6	225.5	174	18	31.7	14	22
GH3684B5L3P2	10.78	56.2	7	191.7	188	21	40.3	12	40
GH3684B5L3P6	10.61	50.9	8	248.8	215	40	35	14	20
GH3684B5L4P8	12.47	42.8	6	206.3	204	16	25.9	17	6
GH3684B4L1P1	11.46	52.6	8	257	170	12	15.3	15	5
GH3684B4L2P5	12.4	28.1	6	231.2	126	29	27.1	17	19
GH3684B4L2P7	15.77	37.8	6	241.2	206	15	20.8	15	16
GH3684B4L4P1	15.04	45.2	6	191.9	116	25	55.1	18	17
GH3684B4L4P3	16.46	41.1	6	233.4	129	23	38	17	13
IT97K-499-35	17.1	27.5	5	101.9	54	20	32.2	13	31

SW= seed weight, VSH= vertical stem height, MB= number of branches, LB= length of branches, NP= number of peduncles, LP= length of peduncles, NSP= number of seeds per pod, NPP= number of pods per plant. Values were means of four replicates.



**Figure 1: Dendrogram of cowpea accessions based on 23 agro-morphological characters as a measure of genetic traits revealing the relationship among 34 samples of cowpea progenies from eight cowpea accessions including an out-group**

### Cluster analysis

The dendrogram (Fig. 1) constructed based on 23 agro-morphological characters revealed significant variations among the cowpea accessions. The 33 samples of the eight cowpea accessions and the out-group were differentiated into two lineages (I and II). The out-group IT97K-499-35 obtained from IITA, Nigeria was distinguished into a single lineage (I). However, the local accessions constituted a giant lineage group (II). A vivid description of the clustering is outlined in Table 4. Bootstrap values at nodes in the dendrogram represent the stability of the clusters associated with the node.

### DISCUSSION

This study sought to identify some segregating lines among second cycle progenies of cowpea accessions obtained from the stock of a previous cultivated germplasm and to evaluate the differences and similarities within the segregating lines using their agro-morphological traits. Earlier studies on cowpeas using morphological traits such as plant pigmentation, growth habit,

root traits, leaf, pod and seed traits as well as grain quality and yield have been carried out by many researchers (Aboagye and Bennett-Lartey, 2001; Roquib and Patnaik, 1990). These traits were all found to be of great importance in assessing genetic variability, and could lead to a better classification of cowpea genotypes. Emebiri (1989) also characterized cowpea cultivars using their flower size and style length and also reported that both characters were highly heritable.

Agro-morphological traits (quantitative and qualitative) are still valuable tools for cowpea genetic diversity studies. Some of the morphological characters used in this study, were colour of matured pods, seed weight, twining tendency, growth habit, immature pod pigmentation and flower colour.

The cowpea seeds were very viable and the seedlings for all the cowpea accessions expressed healthy growth suitable for agro-morphological studies. The samples obtained from the eight cowpea accessions showed significant differences in growth habits including

**Table 4: Cluster distribution of 34 cowpea samples obtained from eight accessions based on 14 qualitative and nine quantitative characters**

Groups	Sample size	Cowpea Population lines
Lineage I	1	IT97K-499-35
Lineage II		
Cluster 1 (A and B) A (a and b)	10	a - GH3684 <sub>BL</sub> L <sub>1</sub> P <sub>1</sub> , GH3684 <sub>BL</sub> L <sub>1</sub> P <sub>5</sub> , GH3684 <sub>BL</sub> L <sub>2</sub> P <sub>7</sub> , GH3684 <sub>BL</sub> L <sub>2</sub> P <sub>3</sub> GH3684 <sub>BL</sub> L <sub>2</sub> P <sub>1</sub> b - GH3684 <sub>BL</sub> L <sub>4</sub> P <sub>6</sub> , GHUCO1 <sub>BL</sub> L <sub>1</sub> P <sub>3</sub> , GHUCO1 <sub>BL</sub> L <sub>2</sub> P <sub>2</sub> , GHUCO1 <sub>BL</sub> L <sub>1</sub> P <sub>6</sub> , GHUCO1 <sub>BL</sub> L <sub>1</sub> P <sub>8</sub> ,
B	4	GHUCO1 <sub>BL</sub> L <sub>2</sub> P <sub>5</sub> , GHUCO1 <sub>BL</sub> L <sub>4</sub> P <sub>1</sub> , GHUCO1 <sub>BL</sub> L <sub>4</sub> P <sub>8</sub> , GH3684B <sub>5</sub> L <sub>2</sub> P <sub>2</sub>
Cluster 2 (C and D) C (c and d)	14	c - GH3684C <sub>2</sub> L <sub>4</sub> P <sub>1</sub> , GH3684C <sub>2</sub> L <sub>4</sub> P <sub>3</sub> d - i) GH3684B <sub>4</sub> L <sub>4</sub> P <sub>1</sub> , GH3684 <sub>4</sub> L <sub>4</sub> P <sub>3</sub> , GH3684B <sub>5</sub> L <sub>4</sub> P <sub>8</sub> , GH3684B <sub>4</sub> L <sub>2</sub> P <sub>5</sub> , GH3684B <sub>4</sub> L <sub>2</sub> P <sub>7</sub> ii) GH3684A <sub>2</sub> L <sub>2</sub> P <sub>1</sub> , GH3684A <sub>2</sub> L <sub>3</sub> P <sub>4</sub> , GH3684 <sub>1</sub> L <sub>1</sub> P <sub>4</sub> GH3684 <sub>1</sub> L <sub>2</sub> P <sub>8</sub> , GH3684 <sub>1</sub> L <sub>2</sub> P <sub>7</sub> , GH3684A <sub>2</sub> L <sub>1</sub> P <sub>6</sub> , GH3684B <sub>4</sub> L <sub>1</sub> P <sub>1</sub>
D	5	GH7184 <sub>BL</sub> L <sub>4</sub> P <sub>1</sub> , GH3684B <sub>5</sub> L <sub>3</sub> P <sub>2</sub> , GH3684B <sub>5</sub> L <sub>3</sub> P <sub>6</sub> , GH3684C <sub>2</sub> L <sub>3</sub> P <sub>6</sub> GH3684C <sub>2</sub> L <sub>4</sub> P <sub>8</sub> .



the out-group. Samples obtained from accession GHUCO1<sub>BL</sub> were prostrate, semi prostrate or semi erect in growth habit. The alleles controlling growth habit in GHUCO1 may be segregating. GH3684B<sub>4</sub>, GH3684<sub>BL</sub> and GH3684A<sub>2</sub> appeared semi-erect but GH3684C<sub>2</sub> and GH7148<sub>BL</sub> were erect. Semi-erect and erect growth habits expressed by the GH3684 cowpea lines suggest that they may be from a common origin. The out-group IT97K-499-35 expressed only erect growth habit, suggesting stability (true breed) of the trait in this cowpea compared to the others.

Accession GHUCO1<sub>BL</sub> produced only intermediate twinning tendency suggesting that this trait may be stable. However, the GH3684 lines expressed slight, intermediate and pronounce twinning tendencies. This is informative, suggesting that more than one allele may be influencing the expression of the trait. The alleles controlling twinning tendency may occupy different loci and their effect on each other, coupled with environmental conditions may produce different phenotypes.

The pods of many cowpea varieties contain anthocyanin and are either partially or wholly purple (Mustapha & Singh, 2008). The purplish green colour of matured pods of most of the cowpea accessions (GH3684B<sub>5</sub>, GH3684B<sub>4</sub>, GH3684A<sub>2</sub>, and GH3684C<sub>2</sub>) could be due to the anthocyanin content. Mustapha and Singh (2008) reported that, wholly purple pods are dominant to green pods and a single gene controls the trait. Sen and Bhowal (1961) suggested that three alleles control green pod with purple tip, green pod with purple ventral suture and purple pod with green sutures; and also identified two additional pod pigmentation genes. One condition is green pods with purple sutures, scattered small purple patches and purple tips; and the other green pods with faintly purple sutures. The matured pods of GHUCO1<sub>BL</sub> were pale green in colour, while accessions GH7184<sub>BL</sub> and IT97K-499-35 had green matured pods. However, GH3684<sub>BL</sub> plants had both pale green and green coloured matured pods. In general only few plants had their matured pods to be green in colour. The allele for

pigmentation may be dominant over that of non pigmentation. Harland (1920) reported that wholly purple pods are dominant over green pods. Complementarities suggested the mode of interaction between the genes controlling the trait such that the two alleles must be present for purple colour to be expressed (Mustapha and Singh, 2008). In a similar investigation, Uguru (1995) showed that pod colour appears to be determined pleiotropically by two allelic pairs. The colour of matured pods of GHUCO1<sub>BL</sub> (light green) confers a genetic lineage to one of the parents, SARC-LO2 (light green pods) [IT97K-499-35 – dark green pods, Apagbaala – green pods]. GH3684 lines may have a common origin from ancestral stock with purplish green pods, however, GH3684<sub>BL</sub> plants alone displayed both green and pale green colour of matured pods and this is an indication of the fact that it could be segregating with regard to pod colour or influenced by the environment.

Most of the cowpea accessions (83.3%) had immature pods with pigmented tips. This could possibly be as a result of a dominant allele factor as suggested by Harland (1920). However, GHUCO1<sub>BL</sub> and GH3484<sub>BL</sub> progenies exhibited both pigmented tip and pigmented tip with suture (14%). Similarly, it has been observed that IT97K-499-35 expressed both pigmented tip and pigmented tip with suture in its immature pods. The expression of both traits among plants from GHUCO1<sub>BL</sub> cowpea accession may appear to be determined pleiotropically by two allelic pairs as suggested by Uguru (1995). This highly supports IT97K-499-35 to be part of a possible parental cross that resulted in GHUCO1<sub>BL</sub> cowpea accession. There is evidence that GHUCO1<sub>BL</sub> may be related to SARC-LO2 and IT97K-499-35, by way of having light green pods and expressing both pigmented tip and pigmented tip with suture on immature pods respectively. It is therefore possible that GHUCO1<sub>BL</sub> is a segregating line that may have resulted from the cross between IT97K-499-35 x SARC-LO2.

Phenotypic differences may also elucidate genetic differences. Autrique *et al.* (1996), Johns *et al.* (1997), and Van Beuningen and Bush

(1997) used morphological, developmental and physiological traits to create distance that was used in evaluating the genetic diversity in large collection of germplasm. Analysis of the quantitative traits (100 seed weight, mean plant height, number of main branches, length of branches, number of leaves, number of peduncles, length of peduncles, number of seeds per pod and number of pods per plant) revealed significant differences ( $p < 0.05$ ) in the various characters assessed among plants of various cowpea accessions studied. This is indicative that the cowpea accessions may be genetically diverse and probably segregating in one trait or the other.

Cluster analysis substantiated the existence of diversity among the samples from the eight cowpea accessions including the out-group for the 23 morphological characters studied. The most divergent accession was IT97K-499-35 (the out-group), which was highly discriminated from other accessions in lineage I. The clustering pattern showed that individual plants were grouped according to the accessions they belonged to; indicating that the eight cowpea accessions studied may differ genetically from each other. However, the parallelism observed among the cowpea lines; GH3684<sub>BL</sub>, GH3684A<sub>2</sub>, GH3684B<sub>4</sub>, GH3684B<sub>5</sub>, GH3684C<sub>2</sub>, GH 3684<sub>1</sub>, GHUCO1<sub>BL</sub>, GH7184<sub>BL</sub> showed close resemblance, an indication that these accessions may have come from a common genetic background. A high level of relationship has also been detected among several cowpea genotypes following the evaluation of the variability in seed proteins among them (D'Urzo et al., 1990). The high level of relationship reported among cowpea varieties may also be due to it being a self-pollinated crop (Padulosi, 1993). On the contrary, there were a few exceptions as some of the different cowpea accessions associated together; GH3684<sub>BL</sub>L<sub>4</sub>P<sub>6</sub> and GHUCO1<sub>BL</sub> in group III (fig. 1), GH3684B<sub>5</sub>L<sub>1</sub>P<sub>2</sub> and GHUCO1<sub>BL</sub> in group IV (figure 1), GH3684<sub>5</sub>L<sub>4</sub>P<sub>8</sub> and GH 3684B<sub>4</sub> in group VI). This could be largely influenced by the fact that most of the cowpea accessions are still segregating mor-

phologically based on some common agro-morphological traits.

On the whole, the study has shown that there were variations or polymorphism in some morphological characteristics expressed by the cowpea accessions and these were segregating in one trait or the other; GHUCO1<sub>BL</sub> alone expressed multiple growth habits (prostrate, semi-prostrate and semi-erect), GH 3684A<sub>2</sub> had both slight and intermediate twinning tendencies. GH3684C<sub>2</sub> produced both purplish green and pale green colours of matured pods. The ANOVA revealed significant differences in 100 seed weight, average plant height, number of branches, length of branches, number of leaves, number of peduncles, length of peduncles, number of seeds per pod and number of pods per plant among the cowpea accessions. An overall relatively high level of dissimilarity was observed among and even within the eight accessions for most of the morphological traits analyzed. The cluster analysis confirmed segregation among the cowpea accessions as it sorted the cowpea accessions into six groups with respect to the segregation patterns of their morphological traits. The bootstrap revealed GH3684C<sub>2</sub> to be the most diverse accession possessing both purple and white flower colours and appeared to associate with other accessions. The cowpeas had some common traits such as plant hairiness, raceme position, immature pod pigmentation, plant vigor and flower pigmentation.

#### CONCLUSION

The evaluation based on agro-morphological characters provided enough evidence to suggest that GHUCO1<sub>BL</sub> may be a descendant from the cross between IT97K-499-35 x SARC-LO2. Similarly, the lines of GH3684 cowpea accessions may have a common ancestry and the diversity exhibited may be due to genotype with environment interactions. Furthermore, the twenty three agro-morphological traits were informative for discriminating the phenotypes to confer trait segregation among the cowpea accessions, except for the out-group, IT97K-499-35. However, it is highly recommended

that molecular characterisation should be carried out to further confirm the current results.

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