

## **Assessment of Genetic Diversity in Pepper (*Capsicum* sp.) Landraces from Ghana Using Agro-morphological Characters**

**Richard Yaw Agyare<sup>1\*</sup>, Richard Akromah<sup>2</sup> and Mashark Seidu Abdulai<sup>1</sup>**

<sup>1</sup>CSIR-Savanna Agricultural Research Institute (SARI), Nyankpala, P.O.Box TL 52, Tamale, Ghana.

<sup>2</sup>Kwame Nkrumah University of Science and Technology (KNUST), PMB University Post Office, Kumasi, Ghana.

### **Authors' contributions**

*This work was carried out in collaboration between all authors. Author RYA used the experiment for his MSc. thesis. Authors RA and MSA supervised the experiment and writing of thesis. The design of the experiment, data analyses and writing of manuscript was done in close collaboration between all authors. All authors read and approved the final manuscript.*

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### **ABSTRACT**

**Aims:** To examine the genetic diversity and relatedness among pepper accessions using agro-morphological markers.

**Study Design:** Augmented design with single rows of each genotype.

**Place and Duration of Study:** Research field, CSIR-Savanna Agricultural Research Institute, Nyankpala-Tamale, Ghana, May to October, 2012.

**Methodology:** Fifty local pepper genotypes from different agro-ecological zones in Ghana were characterized using 35 agro-morphological (11 quantitative and 24 qualitative) traits using standard descriptors for *Capsicum* sp. For quantitative traits, measurements were recorded on ten tagged plants and the mean value used while four tagged plants were scored for the qualitative traits.

**Results:** The first three principal components accounted for 59.61% of the total genetic variance among the genotypes with the larger part of the variance explained by fruit pedicel width, fruit

\*Corresponding author: E-mail: [agyareyaw@live.com](mailto:agyareyaw@live.com);

weight, fruit length, plant height, stem diameter, fruit pedicel length and fruit width. For qualitative traits, the first three principal components contributed to 51.65% of the total genetic variance with leaf pubescence density, fruit position, calyx annular constriction and filament colour as the most important parameters. The study showed a great variation in fruit traits revealing six fruit shapes and four fruit colours. Fruit weight exhibited positive and significant correlations with yield components such as fruit length and fruit width.

**Conclusion:** The study has shown that morphological markers are effective tools in studying genetic diversity in *Capsicum* species. This observed diversity among the pepper genotypes would therefore be used for improving pepper through hybridization and selection.

**Keywords:** Chilli pepper; correlation analysis; genetic diversity; principal components; cluster analysis.

## 1. INTRODUCTION

Pepper, (*Capsicum* sp.), is an economically important crop grown worldwide for vegetable, spice, ornamental and medicinal uses and is a significant source of vitamins A and C [1]. It is one of the most important vegetable crops in Ghana with numerous uses. It is found within the family Solanaceae of the genus *Capsicum* and is believed to have originated from tropical South America with Brazil as the major centre of diversity where all cited levels are found [2]. The genus *Capsicum* has five domesticated species (*C. annuum*, *C. pubescens*, *C. chinense*, *C. baccatum* and *C. frutescens*) which were thought to have been domesticated through at least five independent events [3]. Natural interspecific cross compatibility among these *Capsicum* species often result in complex hybrids difficult to characterize. Pepper was introduced into Europe by Columbus and other early new explorers in the sixteenth century and cultivation spread throughout the world with *C. annuum* being the most widely cultivated [4]. The predominance of *C. annuum* among the cultivated species globally is not attributed to superior agronomic or consumer traits but it was the first to be introduced into Europe [5]. It has therefore become one of the most important spice commodities and as well as essential vegetable crop worldwide [1].

Pepper is a small perennial shrub characterized by white or greenish-white corolla, one or more pedicels at a node with varying fruit sizes and shapes [6]. The wild ancestor of domesticated *C. annuum* has erect, small fruits that are pungent, red in colour, deciduous and soft-fleshed. These traits promote consumption and seed dispersal by birds rather than mammals [7]. Domestication and commercialization of pepper has led to the selection of traits such as compact architecture, increased efficiency of self-pollination, early

flowering and non-deciduous, high fruit set, pendant fruits. Pepper cultivars have been selected for based on the uses of the crop and consumer-preferred fruit traits such as degree of pungency, fruit shape and colour flavour, fruit wall thickness and drying ability [1]. Continuous selection during domestication and monocropping has led to the identification of cultivars with bigger non-pungent fruits with greater variation in shape and remarkable increases in fruit mass [8]. These large-fruited non-pungent bell type peppers were found in pre-Columbian Mexico and were first described about 500 years ago. Although the pungent pepper cultivars are considered the most important spice crop globally, the large non-pungent bell peppers also consumed worldwide, are the most economically important pepper type [1].

Crop improvement programs are aided by the availability of genetically diverse germplasm within the gene pool of a crop species. However, the richness of genetic diversity in a species are barely fully tapped by breeders due to scarcity of information on the extent of diversity among the breeding materials [9]. Genetic diversity of landrace germplasm is considered as one of the criteria for selection of parents for pepper breeding, because of their competitive advantage. Tanksley and McCouch [10] indicated that the genetic base of most crops were narrowed when wild species were domesticated and also when landraces were replaced by modern improved cultivars. These landrace germplasm have higher genetic variability among the different groups of germplasm, as well as better environmental adaptation, and are an irreplaceable source of highly adapted genotypes [11]. Landraces of crops constitute a dynamic and important component of agricultural biodiversity which has been valued almost totally as the source of essential traits that can be used in crop breeding

programs and to improve the productivity of new crop varieties. However germplasm from exotic sources may possess important traits that may not be found within the available germplasm. Therefore assembling landraces and exotic genotypes allow breeders to improve both within and between population variations which will allow these genotypes to cope with variable environmental stresses [12].

Germplasm characterization is useful in detecting variations in different cultivars purposely for identification and elimination of duplicates. It is also used for revealing distinct genotypes that could be used as parental lines to establish hybridization programs. Morphological markers such as plant stature, stem pubescence, fruit weight, flower colour, fruit shape, plant height etc., have been used to distinguish between pepper genotypes and characterize them into groups [13,14]. The use of these agro-morphological markers in describing and classifying germplasm is a fundamental step in genetic diversity assessment [15,16]. It is very useful in describing the genetic variation available within a crop species and to allow the detection of sources of genetic diversity for crop improvement [17]. Estimation of the genetic diversity among cultivated genotypes using agro-morphological characters has become an important requirement of the crop industry for identification, elimination of duplicates and crop improvement [18]. The extent of genetic variability within a species is vital for its continued existence and adaptation in different agro-ecologies. The more diverse the population is the better for the breeder in developing elite cultivars through careful selection of superior parents. Therefore, an understanding of the extent of genetic variability of a population, through the use of agro-morphological markers, is of critical importance in estimating possible loss of genetic variability and developing effective strategies for germplasm conservation and breeding purposes [16,19]. The objective of this work was to characterize pepper genotypes from different geographical regions of Ghana using agro-morphological markers and to determine the genetic relatedness within the germplasm.

## 2. MATERIALS AND METHODS

### 2.1 Study Area

The experiment was conducted at the experimental field of CSIR-Savanna Agricultural

Research Institute (CSIR-SARI), Nyankpala in the Guinea Savanna zone of Ghana (N 09°23'21.4"; W 001°00'13.4"). The zone is characterized by a mono-modal rainfall pattern and receives an average annual rainfall of about 800-1200 mm.yr<sup>-1</sup> with the rainy season falling between May and September. The mean annual temperature is recorded to be 24-34°C. The soil belongs to the Kumayili series and commonly classified as Ferric Luvisols. The field had a gentle slope of about 1-2% with a well-drained sandy-loam soil.

### 2.2 Genotypes Used for the Study

Fifty pepper genotypes comprising forty-eight landraces collected from diverse agro-climatic ecologies in Ghana through regular germplasm collection as well as two improved genotypes obtained from CSIR-SARI were used in the present study (Table 1). The pepper seeds were nursed in seed boxes using potting mix sterilized by steam sterilization method. The potting mix consisted of two parts of top soil to one part of well decomposed cow dung. Nursery management practices, such as shading, forking, thinning, watering and hardening off, were carried out appropriately to ensure that healthy seedlings were produced. The seedlings were transplanted onto ridges 6 weeks after nursing at a spacing of 75 cm x 50 cm. The experimental design used was augmented design with single rows (5 m long) of each genotype. Other agronomic practices such as weeding, fertilizer application, diseases and insect pest control were carried out uniformly as required for the growth of pepper. Morphological data were collected on 35 (24 qualitative and 11 quantitative) traits from seedling emergence to crop maturity adopting standard descriptors for *Capsicum* sp. developed by IPGRI [20] with slight modifications by Asian Vegetable Research and Development Center (AVRDC). Each qualitative trait was scored by observing four tagged plants per genotype. For quantitative traits, measurements were recorded on 10 tagged plants and the mean value used.

Descriptive statistics (mean, standard error, standard deviation, coefficient of variation and frequency distribution), principal component analyses (PCA) and correlations analysis of the morphological traits were carried out using GenStat software version 12.1 [21]. Principal coordinate analysis (PCoA) was carried out to determine the grouping of the genotypes using

DARwin software programme version 5 [22]. Cluster analysis based on Euclidean similarity coefficient was used to generate a dendrogram using GenStat software version 12.1 [21].

**Table 1. Pepper accessions used in the study**

<b>Genotype</b>	<b>Code</b>	<b>Origin</b>	<b>Region</b>	<b>Taxonomy</b>
VR HOE 11	VR 4	Hohoe	Volta	<i>Capsicum annuum</i> L.
VR KPV 1	VR 7	Kpeve	Volta	<i>Capsicum annuum</i> L.
VR KTS 2	VR 8	Kpogen	Volta	<i>Capsicum annuum</i> L.
BA TAN 3	BA 1	Hianmunchend	Brong Ahafo	<i>Capsicum annuum</i> L.
VR HOE 1	VR 3	Ve-Koloenu	Volta	<i>Capsicum annuum</i> L.
VR KTS 13	VR 2	Nogokpo	Volta	<i>Capsicum annuum</i> L.
BA TAN 12	BA 4	Kykyewere	Brong Ahafo	<i>Capsicum annuum</i> L.
ER UMK 2	ER 1	Asesewa	Eastern	<i>Capsicum annuum</i> L.
BA JMS 3	BA 2	Babiania	Brong Ahafo	<i>Capsicum annuum</i> L.
UE KNW 7	UE 1	Paganiani	Upper East	<i>Capsicum annuum</i> L.
UE TND 1	UE 6	Talensi	Upper East	<i>Capsicum annuum</i> L.
UE BOM 2	UE 9	Bolgatanga	Upper East	<i>Capsicum annuum</i> L.
NR TAM 4	NR 5	Tamale	Northern	<i>Capsicum annuum</i> L.
UE BAW 2	UE 2	Bawku	Upper East	<i>Capsicum annuum</i> L.
UE BAW 7A	UE 3	Bawku	Upper East	<i>Capsicum annuum</i> L.
UE BAW 7B	UE 5	Bawku	Upper East	<i>Capsicum annuum</i> L.
NR WMP 4	NR 2	Walewale	Northern	<i>Capsicum annuum</i> L.
GA ACC 1	GA 2	Madina	Greater Accra	<i>Capsicum annuum</i> L.
VR KTS 8	VR 9	Kpogen	Volta	<i>Capsicum annuum</i> L.
UE KNW 3	UE 8	Paganiani	Upper East	<i>Capsicum annuum</i> L.
VR KTS 9	VR 5	Kpogen	Volta	<i>Capsicum annuum</i> L.
ER UMK 3	ER 2	Asesewa	Eastern	<i>Capsicum annuum</i> L.
BA SYW 8	BA 7	Ayakomaso	Brong Ahafo	<i>Capsicum annuum</i> L.
VR HOE 8F	VR 10	Gbi, Hohoe	Volta	<i>Capsicum annuum</i> L.
UE KNE 4	UE 11	Goo, Paga	Upper East	<i>Capsicum annuum</i> L.
NR TKB 9	NR 1	Cheschegu	Northern	<i>Capsicum annuum</i> L.
NR WMP 6	NR 3	Diany	Northern	<i>Capsicum annuum</i> L.
UE BNG 1	UE 15	Bongo	Upper East	<i>Capsicum annuum</i> L.
UE KNE 8	UE 14	Zone J	Upper East	<i>Capsicum annuum</i> L.
UE KNW 13	UE 12	Navrongo	Upper East	<i>Capsicum annuum</i> L.
NR TKB 6	NR 7	Nwogu	Northern	<i>Capsicum annuum</i> L.
GA DWW 7	GA 3	Shai hills	Greater Accra	<i>Capsicum annuum</i> L.
GA ACC 5	GA 1	Madina	Greater Accra	<i>Capsicum annuum</i> L.
UE KNW 8	UE 4	Banyono	Upper East	<i>Capsicum annuum</i> L.
UE KNW 9	UE 10	Banyono	Upper East	<i>Capsicum annuum</i> L.
UE KNE 2	UE 7	Nangali	Upper East	<i>Capsicum annuum</i> L.
VR HOE 10 B	VR 6	Hohoe	Volta	<i>Capsicum annuum</i> L.
BA SYW 6	BA 8	Ayakomaso	Brong Ahafo	<i>Capsicum annuum</i> L.
NR TAM 6	NR 6	Tampeikukuo	Northern	<i>Capsicum annuum</i> L.
VR HOE 4	VR 1	Ur Avegpo	Volta	<i>Capsicum annuum</i> L.
NR SVN 4	NR 4	Libga	Northern	<i>Capsicum annuum</i> L.
BA JMS 4	BA 5	Babiania	Brong Ahafo	<i>Capsicum annuum</i> L.
UE KNE 6	UE 13	Bonia	Upper East	<i>Capsicum annuum</i> L.
ER UMK 1	ER 3	Asesewa	Eastern	<i>Capsicum annuum</i> L.
Legon 18	S 1	SARI	Northern	<i>Capsicum annuum</i> L.
Shito Adope	S 2	SARI	Northern	<i>Capsicum annuum</i> L.
VR KPD 2	VR 11	Kpando	Volta	<i>Capsicum annuum</i> L.
NR TKB 3	NR 8	Nwogu	Northern	<i>Capsicum annuum</i> L.
BA TAN 11A	BA 3	Nsawkaw	Brong Ahafo	<i>Capsicum annuum</i> L.
BA TAN 11B	BA 6	Nsawkaw	Brong Ahafo	<i>Capsicum annuum</i> L.

### 3. RESULTS AND DISCUSSION

#### 3.1 Phenotypic Evaluation of Qualitative Traits

Genetic characterization based on standard descriptors such as plant size, plant growth habit, branching habit, stem pubescence, leaf shape, flower position, fruit shape and colour helps to easily describe the morphological features of a genotype and makes diversity assessment easier [23]. The accessions exhibited a wide variation for several morphological characters studied. Most of the accessions had abundant pubescence on the hypocotyl (Table 2). Cotyledon colour ranged from light green to green with the shape varying from ovate to elong-deltoid. Majority of the accessions had sparse stem pubescence with green colour. Two modes of plant growth were observed (62% compact and 38% erect). Leaf shape varied between deltoid and lanceolate with sparse pubescence characterizing majority of them. Most of the accessions had intermediate plant size with abundant branches and dark green leaves. Yellow-green corolla (Fig. 1A) was common among the accessions with filament colour mostly white. Anther colour varied from pale blue to purple (Fig. 1B). Fruit shape at pedicel attachment ranged from acute to cordate with or without neck at base of fruit. Fruit shape at blossom end varied from pointed to sunken. Fruit cross-section ranged from smooth to corrugate with two or three locules per fruit (Fig. 1C). The study revealed six major classes of fruit shape ranging from elongate to blocky and four fruit colours at mature stage with red as the predominant fruit colour (Fig. 1D). The variations observed in the present study are in consonance with observations by Fonseca et al. [13] who found four fruit shapes varying from elongate to bell and nine fruit colours when they characterized 38 pepper genotypes from Brazil. Manju and Sreelathakumary [23] also found substantial variations in 32 pepper accessions using 18 morphological markers. The presence of wide genetic variation for a trait within a population indicates the potential for genetic improvement of that trait [24]. The variations among the accessions in the present study could be used in future pepper improvement programmes to breed for specific consumer-preferred traits.

#### 3.2 Phenotypic Analysis of Quantitative Traits

Cotyledon leaf length ranged from 1.24 cm in BA JMS 4 to 2.36 cm in VR HOE 11 with a mean of 1.76 cm (Table 3). Cotyledon leaf had widths ranging from 0.45-0.87 cm. The heights of the pepper genotypes ranged from 31.00-91.70 cm with an average height of 49.61 cm. Pepper accessions with intermediate heights would be good for intercropping purposes. The diameters of the stems were from 0.60-1.73 cm. The average genotype used about 41 days for 50% of its population to flower. The days to 50% flowering ranged from 22-58 days after transplanting was done. Days to 50% fruiting ranged from 26-29 days after days to 50% flowering were attained. Fruit pedicel length and width ranged from 1.49-3.21 cm and 0.09-0.39 cm, respectively. The mean fruit length was 4.44 cm with BA TAN 3 and VR KTS 2 having the shortest and longest fruit lengths of 0.70 cm and 10.46 cm, respectively. Fruit width also ranged from 0.63-3.90 cm with an average of 1.58 cm. Fruit weight which is the most important economic trait ranged from 4.50-131.50 g with genotypes UE TND 1 and GA ACC 5 having the smallest and greatest fruit weights respectively. In general, accessions belonging to scotch bonnet big group had the widest and heaviest fruits while those from the long cayenne group had longer fruits. Although quantitative traits are highly influenced by the environmental conditions, they are of major agronomic importance. Pepper accessions with diverse quantitative traits could be identified and selected as parental genotypes for hybridization and improvement purposes. For instance in breeding for pepper varieties with intermediate fruit length, BA TAN 3 which had the shortest fruit length could be hybridized with VR KTS 2 to develop progenies with intermediate fruit length to meet the demand for the export market.

The pepper accessions were also analysed based on the area of collection (region) using four quantitative traits to determine the extent of diversity among the accessions based on their origin (Table 4). For mean cotyledon leaf width, accessions from the Volta region had the least width of 0.67 cm while accessions from Greater Accra had the highest width of 0.78 cm. The overall mean plant height among the accessions was 49.61 cm. The average plant height of accessions from the Brong Ahafo (59.50 cm) was higher than the average plant heights of the accessions from the other regions with Volta

region having the least height of 45.00 cm. Greater Accra had accessions with bigger fruits (5.56 cm long and 3.96 cm wide) than the other regions. Although variations existed among the accessions from the different regions, it can be observed that variations among accessions

within a region were higher than variations among accessions between regions. This means that pepper accessions with diverse characteristics could be identified within regions of choice to minimize the cost associated with germplasm collection in the entire country.

**Table 2. Frequency distribution of 20 qualitative traits among pepper accessions**

No.	Descriptor	Descriptor state (frequency percentage)				
1	Hypocotyl pubescence	Sparse (6%)	Intermediate (16%)	Abundant (78%)		
2	Cotyledon leaf shape	Ovate (6%)	Lanceolate (82%)	Elong-deltoid (10%)		Mixture (2%)
3	Cotyledon leaf colour	Light green (18%)	Green (82%)			
4	Stem colour	Green (72%)	Green with few purple strips (8%)	Green with many purple strips (20%)		
5	Plant growth habit	Compact (62%)	Erect (38%)			
6	Stem pubescence	Glabrous (4%)	Sparse (66%)	Intermediate (26%)		Abundant (4%)
7	Leaf pubescence	Glabrous (16%)	Sparse (58%)	Intermediate (16%)		Mixture (10%)
8	Leaf shape	Deltoid (20%)	Ovate (54%)	Lanceolate (22%)		Mixture (4%)
9	Leaf colour	Light green (8%)	Green (36%)	Dark green (50%)		Mixture (6%)
10	Branching habit	Sparse (2%)	Intermediate (28%)	Abundant (62%)	Mixture (8%)	
11	Plant size	Small (14%)	Intermediate (70%)	Large (16%)		
12	Filament colour	White (76%)	Light purple (12%)	Purple (2%)	Mixture (10%)	
13	Calyx margin shape	Intermediate (74%)	Dentate (26%)			
14	Calyx annular constriction	Absent (2%)	Not clear (16%)	Clear (22%)	Distinct and uniform in whole plant (58%)	Mixture (2%)
15	Fruit position	Declining (44%)	Erect (14%)	Mixture (42%)		
16	Fruit colour at mature stage	Green (4%)	Yellow (2%)	Orange (2%)	Red (86%)	Mixture (6%)
17	Fruit shape at pedicel attachment	Acute (6%)	Obtuse (44%)	Truncate (44%)	Cordate (6%)	
18	Neck at base of fruit	Absent (74%)	Present (26%)			
19	Fruit shape at blossom end	Pointed (60%)	Blunt (22%)	Sunken (16%)	Mixture (2%)	
20	Fruit cross-sectional corrugation	Smooth (6%)	Slightly corrugated (40%)	Intermediate (24%)	Corrugated (30%)	

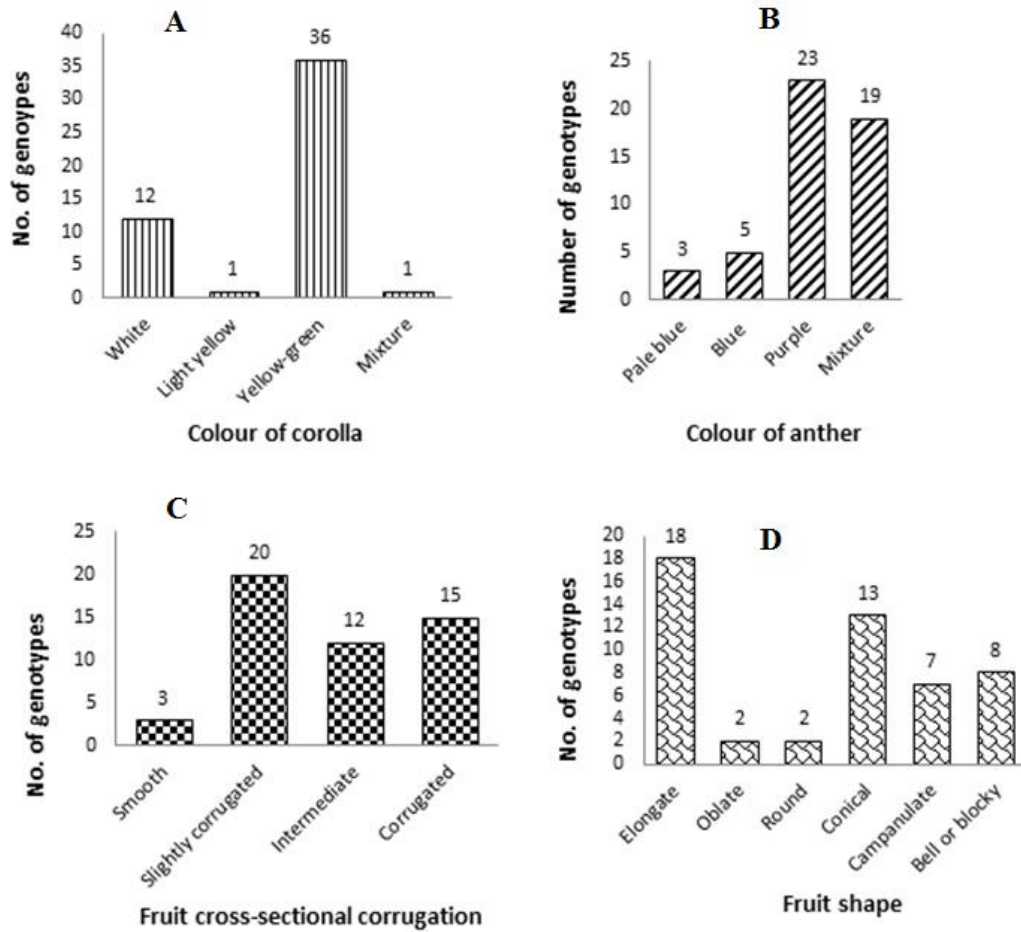


Fig. 1. Frequency distribution of four traits among 50 pepper accessions from Ghana

Table 3. Analysis of 11 quantitative traits among pepper accessions

Parameter	Mean ± SE	Range	SD	CV (%)
Cotyledon leaf length (cm)	1.76±0.03	1.24-2.36	0.24	13.37
Cotyledon leaf width (cm)	0.69±0.01	0.45-0.87	0.09	13.30
Plant height (cm)	49.61±1.66	31.00-91.70	11.71	23.60
Stem diameter (cm)	1.07±0.03	0.60-1.73	0.22	20.52
Days to 50% flowering	40.78±1.34	22.00-58.00	9.46	23.19
Days to 50% fruiting	28.46±0.17	26.00-29.00	1.16	4.09
Fruit pedicel length (cm)	2.30±0.06	1.49-3.21	0.41	17.70
Fruit pedicel width (cm)	0.17±0.01	0.09-0.39	0.06	32.11
Fruit length (cm)	4.44±0.34	0.70-10.46	2.39	53.78
Fruit width (cm)	1.58±0.10	0.63-3.90	0.68	42.60
Fruit weight (g)	35.55±3.72	4.50-131.50	26.33	74.08

### 3.3 Influence of Agro-morphological Traits on Total Genetic Variance as Revealed by Principal Component Analysis (PCA)

Principal component analyses were carried out to determine the most important agro-morphological

traits which contributed significantly to total genetic diversity among the pepper accessions. The first three principal components (PC) accounted for 51.65% of the total genetic variance using the 24 qualitative traits (Table 5). The first PC accounted for 23.22% of the variance with the larger part of the variance

explained by leaf pubescence density, calyx annular constriction, filament colour and fruit position. PC 2 explained 17.82% of variation with anther colour as the predominant trait that accounted for the variation. For PC 3, fruit cross-sectional corrugation, fruit position at blossom end and fruit shape were the most important traits that explained 10.61% the variation observed.

For the 11 quantitative traits, the first three PCs accounted for 59.61% of the total genetic variance (Table 6). PC 1 accounted for 23.32% of the observed variation which was explained by fruit length, fruit pedicel width and fruit weight. PC 2 accounted for 18.79% of the variance with plant height, stem diameter and fruit pedicel length being the most important traits. Fruit width, cotyledon leaf length and days to 50% fruiting were the most significant traits explaining 17.50% of the variance as observed in PC 3. Genetic diversity studies using principal components have been carried out by several authors on pepper. Bozokalfa et al. [25] recorded 54.29% variation in 48 pepper accessions using the first six principal components. Similarly Nsabiya et al. [26] working on 37 pepper genotypes indicated that 55.40% of the total genetic variance was explained by the first 2 PCs. Distinct pepper genotypes can be selected as parental lines using the most important traits contributing more to total variability. Se-Jong et al. [16] reported the use of morphological traits such as flower and fruit characteristics in pepper as the simplest approach for the detection of genotypes and the assessment of genetic diversity.

### 3.4 Correlation Analysis of 11 Morphological Traits

Correlation coefficients of 11 quantitative traits measured among the 50 pepper accessions are presented in Table 7. Cotyledon leaf length possessed significant negative correlation ( $r = -0.375$ ) with cotyledon leaf width but showed significant positive correlation ( $r = 0.305$ ) with days to 50% fruiting. Cotyledon leaf width had non-significant association with all the traits with the exception of cotyledon leaf length. Days to 50% flowering showed significant positive association ( $r = 0.419$ ) with plant height. This result was in consonance with report by Ghosh et al. [27]. Days to 50% fruiting had significant positive and negative correlations ( $r = 0.315$ ,  $r = 0.513$ ,  $r = -0.473$ ) with fruit width, stem diameter and fruit length respectively. Fruit weight

disclosed highly significant positive associations ( $r = 0.436$ ,  $r = 0.527$ ,  $r = 0.710$ ) with fruit length, fruit pedicel width and fruit width. This result was in agreement with Muhammad et al. [28]. However, they reported significant negative correlation between fruit weight and fruit length in tomato. Fruit weight also shared non-significant association with plant height indicating that fruit weight which is the most important economic trait was not influenced by the height of the pepper plants. Plant height showed significant positive correlations ( $r = 0.508$ ,  $r = 0.529$ ) with stem diameter and fruit pedicel width respectively. Fruit length possessed significant positive associations ( $r = 0.419$ ,  $r = 0.408$ ) with fruit pedicel length and fruit pedicel width.

In general, there were significant positive correlations between fruit weight (yield) and yield components such as fruit length and fruit width. Mohammed et al. [29] indicated that correlation analysis is helpful in determining main traits influencing variation in traits of economic importance as well as their interrelatedness to facilitate their simultaneous improvement. Based on the correlations between the agromorphological traits at the phenotypic level, pepper accessions with long fruit length, large fruit pedicel width and large fruit width should be selected as desirable parental lines in efforts towards fruit yield improvement.

### 3.5 Principal Coordinate Analysis (PCoA)

Principal coordinate analysis (PCoA) grouped the pepper accessions into four major clusters with the accessions fairly distributed on the axes (Fig. 2). Cluster A consisted of five accessions (NR 8, UE 14, VR 2, S 1 and UE 15). These accessions had glabrous leaf pubescence, elongate fruit shape and slightly corrugated fruit cross section. Cluster B had the highest number (20) of accessions. These include NR 2, UE 13, NR 5, BA 5, ER 2, UE 6, UE 12, UE 11, UE 3, NR 1, ER 3, UE 2, NR 4, BA 7, VR 9, UE 4, VR 5, VR 11, NR 6 and GA 1. The accessions in this cluster had sparse leaf pubescence, conical fruit shape and corrugated fruit cross section. Cluster C was made up of five accessions. This cluster was made up of accessions UE 9, UE 5, GA 2, BA 8 and UE 7. They clustered together mainly due to their sparse leaf pubescence, white filament and campanulate fruit shape. The accessions that clustered in group D comprised, BA 4, BA 6, UE 8, UE 10 and VR 6. These accessions had intermediate leaf pubescence, distinct and uniform calyx annular constriction





**Table 4. Analysis of four quantitative traits among the pepper accessions based on origin (region)**

Origin of accessions	Cotyledon leaf width (cm)				Plant height (cm)				Fruit length (cm)				Fruit width (cm)			
	Mean	SD	Min	Max	Mean	SD	Min	Max	Mean	SD	Min	Max	Mean	SD	Min	Max
Overall	0.69	0.09	0.45	0.87	49.61	11.71	31.00	91.70	4.44	2.39	0.70	10.46	1.58	0.68	0.63	3.90
Brong Ahafo	0.68	0.12	0.45	0.86	59.50	15.86	42.30	91.70	4.26	2.34	0.70	7.47	1.37	0.48	0.63	2.18
Eastern	0.69	0.10	0.60	0.80	56.57	19.16	39.00	77.00	4.24	3.44	1.15	7.95	1.40	0.37	1.03	1.77
Greater Accra	0.78	0.09	0.68	0.87	46.43	12.61	32.00	55.30	5.56	2.25	3.55	7.99	2.53	1.22	1.58	3.90
Northern	0.71	0.07	0.60	0.84	48.70	10.78	31.00	67.00	3.96	1.38	1.87	6.55	1.40	0.69	0.85	2.71
Upper East	0.68	0.09	0.47	0.84	47.57	9.76	32.30	62.30	4.04	2.02	1.83	9.39	1.60	0.74	0.62	2.94
Volta	0.67	0.07	0.54	0.77	45.00	5.09	38.70	56.00	5.32	3.40	1.52	10.46	1.67	0.44	0.86	2.34

**Table 5. PCA of qualitative traits to total genetic variance using the first 3 PCs**

Traits	PC 1	PC 2	PC 3
Hypocotyl pubescence	0.1113	-0.0657	-0.1092
Leaf pubescence density	0.4453	0.1293	0.3932
Leaf colour	0.0145	-0.1101	0.1212
Leaf shape	-0.1724	0.0688	0.1518
Neck at base of fruit	0.0172	-0.0105	-0.0019
Number of locules	-0.0016	0.0177	-0.0126
Plant size	0.0895	-0.0187	0.0480
Plant growth habit	-0.1301	0.0428	0.1385
Stem pubescence density	0.0596	0.1088	0.1158
Stem colour	-0.1432	0.0383	0.1239
Fruit shape at peduncle attachment	0.1289	0.0659	-0.1774
Fruit shape at blossom end	0.1483	0.0750	0.3978
Fruit shape	0.2949	0.1365	0.3623
Fruit position	0.4577	0.6967	0.1390
Fruit cross sectional corrugation	0.1929	0.1617	0.4541
Fruit colour at mature stage	-0.0154	-0.0752	0.1669
Filament colour	0.3483	0.4628	0.3600
Cotyledon leaf shape	-0.0433	-0.0057	0.0160
Cotyledon leaf colour	-0.0502	-0.0593	0.0905
Corolla colour	0.2779	-0.1143	-0.0664
Calyx margin shape	-0.0715	0.0219	0.0572
Calyx annular constriction	0.3025	-0.0125	-0.0654
Branching habit	0.0714	-0.0658	0.1192
Anther colour	0.1817	0.4057	0.0825
Eigen value	8.042	6.171	3.675
% variance	23.22	17.82	10.61
Cumulative % variance	23.22	41.04	51.65

**Table 6. PCA of quantitative traits to total genetic variance using the first 3 PCs**

Traits	PC 1	PC 2	PC 3
Cotyledon leaf length	0.2635	0.0397	0.2337
Cotyledon leaf width	-0.0876	0.0153	0.0541
Days to 50% flowering	-0.1107	0.3458	-0.1291
Days to 50% fruiting	-0.4557	0.1315	0.2939
Fruit weight	0.3584	0.2948	0.4621
Plant height	-0.1371	0.5840	-0.2065
Stem diameter	-0.3345	0.3657	0.0189
Fruit length	0.4960	0.1437	-0.1143
Fruit pedicel length	0.1905	0.4765	-0.3078
Fruit pedicel width	0.4019	0.0614	0.2895
Fruit width	-0.0042	0.2194	0.6256
Eigen value	2.565	2.067	1.925
% variance	23.32	18.79	17.50
Cumulative % variance	23.32	42.11	59.61

### 3.6 Genetic Relationship among Pepper Accessions Using Morpho-agronomical Traits

Cluster analysis is very useful in revealing complex relationships and genetic relatedness among populations of diverse origins in a more simplified manner [16]. It is also effective in indicating accessions with useful traits belonging to different clusters for hybridization. Genetic

similarity based on the 35 morpho-agronomical traits ranged from 0.88-0.99 (Fig. 3). The 50 pepper accessions were grouped into 2 main clusters at a similarity coefficient of about 88. Cluster A had a very unique accession, BA TAN 3 (late flowering and tiny fruit size) while cluster B had 49 accessions. Although majority of the accessions were grouped into cluster B, there were variations among them resulting in further sub-clustering. Cluster B was further subdivided

into six sub-clusters (Table 8). Sub-cluster B I consisted of accession UE KNW 7. Sub-cluster B II was made up of accessions VR HOE 10B, BA TAN 11A and BA TAN 11B. Accession GA DWW 7 alone was found in sub-cluster B III. Sub-cluster B IV was made up of accession VR KPV 1. Sub-cluster B V had only one accession, BA JMS 4. Sub-cluster B VI consisted of 42 accessions. Even though majority of the accessions clustered into their various groups, clustering did not strictly follow the geographic location from where the accessions were collected but was based on their morphological

features. At a genetic similarity above 98%, NR WMP 4 and UE TND1 as well as UE BAW 7A and UE BAW 2 may be considered as possible duplicates, respectively. Similar results of possible duplicates have been observed by other researchers working on different crops [30,31]. The cluster analysis revealed VR HOE 1 and BA TAN 3 as the more diverse genotypes. Although the dendrogram revealed high genetic relatedness, the diversity within the genotypes could be used for improving desirable traits through selection and hybridization.

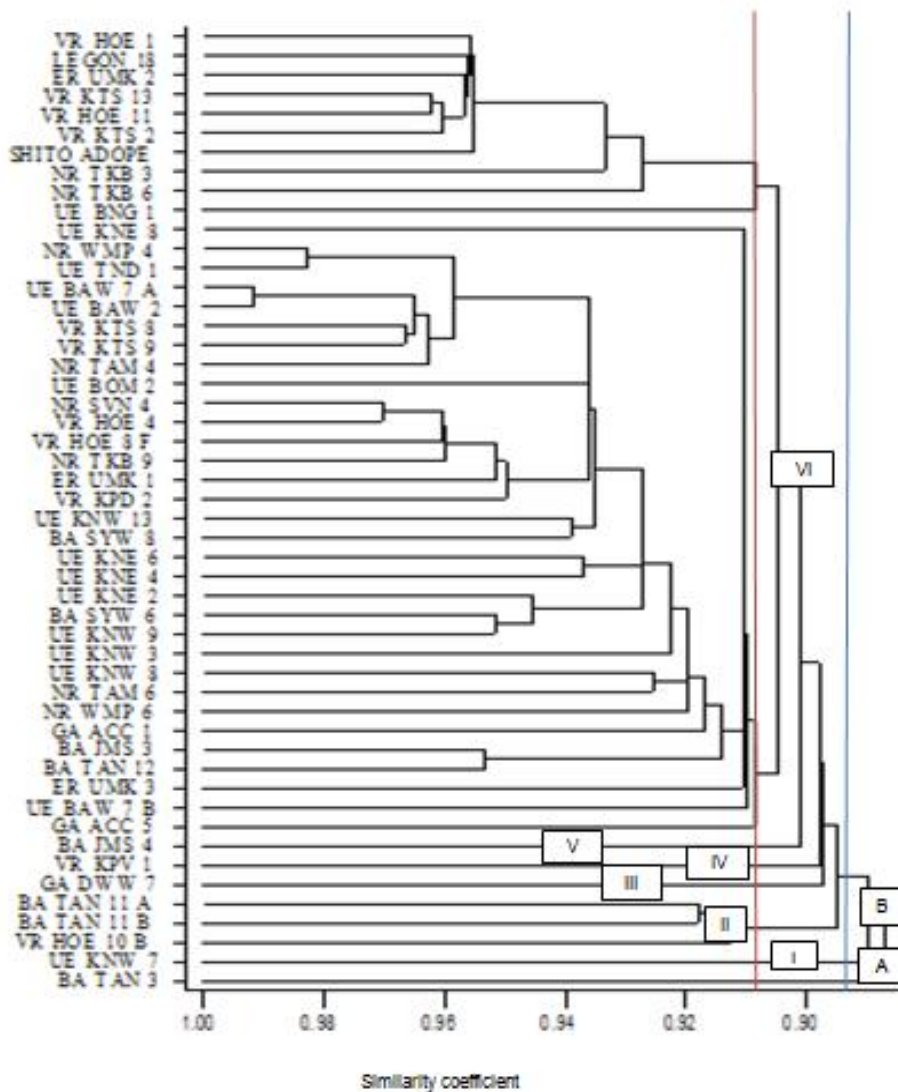


Fig. 3. Genetic relationships among 50 pepper accessions based on morphological traits using coefficient of euclidean, single-linked similarity matrix

**Table 7. Pearson correlation coefficient for 11 morphological traits evaluated among 50 pepper genotypes**

Traits	1	2	3	4	5	6	7	8	9	10	11	
Cot LL (cm)	1	-										
Cot LW (cm)	2	0.305*	-									
D50%Flo	3	-0.026NS	-0.123NS	-								
D50%Fr	4	-0.375**	0.181NS	-0.022NS	-							
F_Wt(g)	5	0.039NS	-0.094NS	0.024NS	-0.122NS	-						
Plt_Ht (cm)	6	0.086NS	0.108NS	0.419**	0.206NS	0.036NS	-					
St_Diam (cm)	7	-0.104NS	0.130NS	0.029NS	0.513***	-0.099NS	0.5081**	-				
Fr_Len (cm)	8	0.232NS	-0.160NS	-0.174NS	-0.473***	0.436**	0.0459	-0.207NS	-			
FrPd_Len (cm)	9	0.142NS	-0.113NS	0.256NS	-0.212NS	0.179NS	0.5298**	0.142NS	0.419**	-		
FrPd_Width (cm)	10	0.168NS	0.115NS	-0.221NS	-0.198NS	0.527***	-0.1339	-0.162NS	0.408**	0.073NS	-	
Fr_Width (cm)	11	-0.174NS	0.045NS	0.134NS	0.315*	0.710***	-0.006	0.089NS	-0.163NS	-0.159NS	0.215NS	-

\*, \*\*, \*\*\* = significant at  $P < 0.05$ ,  $P < 0.01$  and  $P < 0.001$  respectively, NS = not significant ( $P > 0.05$ ), Cot LL = Cotyledon leaf length (cm), Cot LW = Cotyledon leaf width (cm), D50%Flo = Days to 50% flowering, D50%Fr = Days to 50% fruiting, F\_Wt = Fruit weight (g), Plt\_Ht = Plant height (cm), St\_Diam = Stem diameter (cm), Fr\_Len = Fruit length (cm), FrPd\_Len = Fruit pedicel length (cm), FrPd\_Width = Fruit pedicel width (cm), Fr\_Width = Fruit width (cm)

**Table 8. Clustering of accessions based on morphological traits**

Cluster	Similarity coefficient	Accessions
A	0.88	BA TAN 3
B I	0.905	UE KNW 7
B II	0.905	VR HOE 10B, BA TAN 11A and BA TAN 11B
B III	0.905	GA DWW 7
B IV	0.905	VR KPV 1
B V	0.905	BA JMS 4
B VI	0.905	GA ACC 5, UE BAW 7B, ER UMK 3, BA TAN 12, BA JMS 3, GA ACC 1, NR WMP 6, NR TAM 6, UE KNW 8, UE KNW 3, UE KNW 9, BA SYW 6, UE KNE 2, UE KNE 4, UE KNE 6, BA SYW 8, UE KNW 13, VR KPD 2, ER UMK 1, NR TKB 9, VR HOE 8F, VR HOE 4, NR SVN 4, UE BOM 2, NR TAM 4, VR KTS 9, VR KTS 8, UE BAW 2, UE BAW 7A, UE TND 1, NR WMP 4, UE KNE 8, UE BNG 1, NR TKB 6, NR TKB 3, Shito Adope, VR KTS 2, VR HOE 11, VR KTS 13, ER UMK 2, Legon 18 and VR HOE 1

#### 4. CONCLUSION

The study revealed the existence of considerable variation among the germplasm accessions. Principal component analysis of both qualitative and quantitative traits revealed the most important agro-morphological traits which contributed more to the total genetic variance. Relevant traits accounting for this variation were plant height, stem diameter and fruit traits such as shape, colour, weight, length and width. Significant and positive associations were found among majority of the traits with fruit width and fruit weight as the highly correlated. The cluster analysis revealed VR HOE 1 and BA TAN 3 as the more diverse genotypes while UE BAW 7A and UE BAW 2 were closely related. Principal coordinate analysis revealed clustering of the accessions did not follow geographical origin of the accessions but on the morphological traits studied. The observed diversity can be used for improving desirable traits through selection and hybridization.

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#### COMPETING INTERESTS

Authors have declared that no competing interests exist.

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