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## KARYOTYPE ANALYSIS OF TEN ACCESSIONS OF HAUSA POTATO IN NIGERIA

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### ABSTRACT

Plant species may be classified according to their karyotype features. Variation in chromosome features is believed to have accompanied evolutionary divergence of many plant and animal species. The cytological characteristics of crop species vary with geographical location of plants. Knowledge of the karyotype relationships can be explored for effective genetic and breeding studies, especially in crops like the Hausa potato (*Solenostemon rotundifolius*) that have not received adequate research attention. This paper reports the results of the karyotype analysis of ten accessions of the Hausa potato cultivated in some parts of Nigeria. The accessions were raised in plastic bowls containing vermiculite soil, from which root-tips were harvested for slide preparation and karyotyping. The conventional squashing in aceto-orcein of root tissues after heating was used. The tissues were photographed under Nikon Universal Microscope, equipped with an MC 100 camera. The chromosomes were then measured under x400 magnification using a micrometer. Results showed that all the accessions were diploid with somatic chromosome number of  $2n = 2x = 64$ . The total length of long-arms ranged from 108.80  $\mu\text{m}$  in accession Pankshin to 118.14  $\mu\text{m}$  in accession NRCRI (1). The total length of short arms ranged from 81.88  $\mu\text{m}$  – 89.34  $\mu\text{m}$ . The total length of long plus short arms ranged from 199.88  $\mu\text{m}$  - 200.06  $\mu\text{m}$ . The mitotic phases varied with accessions. Similarly, the arm ratio, r-value, centromeric index, coefficient of variation, total form, intra-chromosomal index and inter-chromosomal index varied with the accessions. The accessions were grouped into four clusters: accessions Hong (1), Hong (2), Manchok and Gembu in cluster I; accessions Pankshin and Langtang in cluster II; accessions NRCRI (1) and NRCRI (2) in cluster III; accessions Bokkos (1) and Bokkos (2) in cluster IV. The principal component analysis showed that variation in the complement length and the centromeric position accounted for 99.997% of the total variation amongst the accessions. The study demonstrated that cytological differences exist in the Hausa potato. Some accessions showed close phylogenetic relationship, but others were distantly related. These differences could be explored for the improvement of the Hausa potato accessions cultivated in Nigeria.

**Key Words:** Centromeric index, *Solenostemon rotundifolius* (Poir) J.K. Morton

## RÉSUMÉ

Les espèces végétales peuvent être classées selon leurs caractéristiques de caryotype. On pense que la variation des caractéristiques chromosomiques a accompagné la divergence évolutive de nombreuses espèces végétales et animales. Les caractéristiques cytologiques des espèces cultivées varient selon la situation géographique des plantes. La connaissance des relations de caryotype peut être explorée pour des études génétiques et de sélection efficaces, en particulier dans des cultures comme la pomme de terre de Haoussa (*Solenostemon rotundifolius*) qui n'ont pas reçu une attention adéquate dans la recherche. Cet article présente les résultats de l'analyse du caryotype de dix accessions de la pomme de terre de Haoussa cultivée dans certaines régions du Nigéria. Les accessions ont été élevées dans des bols en plastique contenant de la terre de vermiculite, à partir desquels les extrémités des racines ont été récoltées pour la préparation des lames et le caryotypage. L'écrasement classique dans l'acéto-orcéine des tissus racinaires après chauffage a été utilisé. Les tissus ont été photographiés au microscope universel Nikon, équipé d'une caméra MC 100. Les chromosomes ont ensuite été mesurés sous un grossissement x400 en utilisant un micromètre. Les résultats ont montré que toutes les accessions étaient diploïdes avec un nombre de chromosomes somatiques de  $2n = 2x = 64$ . La longueur totale des bras longs variait de 108,80  $\mu\text{m}$  dans l'accession Pankshin à 118,14  $\mu\text{m}$  dans l'accession NRCRI (1). La longueur totale des bras courts variait de 81,88  $\mu\text{m}$  à 89,34  $\mu\text{m}$ . La longueur totale des bras longs et courts variait de 199,88  $\mu\text{m}$  à 200,06  $\mu\text{m}$ . Les phases mitotiques variaient avec les accessions. De même, le rapport de bras, la valeur r, l'indice centromérique, le coefficient de variation, la forme totale, l'indice intra-chromosomique et l'indice inter-chromosomique variaient avec les accessions. Les accessions ont été regroupées en quatre groupes: les accessions Hong (1), Hong (2), Manchok et Gembu dans le groupe I; accessions Pankshin et Langtang dans le groupe II; accessions NRCRI (1) et NRCRI (2) dans le groupe III; accessions Bokkos (1) et Bokkos (2) dans le groupe IV. L'analyse en composantes principales a montré que la variation de la longueur du complément et de la position centromérique représentait 99,997% de la variation totale entre les accessions. L'étude a démontré qu'il existe des différences cytologiques chez la pomme de terre de Haoussa. Certaines accessions ont montré une relation phylogénétique étroite, mais d'autres étaient liées de loin. Ces différences pourraient être explorées pour l'amélioration des accessions de pommes de terre de Haoussa cultivées au Nigéria.

*Mots Clés:* Index centrométrique, *Solenostemon rotundifolius* (Poir) J.K. Morton

## INTRODUCTION

Chromosome number is an important character used for evolutionary studies of plants, providing information about polyploidy and genome changes (Guerra, 2008; Louzada *et al.*, 2010). Data generated from such studies are a useful tool for systematic comparisons of geographic and taxonomic groups of plants (Peruzzi *et al.*, 2012). Karyotype analysis enhances understanding of phylogenetic relationships at different taxonomic levels.

In plant systematics, chromosome morphology and number are useful for the clarification of the origin and phylogenetic

relationships of plants. Stebbins' classification has been used to assess the karyotype asymmetry and to establish karyotype relationship between different taxa (Stebbins, 1971; Cai *et al.*, 2004; Pavlova and Tosheva, 2005; Eroglu *et al.*, 2013; Ozcan *et al.*, 2014). The centromere position and the relative chromosome length are the most important karyotypic features used to assess chromosomal affinities based on the concept of symmetry and asymmetry (Lavnica and Srivastava, 1992).

The Hausa potato [*Solenostemon rotundifolius* (Poir) J.K. Morton] is a tropical minor tuberous root crop ( $2n=2x=64$ ), with

distinctive fragrance, medicinal, nutritional and economic values (Nanema *et al.*, 2009). Species have been reported to have either metacentric or sub-metacentric chromosomes, which differ in length. Fujita (1970) reported variations in karyotype between and within plant species. Martin-Estra *et al.* (2011) reported the existence of intraspecific polyploidy within several species of the Lamiaceae family to which the Hausa potato belongs. The cytogenetic characteristics of crop species have been reported to vary with geographic location of the plants (Awe and Akpan, 2017). Most of the cultivated varieties of the Hausa potato in Nigeria are landraces held by smallholder farmers, which are yet to be scientifically characterised. These, like other plant species the world over, need to be continually documented and studied. There is the need for cytogenetic studies to establish the phylogenetic relationships of such species (Paknia and Karimzadeh, 2011; Onyutsetseg *et al.*, 2013; Awe and Akpan, 2017). Data generated from such studies could be used to characterise and improve the crop species. This paper reports the results of the karyotype analysis of ten accessions of the Hausa potato cultivated in some parts of Nigeria.

## MATERIALS AND METHODS

The seedlings were raised in the Biology Laboratory of the Department of Botany, Ahmadu Bello University, Zaria, Nigeria. The accessions used in this study were sourced from the germplasm collection of the National Root Crops Research Institute (NRCRI), Kuru and from some farmers in Manchok, Hong, Pankshin, Gembu, Langtang and Bokkos, spread across four states of Kaduna, Plateau, Adamawa and Taraba in Nigeria. These accessions include NRCRI (1), NRCRI (2), Manchok, Hong (1), Hong (2), Pankshin, Gembu, Langtang, Bokkos (1) and Bokkos (2). The agronomic characteristics of the accessions are shown in Table 1.

TABLE 1. Agronomic characteristics of accessions of the Hausa potato used in the study

| Accession  | Agronomic characteristics  |
|------------|--|
| Manchok    | A local farmer's accession with yellowish round tubers   |
| NRCRI(1)   | An improved variety with tubers which have white skin  |
| NRCRI(2)   | An improved variety with tubers which have black skin  |
| Hong (1)   | A local accession sourced from Hong in Adamawa State. It is tolerant to rot and dryness when kept for several months. It is also characterised by large and round tubers |
| Hong (2)   | It is tolerant to rot and dryness when kept for several months. It is characterised by large and longer tubers than Hong 1   |
| Pankshin   | It is characterised by large tubers, yellow skin, tolerance to rot and dryness when kept for several months  |
| Gembu      | It is characterised by yellow skin, early sprouting and large tubers and can also be cultivated under irrigation   |
| Langtang   | It is characterised by distinct traits, which include long tubers and dark spots around the sprouting region   |
| Bokkos (1) | It is characterised by dark, roundish tubers and early sprouting   |
| Bokkos (2) | It is characterised by dark, oblong tubers and early sprouting   |

Source: Egbaji, 2019

**Karyotype study.** Fresh root tips of 1-1.5 cm long were cut from rapidly growing seedlings (3-4 weeks after planting). The root tips were pre-treated with 0.5 g of Feulgen dissolved in 100 ml of distilled water at room temperature for 3 hr. The roots were washed with distilled water for 5 min at room temperature; thereafter, they were fixed in Carnoy's fixative (glacial acetic acid: ethanol, 3:1) overnight at room temperature (25 °C). After thorough washing with distilled water, 1N HCl was added using a dropper to hydrolyse the cells. The root tips were allowed to stand for 10 minutes to hydrolyse the cells. The HCl was removed from the Petri-dish using the dropper. The Petri-dish was then refilled with distilled water twice. A microscope slide was placed on a paper towel. Three drops of 2% aceto-orcein stain were placed in the centre of the slide. The root tip was transferred from the Petri-dish to the stain in the slide, using a pair of forceps, and was allowed to remain in the stain for 10-15 minutes to pick up the stain.

Triplicates of well-spread metaphase plates in terms of clarity and organisation, from different individuals, were processed and analysed for each accession. The best metaphase plates were photographed using an external camera (Celestron digital microscope imager 2.0) attached to the BX50 Olympus microscope, and scanned at 100-resolution. All measurements were recorded using the Software Image J (Abramoff *et al.*, 2004). Chromosome morphology was described using nomenclatures proposed by Levan *et al.* (1964). Numerical characterisation was carried out on the following parameters:

The arm ratio (AR) was computed as the ratio of long arm length of a chromosome pair to the short arm length of the chromosome pair using the formula:

$$AR = \frac{L}{S} \dots\dots\dots \text{Equation 1}$$

Where:

L = Long arm length of chromosome; and S= Short arm length of chromosome

The total chromosome length (TL) of each pair was calculated using the formula:

$$TL = L+S \dots\dots\dots \text{Equation 2}$$

Where:

L = Long arm length; and S = Short arm length

The ratio of the shortest arm chromosome length to the longest arm chromosome length (r-value) was computed using the formula:

$$r\text{-value} = \frac{S}{L} \dots\dots\dots \text{Equation 3}$$

Where:

S = Short arm length of chromosome; and L= Long arm length of chromosome

The total form percentage (% TF) was computed as the ratio of the summation of short arm length to the summation of long arm length and multiplied by one hundred (100) using the formula:

$$\%TF = \frac{\sum s}{\sum L} \times 100 \dots\dots\dots \text{Equation 4}$$

Where:

L = Long arm length of chromosomes; and S= Short arm length of chromosomes

The values of Dispersion Index (DI) of a given karyotype were estimated from the following equation:

$$CG = \frac{SX}{TLX} \times 100 \dots\dots\dots \text{Equation 5}$$

Where:

CG = Centromeric gradient; Sx = Length of median short arm; and Lx= Total length of median chromosome

$$CV = \frac{SD}{\bar{X}} \times 100 \dots\dots\dots \text{Equation 6}$$

Where:

SD = Standard deviation, X = Mean chromosome length; and CV = Coefficient of variation for chromosome length; DI = Proportionate measure of CG with respect to CV.

Karyotype asymmetry was estimated using two numerical parameters according to the method of Romero-Zarco (1986) as follows:

$$\sum_{i=1}^n \frac{Sx}{Lx} \dots\dots\dots \text{Equation 7}$$

$$A_1 = \frac{\dots\dots\dots}{n}$$

Where:

Sx = Mean length of the short arm of each pair of homologues; and LX = Mean length of long arm of each chromosome

n = Number of homologues (n = 32)

A<sub>1</sub> = Intrachromosomal index

$$A_2 = \frac{S}{X} \dots\dots\dots \text{Equation 8}$$

Where:

S = Standard deviation,  
 X = Mean chromosome length; and  
 = A<sub>2</sub> = Interchromosomal index

**Statistical analysis.** The data collected were subjected to the one-way analysis of variance (ANOVA) test, using the Statistical Analysis

System (SAS), version 9.2 software. Means were compared using the least significant difference (L.S.D) test at 5% level of probability.

Cluster analysis was used to determine the relative closeness of one accession to the other so that all the accessions in the populations could be arranged in specific groups according to Peters and Martineli (1985). Cluster analysis was performed using the Cophenetic Coefficient (CP). Principal component analysis (PCA) was carried out to differentiate the studied populations based on the karyotype parameters. Dendrogram and principal component analysis (PCA) were analysed using the Unweighted Pair Group Method with Arithmetic Mean (UPGMA) software.

**RESULTS**

The short arm length varied from 1.285 µm in accession NRCRI (1) to 1.431 µm in the accession Pankshin (Table 2); but did not differ significantly among the ten accessions used in the study (Table 2). The total length was statistically similar in all the accessions of the Hausa potato studied (Table 2). The arm ratio varied from 1.189 µm in the accession Pankshin to 1.438 µm in the accession NRCRI (1) (Table 2).

The r-value varied from 0.695 µm in accession NRCRI (1) to 1.844 µm in accession Hong (1). The r-value did not also differ significantly (P>0.05) among the accessions of the Hausa potato studied (Table 2).

The coefficient of variation (CV) varied from 14.00% in the accession NRCRI (1), to 32.50% in the accession Hong (2) (Table 3). The total form percentage of the Hausa potato accessions used in this study varied from 40.9% in the accession NRCRI (1) to 45.5% in the accession Pankshin (Table 3).

The highest disparity index of 50.8% was observed in accession Hong (2), followed by accessions Langtang (50.2%), Hong (1) (49.8%), Bokkos (2) (48.7%), Manchok

TABLE 2. Chromosomal characteristics of some Hausa potato accessions

| Accession  | Short arm length (S) ( $\mu\text{m}$ ) | Long arm length (L) ( $\mu\text{m}$ ) | Total length (L+S) ( $\mu\text{m}$ ) | Arm ratio (L/S) ( $\mu\text{m}$ ) | R-value (S/L) ( $\mu\text{m}$ ) | Centromeric index (S/L+S) ( $\mu\text{m}$ ) |
|------------|--|---------------------------------------|--------------------------------------|-----------------------------------|---------------------------------|---|
| Manchok    | 1.362 $\pm$ 0.122                      | 1.811 $\pm$ 0.146                     | 3.173 $\pm$ 1.589                    | 1.330 $\pm$ 0.174                 | 0.752 $\pm$ 0.094               | 0.429 $\pm$ 0.054                           |
| NRCRI (1)  | 1.285 $\pm$ 0.115                      | 1.848 $\pm$ 0.189                     | 3.133 $\pm$ 1.567                    | 1.438 $\pm$ 0.180                 | 0.695 $\pm$ 0.087               | 0.410 $\pm$ 0.051                           |
| NRCRI (2)  | 1.359 $\pm$ 0.178                      | 1.771 $\pm$ 0.207                     | 3.130 $\pm$ 1.565                    | 1.303 $\pm$ 0.163                 | 0.767 $\pm$ 0.096               | 0.434 $\pm$ 0.054                           |
| Hong (1)   | 1.387 $\pm$ 0.056                      | 1.728 $\pm$ 0.118                     | 3.115 $\pm$ 1.558                    | 1.250 $\pm$ 0.156                 | 0.803 $\pm$ 0.100               | 0.445 $\pm$ 0.056                           |
| Hong (2)   | 1.398 $\pm$ 0.071                      | 1.729 $\pm$ 0.117                     | 3.127 $\pm$ 1.564                    | 1.236 $\pm$ 0.155                 | 0.809 $\pm$ 0.101               | 0.447 $\pm$ 0.056                           |
| Pankshin   | 1.431 $\pm$ 0.134                      | 1.702 $\pm$ 0.150                     | 3.133 $\pm$ 1.567                    | 1.189 $\pm$ 0.149                 | 0.841 $\pm$ 0.105               | 0.457 $\pm$ 0.057                           |
| Gembu      | 1.367 $\pm$ 0.193                      | 1.733 $\pm$ 0.022                     | 3.100 $\pm$ 1.546                    | 1.270 $\pm$ 0.158                 | 0.790 $\pm$ 0.099               | 0.441 $\pm$ 0.055                           |
| Langtang   | 1.373 $\pm$ 0.101                      | 1.753 $\pm$ 0.155                     | 3.126 $\pm$ 1.563                    | 1.275 $\pm$ 0.160                 | 0.783 $\pm$ 0.098               | 0.439 $\pm$ 0.055                           |
| Bokkos (1) | 1.375 $\pm$ 0.137                      | 1.754 $\pm$ 0.151                     | 3.129 $\pm$ 1.565                    | 1.276 $\pm$ 0.159                 | 0.784 $\pm$ 0.098               | 0.439 $\pm$ 0.055                           |
| Bokkos (2) | 1.366 $\pm$ 0.381                      | 1.758 $\pm$ 0.050                     | 3.124 $\pm$ 0.562                    | 1.290 $\pm$ 0.161                 | 0.777 $\pm$ 0.098               | 0.437 $\pm$ 0.055                           |
| LSD(0.05)  | 0.361                                  | 0.462                                 |                                      |                                   |                                 |   |
| CV (%)     | 25.274                                 | 25.335                                |                                      |                                   |                                 |   |

TABLE 3. Haploid karyotype parameters measured in ten accessions of the Hausa potato cultivated in some parts of Nigeria

|            | CV    | TF (%) | DI (%) | A <sub>1</sub> | A <sub>2</sub> | KF        |
|------------|-------|--------|--------|----------------|----------------|-----------|
| Manchok    | 14.5  | 42.1   | 47.8   | 0.022          | 0.039          | 28M + 4Sm |
| NRCRI (1)  | 14.5  | 40.9   | 39     | 0.021          | 0.046          | 25M + 7Sm |
| NRCRI (2)  | 14    | 43.5   | 42     | 0.024          | 0.06           | 29M + 3Sm |
| Hong (1)   | 30    | 44.7   | 49.8   | 0.025          | 0.029          | 32M       |
| Hong (2)   | 32.5  | 44.6   | 50.8   | 0.025          | 0.029          | 32M       |
| Pankshin   | 21.5  | 45.6   | 47.7   | 0.026          | 0.05           | 32M       |
| Gembu      | 21.8  | 43.5   | 45.7   | 0.024          | 0.065          | 30M + 2Sm |
| Langtang   | 25.59 | 43.9   | 50.2   | 0.025          | 0.039          | 30M + 2Sm |
| Bokkos (1) | 26.59 | 43.9   | 45.6   | 0.025          | 0.023          | 26M + 6Sm |
| Bokkos (2) | 28.9  | 43.9   | 48.7   | 0.024          | 0.047          | 30M + 2Sm |

CV = Coefficient of variations; TF = Total form; DI = Disparity index; A<sub>1</sub> = Intrachromosomal index; A<sub>2</sub> = Interchromosomal index; KF = Karyotype formula

(47.8%), Pankshin (47.7%), Gembu (45.7%), Bokkos (1) (45.6%) and NRCRI (2) (42.0%). The lowest disparity index of 39.0% was observed in the accession NRCRI (1) (Table 3).

The intrachromosomal index ranged from 0.021 in accession NRCRI (1) to 0.026 in

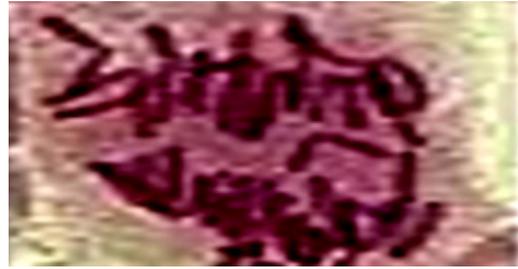
accession Pankshin. The interchromosomal index was highest (0.065) in accession Gembu and lowest (0.023) in accession Bokkos (1) (Table 3). The chromosomes were observed to be either metacentric or sub-metacentric (Fig. 1; Plate 1).



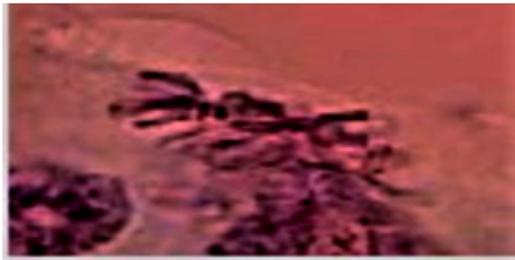
Figure 1. Ideograms of somatic cells of some Hausa potato accessions.



Manchok



NRCRI (1)



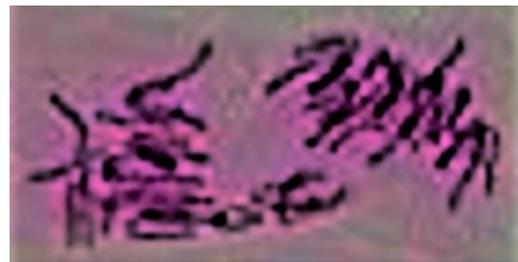
NRCRI (2)



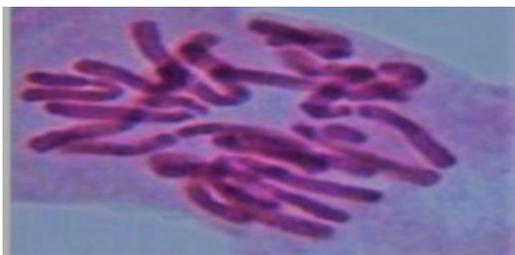
Hong (1)



Hong (2)



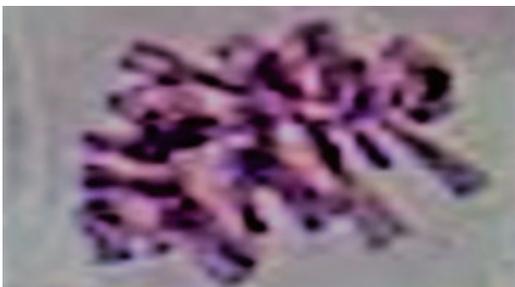
Pankshin



Gembu



Lantang



Bokkos (1)



Bokkos (2)

Plate 1. Somatic cells of ten accessions of the Hausa potato.

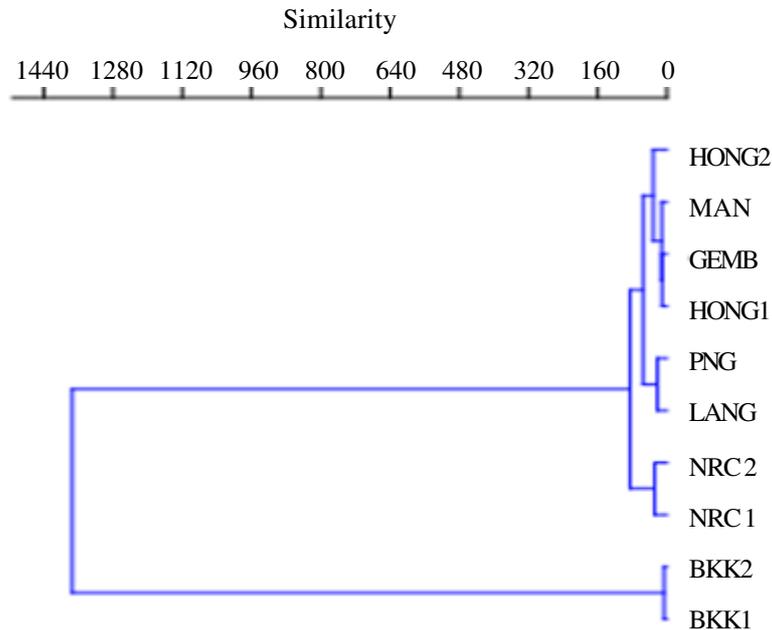


Figure 2. Dendrogram showing the phylogenetic relationship amongst ten accessions of the Hausa potato (constructed based on the Ward's method which is the matrix of karyotype distances) Cophenetic Correlation Coefficient (CP) = 0.462959403104521. Key: HONG2 = Hong (2), Man = Manchok, Gemb = Gembu, HONG1 = Hong (1), PNG = Pankshin, Lang = Langtang, NRC 2 = NRCRI (2), NRC 1 = NRCRI (1), Bkk2 = Bokkos (2), Bkk1 = Bokkos (1).

In accession Manchok, twenty-eight chromosomes were metacentric; while four were sub-metacentric (28M+4Sm). In the accession NRCRI (1), twenty-five chromosomes were metacentric; while seven were sub-metacentric (25M+7Sm). In accession NRCRI (2), twenty-nine chromosomes were metacentric; while three were sub-metacentric (29M+3Sm). In accessions Hong (1), Hong (2), Pankshin and Bokkos (2) all the thirty-two chromosomes were metacentric (32M). In accessions Gembu and Langtang, thirty chromosomes were metacentric; while two were sub-metacentric (30M+2Sm). In accession Bokkos (1), twenty-six chromosomes were metacentric while six were sub-metacentric (26M+6Sm) (Table 3).

The phylogenetic relationships among the accessions were assessed using the cluster analysis. Grouping was based on the Euclidean distance co-efficient, using the Pearson's correlation. The accessions were grouped into

four clusters. Cluster I consisted of four accessions (Hong (2), Manchok, Gembu and Hong (1)); cluster II consisted of two accessions (Pankshin and Langtang); cluster III consisted of two accessions (NRCRI (1) and NRCRI (2)), while cluster IV consisted of two accessions (Bokkos (1) and Bokkos (2)) (Fig. 2).

The principal component analysis (PCA) based on karyotype parameters, showed that the first two components ( $PC_1$  and  $PC_2$ ) accounted for 99.997% of the total variation, and these were projected in two dimensional graphic (Fig. 3).

## DISCUSSION

The basic chromosome number of  $2n = 2x = 64$  as was reported by Nkansah (2004) was confirmed in this study. The chromosomes were observed to be metacentric and sub-metacentric (Fig. 1; Plate 1). Variations in

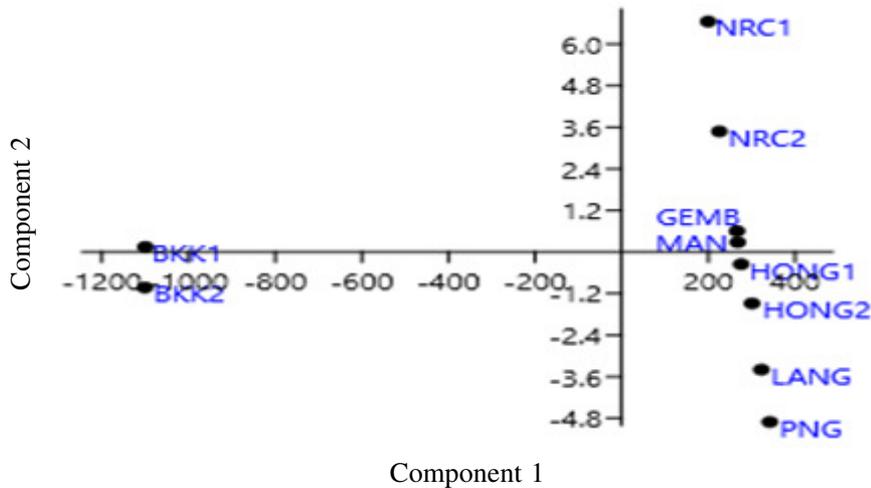


Figure 3. Diagrammatic result of principal component analysis of ten accessions of the Hausa potato grown in Jos NRC1 = NRCRI (1), NRC2 = NRCRI (2), GEMB = Gembu, MAN = Manchok, HONG1 = Hong (1), HONG2 = Hong (2), LANG = Langtang, PNG = Pankshin, BKK1 = Bokkos (1), BKK2 = Bokkos (2).

chromosome structure among the accessions were observed, as has also been reported for many plant groups (Maffei *et al.*, 1999). Six karyotype classes were observed in the accessions studied. All the chromosomes in accessions Hong (1), Hong (2) and Pankshin were metacentric (32M).

Differences in the karyotype parameters among members of the same species, as observed in this study, have been reported to be due to the differences in relative length of haploid complement of chromosomes, arm ratio, centromeric index and chromosome type (Awe and Akpan, 2017). These differences may be due to chromosomal re-arrangements such as translocation, deletion or inversion (Mukherje and Ray, 2012). The karyotype can also be changed through inter-specific hybridisation or mutations in the natural populations (Awe and Akpan, 2017). Structural alteration of chromosomes is believed to result in the evolution of races, while the constancy of the karyotype within the population suggests adaptability to the micro-environmental condition to which they are subjected (Awe and Akpan, 2017). Differences in the

karyotype formula (asymmetric karyotype) may be due to different geographic locations, suggesting that the genus *Solenostemon* has evolved into many different strains in different locations overtime (Awe and Akpan, 2017).

The coefficient of variation, total form (%TF) and disparity index varied with the accessions (Table 3). The CV % estimated for the homology of chromosome arms, spread over populations is used to determine the extent of variation among populations. Generally, the karyotypes of the populations in this study had either metacentric (centromere at median region) or sub-metacentric chromosome types. In other words, three populations were metacentric (32M), followed by 30M+2Sm (3 populations), 29M+3Sm (one population), 28M+4Sm (one population), 26M+6Sm (one population) and 25M+7Sm (one population).

The disparity index (DI) has been reported as a useful tool to differentiate quantitatively and closely related karyotypes belonging to the same clan of symmetry (Lavania and Srivastava, 1992). The high values of DI observed in this study suggests high levels of

karyotype differentiation. The intrachromosomal index ( $A_1$ ) and interchromosomal index ( $A_2$ ) showed slight variations among Hausa potato accessions studied. Variations in long and short arm lengths within and between populations form the basis of morphological variations among different accessions of the Hausa potato observed in this study. These variations could be used to determine the slight differences among populations (Romero-Zarco, 1986).

The results of cluster analysis showed that the accessions belonged to four clusters (Fig. 2). Some clusters were closely related, others were distantly related, suggesting genotypic or environmental differences.

In developing a crop improvement programme, a cross between distantly related accessions could result in a high degree of heterosis (hybrid vigour) in the first filial generation ( $F_1$ ) and subsequent generations. Ghaderi *et al.* (1984) suggested that parents that are distantly related have the contrasting alleles at different loci, which recombine in  $F_2$  and  $F_3$  generations following crosses between the distantly related parents. Such crosses and recombinations provide opportunities for effective selection and crop improvement. Consequently, accessions in cluster I in this study could be crossed with those in cluster III; while those in cluster II could be crossed with those in cluster IV.

Principal component analysis was used to determine the variation in distance among the accessions studied. The principal components,  $PCA_1$  and  $PCA_2$ , which were extracted from the original karyotype data, had a latent root greater than 1, and accounted for 99.997% of the total variation among the accessions studied. Characters with high absolute values within the first principal component are believed to influence clustering more than those with lower absolute values (Chahal and Gosal, 2002). In this study, the differentiation of the accessions into clusters might have resulted from a large contribution of a few characters (centromere position and

complement length), rather than small contributions of many characters. The arrangement of the accessions based on PCA conformed to the result of the cluster analysis. Differences in the karyotype formula and asymmetric indices found among the Hausa potato accessions, suggest that structural changes might have contributed to the diversification of the accessions studied.

Generally, crop improvement techniques such as selection and hybridisation depend, to a large extent, on the existence of variability. Genetic diversity or variations that relate to karyotype forms have been employed as a useful tool in assessing the crop improvement potentials of some crops (Bakshi *et al.*, 2004; Dhamavanthi, 2005; Oyama *et al.*, 2006).

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