# Phenotypical characterization of cassava (*Manihot Esculenta* Crantz) accessions in Cameroon's mono-modal rainforest zone

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*Abstract— One hundred and five (105) accessions of cassava collected in the South West and Littoral Cameroon regions were evaluated on a morphological and epidemiological basis. The objective was to study the phenotypic diversity of accessions and its structure based on variables selected among the cassava (Manihot esculentaCrantz) descriptors. Descriptive analysis showed significant phenotypic differences for the traits. Principal component analysis confirmed this important morphological variability. The hierarchical ascending classification made it possible to structure the accessions into 6 and 4 groups. In Ekona, group I consists of accessions with high incidence (IN = 54.03 ± 20.41), group II contains high height (H = 2.01 ± 0.41m), group IV consists of accessions with high severity (SE = 40.44 ± 11.68), petiole length (LP = 39.66 ± 0.03), lobe length (LL = 19.00 ± 0.2 cm) and lobe number (NL = 7.66 ± 0.2).In Njombé, group I consists of accessions with a high incidence (IN = 59.31 ± 20.38), lobe length (LL = 18.08 ± 1.00 cm) and considerable lobe number (NL = 7.44 ± 0.2). These groups offer a wide range of broodstock choices for the creation of improved cassava varieties with interesting potential and adapted to these agro-ecological zones.*

*Keywords— **Manihot esculenta, Accession, Cameroon, cassava, morphological diversity.***

## I. INTRODUCTION

Cameroon is a country whose economy remains heavily dependent on its agricultural sector, which employs nearly 68% of the working population and accounts for a significant share of its GDP and about 15% of public budget resources. Cassava (*Manihot esculenta* Crantz) is a staple food crop and contributes to food security in Cameroon. World cassava production is estimated at more than 268.28 Mt. In Cameroon, national production is estimated at 5.83Mt [1]. Its importance is

attested not only by the enthusiasm of the population for its cultivation but also by the diversity of its use in both food and industry. Local and improved varieties of cassava are cultivated in all the agro-ecological zones of the country as combined crops or often as pure crops, depending on the objectives set by the farmer [2]. The ease of cultivation of this plant, its adaptability to different soil types and its tolerance to drought have contributed to the expansion of its cultivation [3]. This plant is cultivated for its starchy tubers, which provide food for more than 500

million people worldwide, particularly in tropical countries [4]. World production is estimated at more than 268.28 Mt. In Cameroon, national production is estimated at 5.83Mt [1]. Despite these somewhat laudatory figures, much remains to be done due to the fact that the phenotypic diversity of the cassava varieties grown in Cameroon is poorly known and therefore little valued on the one hand, and on the other hand due to the susceptibility of cassava to diseases and pests. It is very important to have a perfect knowledge of the phenotypic diversity of cassava accessions in some production areas in Cameroon.

The exploitation of this genetic diversity is of particular importance for maintaining and improving the productivity of this species in developing crops. Numerous procedures have been developed to quantify and analyses the existing genetic diversity. Any varietal improvement programme requires more and more information about the structuring and spatial distribution of the diversity to be conserved. This goes through the process of characterization in order to determine the real varietal potential. Phenotypic identification has already been used in genotypic and taxonomic classification [5]. In the absence of molecular markers, the use of morphological descriptors remains the most widely used method to study variety diversity. Farmers' varieties, the basis of ex situ collections, are recognized as reservoirs of genes useful for the improvement of the plants used [6]. A good knowledge of the forms of this traditional varietal diversity is necessary because it constitutes the reservoir of genetic variability. The analysis of morphological descriptors makes it possible to reveal the diversity as it is perceived and selected by local farmers and the main stakeholders in the management of varietal diversity [7]. It is the most practical approach for phenotypic differentiation provided it is combined with a statistical tool that estimates the variation related to the experimental environment [8]. Morphological descriptors have made it possible to describe and classify thousands of forms in maize ([9]; [10]; [11]; [12]; [13]. The existence of significant variability for most agro-morphological traits in Cameroon

has been demonstrated on several crops such as *Dioscoreadumetorum* [14]. The study of the diversity of these genetic resources is essential to create new varieties with interesting characteristics, adapted to climatic variations and resistant to diseases. The objective of this study is to assess the morphological diversity of 105 cassava accessions originating from several localities in the South-West and Littoral regions of Cameroon. The production of roots and tubers, especially cassava, is hampered by various constraints. In Cameroon, diseases and pests are among the main constraints to production. The most common diseases of cassava are: cassava mosaic, bacterial blight, anthracnose, bud necrosis and root rot, brown streak disease. In the south-western regions (Ekona) people tend to attribute less importance to cassava cultivation due to the unsuitability of the varieties present to the climatic conditions.

## II.     MATERIEL AND METHODS

### 2.1. Study sites

The study took place in 2014/2015 and 2015/2016 in the stations of the Agricultural Research Institutes for Development (IRAD) of Njombé and Ekona respectively and had the following characteristics: Ekona is 16 km from Buea and 10 km from Muyuka on the No8 Buea-Kumba road axis in Cameroon with an altitude of 400 m and covers an area of 55,000 km2. The IRAD station is located at 06° 30' 00 latitude N and 08° 30' 00 longitude East.

Njombé is located 80 km from Douala, the economic capital of Cameroon with an altitude of 80 m; latitude 4° 35' North and 9° 39' East. The climate is equatorial-Guinean, with relative humidity between 32 and 100 percent and an average of 72 percent. The average rainfall is 2086 mm with approximately 161 rainy days per year. Temperatures vary between 22.1 and 32.2°C with an average of 27.1°C. The relief is a plain, the slope is between 0 and 16%, the soil is volcanic, brown and eutrophic.
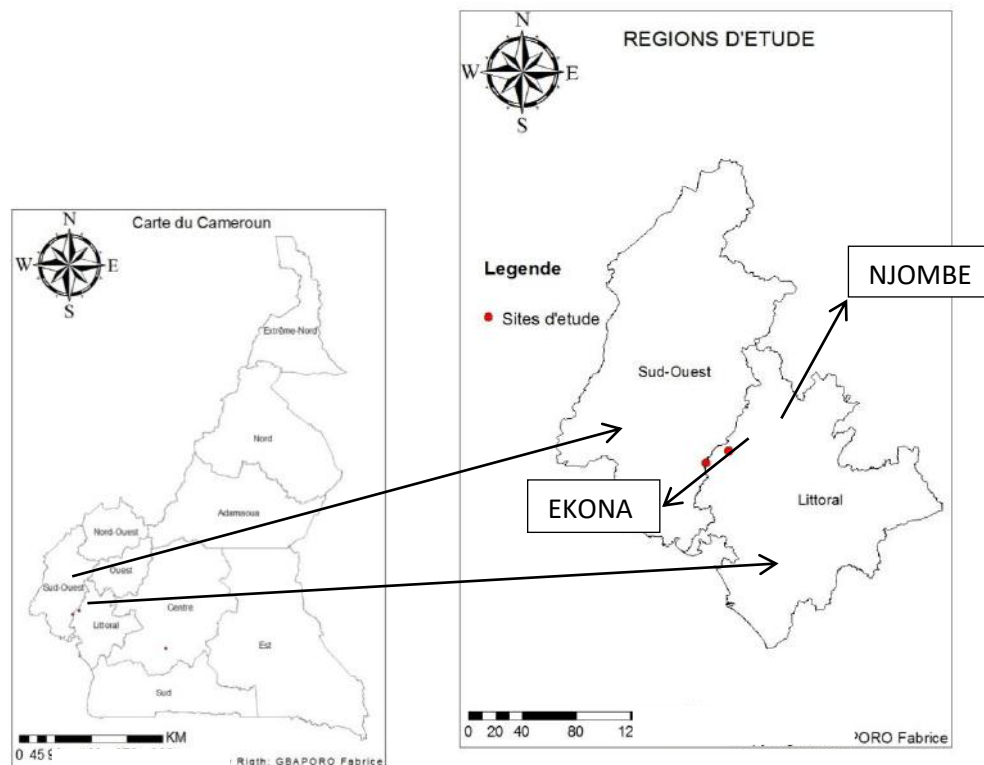
*Fig. 1. Sites of study*

## 2.2. Experimental design

The experimental design was non-statistical and consisted of a block in which the varieties were arranged in rows with 30 plants per row per variety. The distance between lines was 1 m and the distance between bunches in the same line was 0.50 m. The sowing was carried out with a 20 cm cutting with 6 knots per bunch. Regular weeding was carried out during the vegetative phase of the crop.

## 2.3. Data collection

Measurements were made on all 30 plants per variety. Five characteristics selected from the descriptors of cassava (Manusset) were retained. These were plant height (H), number of lobes (NL), length of lobe (LL), length of petiole (LP), color of petiole (CP), number of branches (NR) and two epidermal indices namely incidence (IN) and severity (SE).

## 2.4. Statistical analysis

Multivariate analysis : The principal component analyses were done using SPAD V55 software. The phylogenetic tree was constructed using the R software and the Ward D method was used to calculate the Euclidean distance. The SAS V9 software for the ANONA.

## III. RESULTS AND DISCUSSION

### 3.1. Results

### 3.1.1. Descriptive analysis of morphological characteristics

Descriptive statistics revealed a wide variation in morphological traits (LL, LP, RA, LL, NL) among cassava varieties.

The mean, minimum, maximum values of the morphological variables are grouped in Table I and II. In Ekona, large differences between minima and maxima were observed for important morphological traits such as petiole length (LP), lobe length (LL), branching (RA) and very large differences between maxima and minima of the epidemiological variables. On average, accessions have a severity of $36.18 \pm 16.1$; an incidence of $66.12 \pm 3.02$; a petiole length of $32.42 \pm 8.59$ and a lobe length of $18.07 \pm 2.40$ (Table 1).

At Njombé, large differences are also observed between minima and maxima for morphological traits such as lobe number (NL), lobe length (LL), petiole length (LP) and very large differences between minima and maxima in epidermal indices. On average, a severity of $29.59 \pm 17.44$; incidence of $49.81 \pm 11.61$; petiole length of $20.32 \pm 6.94$; LL ($15.44 \pm 3.16$) (Table 2).

*Table 1. Minimum, maximum, mean values of morphological characteristics and two Ekona epidermal indices.*

| Variable wording | Minimum | Maximum | Mean± standard deviation |
|---|---|---|---|
| SE | 0.000 | 60.000 | 36.18 ± 16.1 |
| IN | 0.000 | 100.000 | 66.12 ±3.02 |
| LP | 19,000 | 48.000 | 32.4 ± 8.59 |
| LL | 14.000 | 23.000 | 18.07±2.4 |
| NL | 6.000 | 9.000 | 7.47 ± 0.73 |
| RA | 0.000 | 4.000 | 2.73 ± 0.78 |
| H | 0.800 | 2.42 | 1.71 ±0.36 |

SE: severity; IN: incidence; LP: petiole length; LL: lobe length; NL: number of lobes; RA: branching; H: height.

*Table 2. Minimum, maximum, mean values of morphological characteristics and two epidermal indices of Njombé.*

| Variable wording | Minimum | Maximum | Mean± standard deviation |
|---|---|---|---|
| SE | 0.000 | 80.000 | 29.59 ± 17.44 |
| IN | 0.000 | 100.000 | 49.81 ±5.02 |
| LP | 3.000 | 37.000 | 20.32 ± 6.94 |
| LL | 9.000 | 26.000 | 15.44±3.16 |
| NL | 3.000 | 9.000 | 6.01 ± 1.52 |
| RA | 0.000 | 4.000 | 2.51 ± 1.52 |
| H | 1.100 | 3.400 | 2.26 ±0.58 |

SE: severity; IN: incidence; LP: petiole length; LL: lobe length; NL: number of lobes; RA: branching; H: height.

**3**

**.1.2. Structuring morphological diversity**

The correlation matrix of the different characteristics studied are reported in Tables 3 and 4. Significant correlations (≥ 0.50) were obtained between several pairs of variables. The correlation coefficient index greater than 6 for specific pairs of traits indicates that there is a statistically acceptable factorial solution. We observe positive and perfect correlations between severity and incidence ($r = 0.70$), between lobe length and petiole length ($r = 0.80$) and between petiole length and number of lobes ($r = 0.62$) (Table 3). Similarly, in Ekona correlations were observed between height and severity ($r = 0.79$), incidence and severity ($r = 0.79$), height and incidence ($r = 0.68$) and length and number of lobes ($r = 0.62$) (Table 4)

*Table 3. Correlation matrix between the variables measured in the Njombé collection*

|  | SE | IN | H | LL | LP | RA | NL |
|---|---|---|---|---|---|---|---|
| SE | 1,00 | | | | | | |
| IN | **0,70***  | 1,00 | | | | | |
| H | 0,09 | -0,09 | 1,00 | | | | |
| LL | 0,14 | 0,26 | 0,10 | 1,00 | | | |
| LP | 0,26 | 0,28 | 0,17 | **0,80*** | 1,00 | | |
| RA | -0,15 | -0,06 | -0,13 | -0,12 | -0,22 | 1,00 | |
| NL | 0,22 | 0,20 | 0,14 | 0,53 | **0,62*** | -0,24 | 1,00 |

SE: severity; IN: incidence; LP: petiole length; LL: lobe length; NL: number of lobes; RA: branching; H: height; * significant correlation

*Table 4. Correlation matrix between the variables measured in the Ekonacollection*

|        | SE     | IN     | H      | LP     | LL     | NL     | RA   |
|--------|--------|--------|--------|--------|--------|--------|------|
| SE     | 1,00   |        |        |        |        |        |      |
| IN     | **0,79*** | 1,00   |        |        |        |        |      |
| H      | **0,79*** | **0,68*** | 1,00   |        |        |        |      |
| LP     | 0,41   | 0,28   | 0,51   | 1,00   |        |        |      |
| LL     | 0,01   | -0,04  | -0,05  | 0,58   | 1,00   |        |      |
| NL     | 0,45   | 0,32   | 0,26   | **0,62*** | 0,35   | 1,00   |      |
| RA     | 0,31   | 0,55   | 0,43   | 0,06   | -0,09  | -0,06  | 1,00 |

SE: severity; IN: incidence; LP: petiole length; LL: lobe length; NL: number of lobes; RA: branching; H: height; * significant correlation

### 3.1.3. Principal Component Analysis

Tables 5 provide an estimate of the variability represented by each axis. Two (02) axes with an eigenvalue greater than 1 were obtained at Ekona and three (03) were obtained at Njombé. These axes explain 72.40% and 74.37% of the variance present in the variables in Ekona and Njombé respectively. The variance accumulation test confirms that these different axes are relevant and will be used to describe the total variability of the accessions.

In Ekona, the first axis describes 46.96% of the variation. This component is defined by severity (SE), incidence (IN), height (H) and petiole length (LP). The second component (axis 2) describes 25.44% of the variable. It is defined by petiole length and lobe length. All these variables are negatively correlated to the axes (Fig.2).
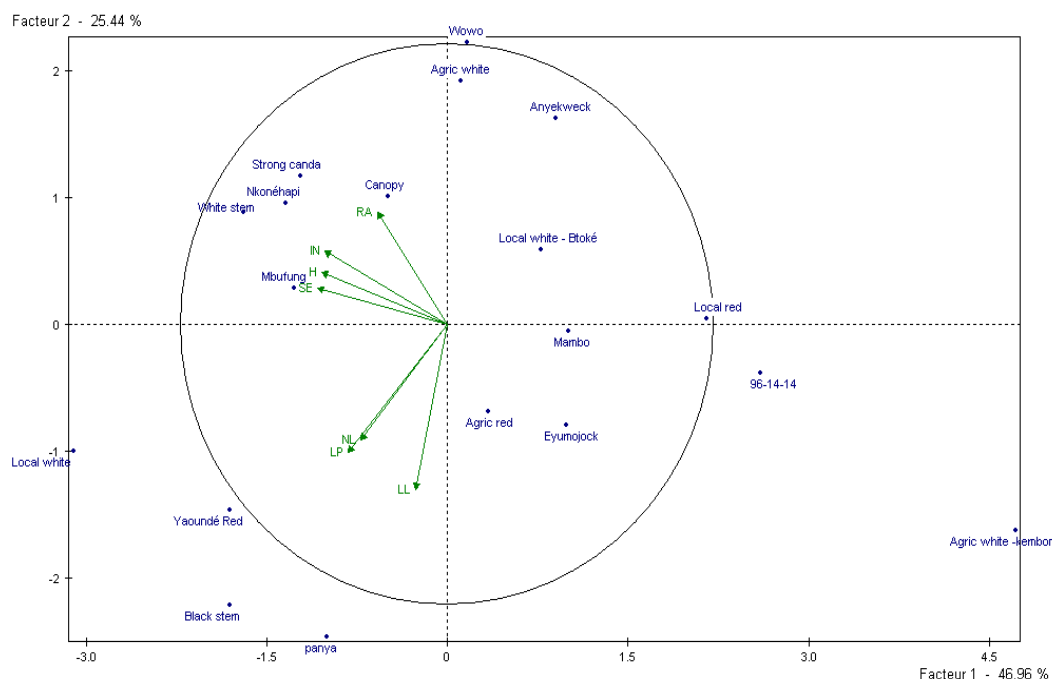


*Fig.2. Distribution of variables on axes 1 and 2 of the main component*

In Njombé, axis 1 describes 39.20 % of the total variable, it is defined by the number of lobe (NL), the length of the lobe (LL), the length of the petiole (LP). Axis 2 describes 20.19% of the total variable and is defined by severity (SE) and incidence (IN). The third component describes 14.97% of the variable and is defined by plant height (H) and number of branches (NR). All of these variables are negatively correlated to the axes except for the third component where branching is positively correlated to axis 3 (Fig. 3).
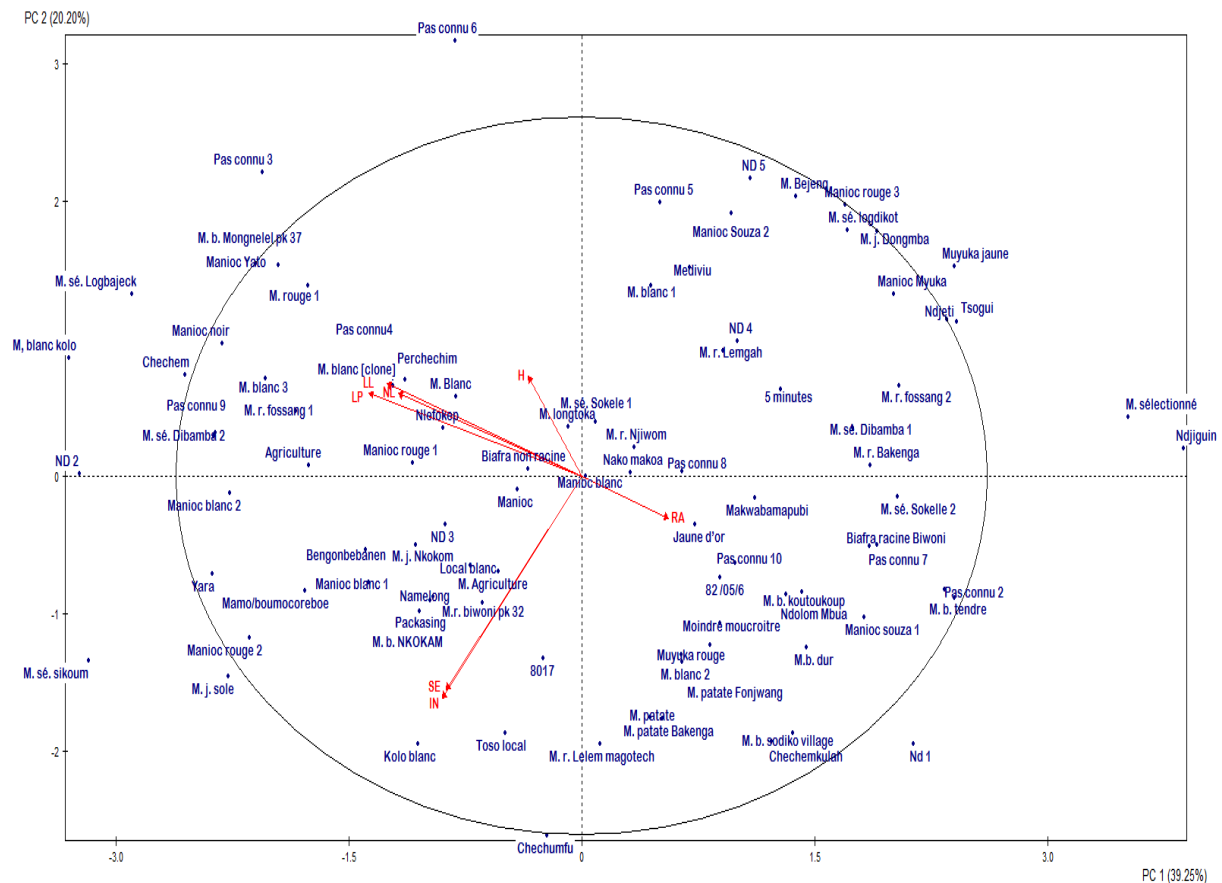
*Fig.3. Distribution of variables on axes 1 and 2 of the main component*

*Table V. Own vectors and percentage of variation expressed by the axes from the characteristics analysed in Ekona and Njombé*

| Main components | Ekona | | Djombe | | |
|---|---|---|---|---|---|
| | Axe1 | Axe 2 | Axe 1 | Axe 2 | Axe 3 |
| 0wn variance | 3.287 | 1.7807 | 2.7441 | 1.413 | 1.047 |
| Total variance | 46.96 | 25.44 | 39.2 | 20.19 | 14.97 |
| Cumulative variance | 46.96 | 72.4 | 39.2 | 59.4 | 74.37 |
| SE | **-0.88**[*] | 0.17 | -0.55 | **-0.71**[*] | -0.24 |
| IN | **-0.84**[*] | 0.35 | -0.57 | **-0.73**[*] | 0.04 |
| H | **-0.85**[*] | 0.25 | -0.22 | 0.33 | **-0.68**[*] |
| LP | **-0.68**[*] | **-0.61**[*] | **-0.79**[*] | 0.31 | -0.33 |
| LL | -0.22 | **-0.78**[*] | **-0.87**[*] | 0.28 | 0.18 |
| NL | -0.59 | 0.55 | 0.35 | -0.14 | **0.61**[*] |
| NR | -0.47 | 0.53 | **-0.75**[*] | 0.28 | 0.06 |

**3.1.4. Diversity Analysis by Ascending Hierarchical Classification**

The dendrograms obtained show a clear separation of accessions and structure the diversity into four (4) groups in Ekona and six (6) groups in njombé (Fig.1 and 2 respectively).
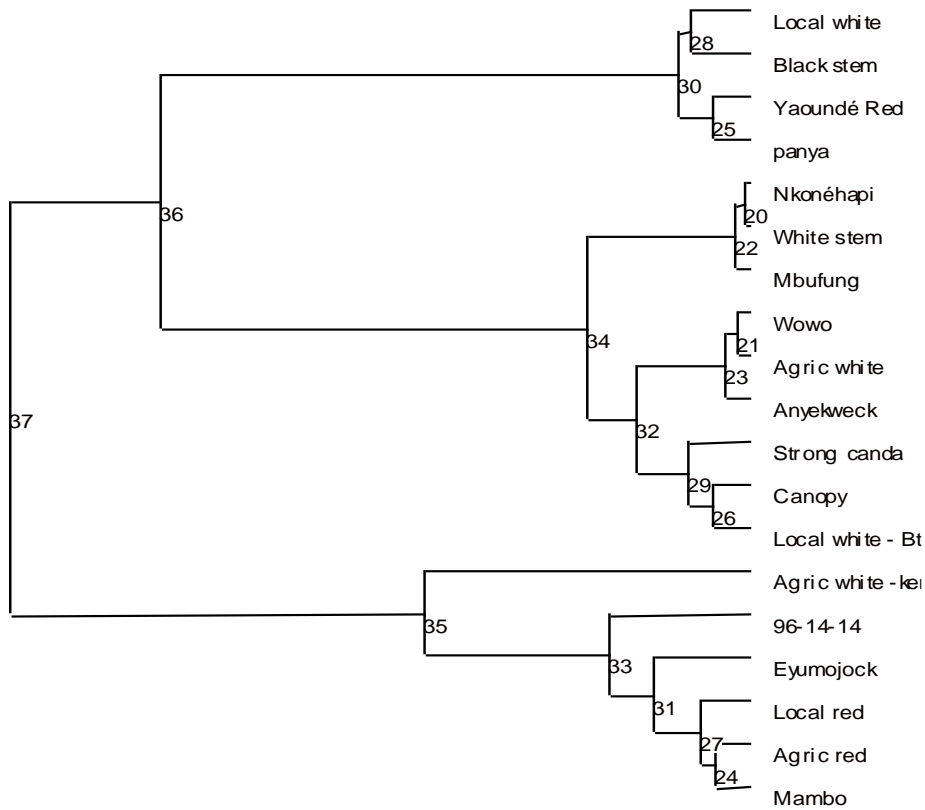


*Fig.4.Ascending hierarchical classification (AHC) of the 19 cassava accessions according to the aggregation criterion of weighted averages*
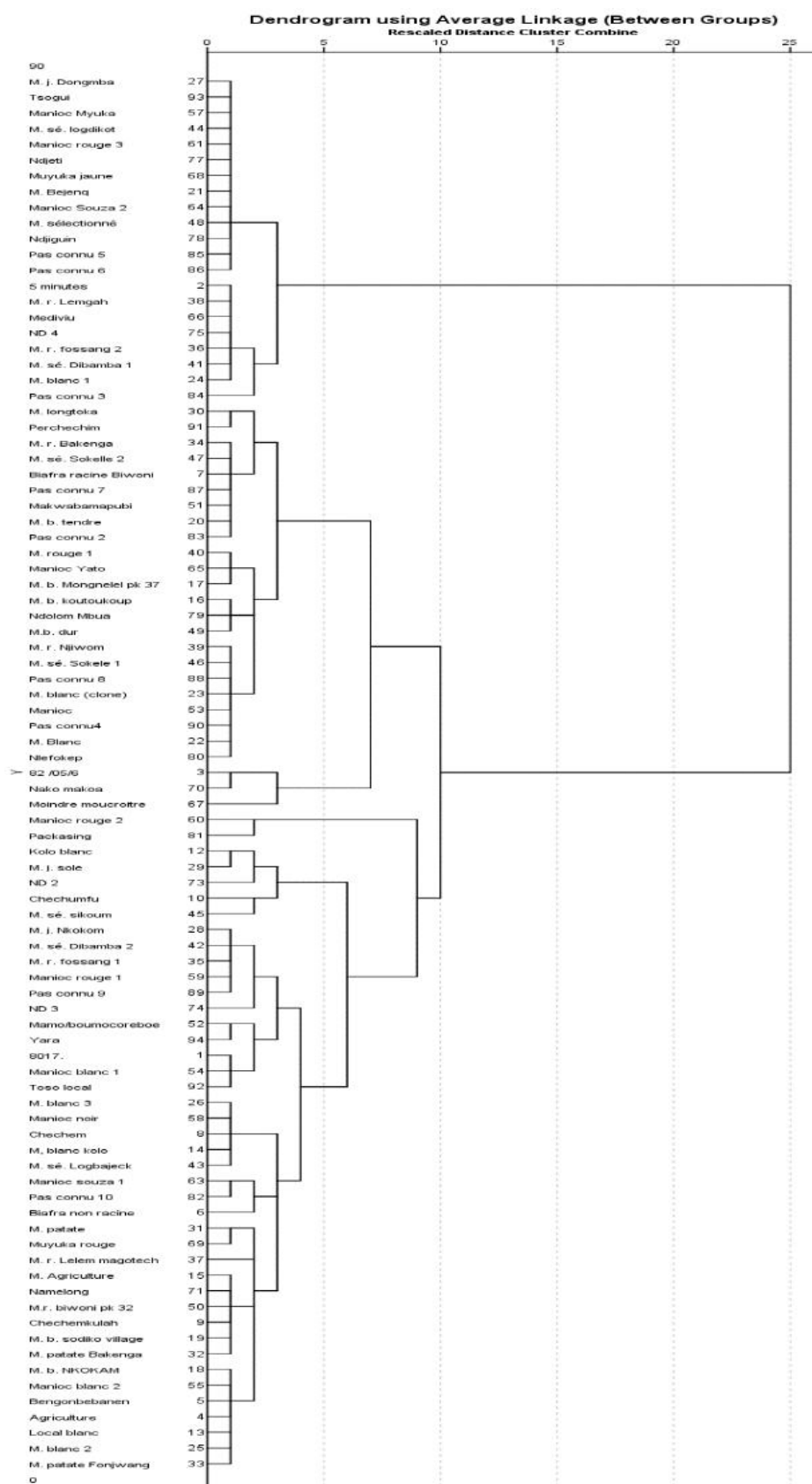
*Fig.5: Ascending hierarchical classification (AHC) of the 96 cassava accessions according to the aggregation criterion of weighted averages*

### 3.14.1. Cluster obtained from AHC

The family tree divides the varieties into several groups. In Ekona, group I consists of accessions with high incidence (IN = 54.03 ± 20.41), group II contains accessions with high height (H = 2.01 ± 0.41m), group IV consists of accessions with high severity (SE = 40.44 ± 11.68), petiole length (LP = 39.66 ± 0.03), lobe length (LL = 19.00 ± 0.2) and lobe number (NL = 7.66 ± 0.2). Whereas in Njombé,

group I consists of accessions with a high incidence (IN = 59.31 ± 20.38), lobe length (LL = 18.08 ± 1.00) and considerable lobe number (NL = 7.44 ± 0.2). Group II consists of the significantly branched accessions (RA = 5,22 ± 0,2). Group V consists of the high height accessions (H = 2.28 ± 0.60) and Group VI consists of the high severity accessions (41.30 ± 12.53) (Tables 6 and 7).

*Table 6: Main characteristics of the different groups formed by CAH at Ekona*

| Variables | GI | GII | GIII | GIV |
|---|---|---|---|---|
| SE | 35.8 ± 12.63 | 00 ± 00 | 22 ± 5.7 | 40.44 ± 11.68 |
| IN | 54.03 ± 20.41 | 00 ± 00 | 20.03 ±6.17 | 49.84 ± 17.49 |
| H | 1.71± 0.34 | 2.01± 0.41 | 1.85 ± 0.37 | 1.70 ± 0.30 |
| LP | 32.27 ± 1.04 | 27.5 ± 0.06 | 21.2 ± 0.02 | 39.66 ± 0.03 |
| LL | 17.74 ± 0.4 | 16.5 ± 0.05 | 12.50 ± 0.01 | 19.00 ± 0.22 |
| NL | 7.45 ± 0.3 | 7.00 ± 0.01 | 6.5 ± 0.11 | 7.66 ± 0.2 |

*Table 7: Main characteristics of the different groups formed by CAH at Njombe*

| Variables | GI | GII | GIII | GIV | GV | GVI |
|---|---|---|---|---|---|---|
| SE | 32.91±9.89 | 24.41± 5.62 | 39.08±17.83 | 23.30±7.19 | 37.47±15.98 | **41.30±12.53** |
| IN | **59.31±20.38** | 20.58±6.73 | 21.65±8.85 | 37.65±10.99 | 57.66±22.01 | 42.38±11.1 |
| H | 2.26±0.52 | 1.98±0.33 | 2.01±0.50 | 2.15±0.25 | **2.28±0.60** | 2.20±0.58 |
| LL | **18.08±1.00** | 16.07±1.02 | 12.5±0.22 | 14.53±0.1 | 17.94±0.03 | 13.75±0.34 |
| NL | **7.44±0.2** | 6.55±0.01 | 5.5±0.04 | 4.70±0.01 | 6.4±0.15 | 6.5±0.01 |
| RA | 4.71±0,23 | **5.22±0.2** | 2.5±0.2 | 3.34±0.02 | 2.4±0.01 | 1.00±0.00 |

### 3.1.4.2. Number of varieties obtained per Clusters

The percentage of each group is high in group I (58.89%) followed by group IV (21.05%) and relatively low at around 10.52% for groups II and III of the Ekona varieties,

while in Njombé 40.89% was recorded in group I followed by 24.41% and 25.58% for groups II and IV respectively. Small numbers were obtained in groups III, V and VI with values of 3.48%, 5.81% and 2.32% (Table 8).

*Table VIII. Percentage distribution of genotype groups (clusters) according to sites*

| Ekona | GI | GII | GIII | GIV |
|---|---|---|---|---|
| Effective (%) | 57.89 | 10.52 | 10.52 | 21.05 |

| Njombé | GI | GII | GIII | GIV | GV | GVI |
|---|---|---|---|---|---|---|
| Effective (%) | 40.69 | 24.41 | 3.48 | 25.58 | 5.81 | 2.32 |

## IV.    DISCUSSION

Principal Component Analysis (PCA) is a statistical method commonly used in population genetics to identify structure in the distribution of genetic variables, across geographic location and ethnic knowledge [15]. The aim is to assess the importance of each variable in the relationship to the total variable between genotypes. This

method offers possibilities to exclude the less important traits in each study group and simultaneously retain the most salient traits to clarify diversity [16].

Knowledge of genetic variability is essential in varietal selection. Highlighting this genetic variability is the first essential step in the description of genetic resources [17].

In this study, lobe length, lobe number, branching, height, incidence and severity are the traits or variables.

The analysis of the agro-morphological diversity of local accessions of cassava grown in certain regions of Cameroon revealed significant differences between the traits analysed, indicating strong phenotypic heterogeneity among the 105 accessions. This morphological and epidermal diversity was structured into 04 groups in Ekona and 06 groups in Njombé.

These different groups taken separately have distinctive and similar characteristics such as plant height, number of lobes, severity and incidence. These results are similar to those of [18].Who, however, was working on maize accessions. This structuring of morphological diversity shows that in cassava, morphological differentiation is most often based on agronomic traits ([8]; [19].).

Peasant phenotypic selection based on perceptible traits could explain the contribution of these variables to structuring variability. According to [20]., vegetative characteristics such as plant height and number of branches are the main characteristics used by farmers to identify varieties. In addition to these characteristics, the epidemiological factor also plays an important role in structuring morphological diversity. The evaluation of the genetic diversity of the germplasm is not only necessary but also constitutes a prerequisite in the hybridization programme and helps to promote the efficiency of the genetic variables used ([20]; [21]. To promote the efficiency of a crop, it is important to obtain information on genetic diversity and kinship through correlations between the variables highlighted. This is because the assessment of genetic diversity is essential not only for crop improvement but also for stewardship and germplasm conservation. In this study, the focus on incidence and severity will now enable us to control varieties that are resistant and susceptible to the flagship cassava disease, which is the mosaic in the different zones investigated in Cameroon.

## V.    CONCLUSION

Preliminary results on the diversity and morphological structuring of cassava in the single-mode rainforest zone of Cameroon clearly show that there is a high phenotypic diversity within cassava cultivars, via the descriptors used. Several distinct groups have been identified and each group has clear traits of specificity for which it differs from the others. The accessions analysed show variation for all the traits used, especially those related to phenology and architecture (branching). The accessions are grouped according to their geographical origin. This genetic variability observed between the

groups resulting from the hierarchical classification indicates that those with interesting characteristics such as mosaic resistance, a large number of lobes will serve as a source of broodstock in programmes aimed at improving cassava productivity. However, it is important to combine morphological characteristics with molecular techniques, such as microsatellites, to better characterize accessions within the different groups.

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