IOSR Journal of Agriculture and Veterinary Science (IOSR-JAVS)
e-ISSN: 2319-2380, p-ISSN: 2319-2372. Volume 11, Issue 11 Ver. II (November 2018), PP 01-07
www.iosrjournals.org

Morphoagronomic Evaluation And Clustering Analysis In cassava (*ManihotEsculenta* Crantz) Varieties In The Agro-Ecological Conditions of Malanje In Angola.

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Date of Submission: 17-11-2018 Date of acceptance: 03-12-2018

I. Introduction

The cassava (*Manihot Esculenta* Crantz), it constitutes the only species of the gender *Manihot*, as a consequence of their roots rich tuberoses in carbohydrates that are transformed in several products in several countries of the world [3]. However, that is not the only cassava species used by the man, it increases the same author.

The cassava is a plant that possesses great accommodation the climatic and pedologic conditions, it plants perennial, that for besides being a source of human feeding, it is for decrease of the costs of the rations, however great part of his/her stem is left in the plowings (field) and the other, it is taken advantage for the other agricultural time as it happens in Angola [14]. The cultivation of the cassava in Africa remounts to the year of 1558 was destined exclusively to provide food to the ships that transported slaves, even about the years 1600 [10].

During the centuries XVI and XVII, happened the introduction of the cassava in Angola, becoming one of the main alimentary cultures of their inhabitants' great importance. The production of the cassava didn't meet great progressive development up to 1975, as a subsistence culture, because, it is considered like this by many, strongly neglectful of the national politics of agricultural development, receiving biotechnological studies and in genetic improvement, however, it is less known than the remaining of the great alimentary cultures. Although the documentation is scarce, something one find described in historical and cinematographic documents.

For Ferrão[9], it defends that the cassava when arriving in Africa, went first by São Tome, after its recognition as alimentary culture, today capable to substitute the cereals, even in manufacture of the bread and beer, it was verified its diffusion quickly by everybody tropical, could be admitted that it will have been one of the first plants of American origin to be introduced in Africa, after the discoveries.

In accordance with Jones [10], the Portuguese travelers introduced the cassava in the basin of the river Congo in 1558, spreading quickly for the bordering territories. The cassava was just imported for Madagascar by the Portuguese exploiters and Arabs in the century XVIII. Opinion also accepts for researcher [2].

Carter [4], mentioning Fernando Pó, he affirms that the first introductions will have happened for the following order: Bioko in Equatorial Guinea, San Tome and Prince, Saws Lioness and in the Angolan coast between Luanda and the river Zaire. For Jones [10], the culture of the cassava arrived in Africa Central, later, in the century XIX, having been incorporate with success in several cultivation systems.

However, Rossel and Thottapilly[18], they defend that the first cultivation of the cassava in Africa Central happened in 1611. It is verified as soon as, still today, there is no agreement among the several researchers as for the origin and diffusion of the cassava in African territory.

However, starting from the Angolan backs the cassava penetrated deeply for Africa Headquarters' heart, ever since playing an important part in the history of the agriculture of these societies, [13].

The cassava constitutes a food of capital importance in the human feeding in Angola, mainly in the North area and East, for they be the areas where concentrate the largest productions of the culture on the country, consuming their roots and leaves.

To distinguish a germplasm, basically is, to identify and to describe differences among varieties. Therefore, differentdescriptorsare used in this work, standing out the morphologic ones and agronomics. Independently of the describers used in the evaluations, the results should make possible the distinction of the varieties, to identify copies and varieties with relevant characteristics and of interest to the several improvement programs and development in the culture of the cassava, as resistance to the diseases and some curses, production potential, among other [6].

In the largest of the alternatives, it takes place a previous characterization and evaluation, using morphoagronomic descriptors, because, besides making possible the regeneration of the genetic material, the experiments are of reduced cost and most of these healthy descriptors of easy evaluation when compared with molecular data. However, each describer has its importance, being possible that the germplasm bank is studied seeking to give support to the investigation and the database of the collection thoroughly [15].

Evaluating and characterizing the varieties of the Angolan cassava, it is believed that can influence in the improvement of the system of production of the culture, in the political and technical decisions addressed to the improvement of the agricultural sector (of the cassava in matter) and of the atmosphere, contributing to the improvement of the social conditions, creation of new sources of collection of incomes for the State, tends in view the economic diversification, benefitting the farmers and the final consumers.

Besides, it is possible through the data of characterization of the accesses to accomplish analyses multivariate, which will allow that it is dear the genetic divergence among the accesses of the germplasm bank. To enhance that, this study makes possible that it is known the available germplasm better, in the sense of facilitating the conservation work, however, the very close accesses genetically are possible be discarded, reducing the size of BAG, besides making possible to choose the most important characters for they be used in the characterization of accesses.

The present study had as objective evaluates the characteristics morphoagronomicsof 40 cassava varieties in the Experimental Station of the Company of Foods of Malanje, with base in methods multivariate, in order to they be used in programs of fomentation of the cultivation of the cassava in Angola.

II. Materials And Methods

The study was conducted in the experimental field of Malanje Food Company for two consecutive crops (2015/16 and 2017/18). Forty cassava genotypes provided by the germplasm of the Agronomic Investigation Institute (AII) of Malanje Agricultural Experimental Station, and by Institute of Agrarian Development(IAD) of Cuanza Norte and Uíge, were assessed. These provinces are located at latitude 8^o 49' South and longitude 13^o 13' eastern, altitude 368m [11]and cover a total area of 8,960 m^2. ThefortygenotypeswereWaticamana, Maria dia Pedro, Hoto, Mata Capim, Kambaxi, Paco Vermelho, Tio Jojo, Verdinha, MukotowaNguandi (Pé de perdiz), Paco Branco, Munenga, Kimbanda, Suzi, Jaca Branca, Jaca Vermelho, Kalazula, Ngana Rico 1 (Uíge), TMS3, Banana, Rio Dange, Cassendi, Vermute, Guita, Chico Diakombe, TMS 4025 (Early in Angola), Kalami, Baco, Katenda, Malanje, Ngana Rico 2 (Malanje), Kalawenda, Gonçalo, Mundele Paco, Suingue, NganaYuculu, Muringa, Kinzela, Mpelo, GuetiandKapumba.

The local soil was classified as fersialitic[8]. According to the classification by [12], the climate in the assessed region is humid subtropical and annual mean temperature reaches 26°C – thermal amplitude 14°C, relative humidity between 80% and 85%, mean annual rainfall well distributed between 1000 and 1200mm.

The study followed a completely randomized block design with four repetitions. Each plot encompassed five rows of 10 plants, thus totalizing 50 plants per plot. Each row was 10m long, spaced 0.90m from each other and 0.90m between plants. The experiment used an area of approximately one hectare and assessed 160 plots, in total.

The soil was prepared through conventional procedure with plowing and harrowing before sowing. The soil was fertilized with 350 kg ha^{-1} of the formula 12-24-12. Cover fertilizer was performed six months later with 250 kg/ha^{-1} of NPK (16-8-12). Sowing was mechanically performed with an 80HP tractor and counted on healthy stakes of the 40 cassava genotypes. The tractor was coupled to a two-row cassava planter (bazuca 1), 13.5cm long stakes were used and horizontally arranged in 0.10m deep grooves.

Stakes were irrigated before cultivation for five minutes with an 80% Maconzebe (1Kg) and 80% Fipronil (1Kg), Boron (1L), Manganese (1L) solution in 15000L/water. Culture managements were performed

based on recommendations for the culture. The manual control method with hoes was applied to control weeds in different culture-development phases and stages. Herbicides such as Capizade and Flumioxazinewere used at planting in order to avoid weeds during the initial growth of cassava plants.

Cuts were performed in December 02, 2016 and in February 21, 2018. All plants in the five rows of each plot were harvested. The number of braches (NB) resulted from the ratio between the sum of the number of sprouts in the stem cutting and the respective number of plants subjected to evaluation; plant height (PH in cm) was calculated from ground level until the most distal tip; stem diameter (SD in cm) was measured with a caliper 10cm from ground level; internode distance (ID in cm) was found by measuring the distances between knots in plant stems; height of the first branch (HFB) was measured from ground level until the first branch; number of roots (NR) was found through the ratio between the number of roots in the stem cuttings and the respective number of plants subjected to evaluation; root diameter (RD in cm) was measured from the diameter of ten roots randomly sampled in each experimental plot; root length (RL in cm) was found by measuring the length of ten randomly sampled roots in each experimental plot; shoot yield (SY in Kg) was recorded by weighing the shoot of all useful plants in the experimental plots; and root yield (RY in Kg) measured by weighing the roots of all useful plants in the experimental plots.

Harvests were conducted through mechanized method and preceded by plant cutting after the vegetative cycle of the culture. Harvest was performed with tuber crops harvester (P9000) coupled to the tractor.

The data obtained in the field, they were submitted to the variance analysis, for the selection of the quantitative descriptors it was performedfor the grouping analysis with the job of the distance of standardized medium Mahalanobis, once the varieties are established without obeying it's any experimental outline[7]. This analysis involved all of the characters and it was executed with base in the average of the taken measures of each descriptor, starting from the correlation head office, being used the procedure PRINCOMP of the SAS ones, version 9.0 [19]and the program computational GENES.

Dissimilarity dendrogram based on the distance of Mahalanobis and the grouping method UPGMA the program Statistical 7.1 was used [21].

For genetic diversity, the analysis of Singh was accomplished [20], the minimum values, maximum, average, standard deviation, variation coefficient, normality test and coefficients of correlation of Pearson in the quantitative descriptors, used in the software SAS [19].

III. Results

Analyzing the descriptive statistics Table 1, the width of the variation coefficients (CV), it varied from 16,21% to 80,87 % to the variables related to the medium diameter of roots and medium production of roots, respectively.

It is possible to observe that the largest variations happened in the variables plant height (PH) (113,82 to 325,65), presenting an average of 193,87; shoot yield (SY) (4,00 to 146,00), with average of 32,26; root yield (RY)(5,50 to 128,00), that it presented an average of 18,91 and height of the first branch (HFB)(12,54 to 113,03), with an average of 46,68(Table 1).

Table 1. Values minimum, maximum, average, standard deviation, variation coefficient and normality test for the quantitative variables, in the which follows the order: number of braches (NB), plant height (PH), stem diameter (SD), internode distance (ID), height of the first branch (HFB),number of roots (NR),root diameter (RD), root length (RL), shoot yield (SY), root yield (RY).

Variables	Minimum	Maximum	Average	Standard deviation	CV (%)	Normality test
NB	1,29	6,86	2,35	0,71	30,46	0,85**
PH	113,82	325,65	193,87	40,89	21,11	0.98*
SD	4,45	19,58	8,98	2,71	30,19	0,98*
ID	5,41	12,25	8,33	1,35	16,21	0,98*
HFB	12,54	113,03	46,68	16,13	34,55	0,92**
NR	0,54	7,65	2,63	1,29	49,24	0,94**
RD	9,70	35,20	21,94	3,69	16,82	0,97*
RL	15,20	62,60	30,44	7,00	23,01	0,91**
SY	4,00	146,00	32,26	26,09	80,87	0,94**
RY	5,50	128,00	46,02	24,51	53,25	0,93**

** e * significant difference at 1% and 5% probability, respectively, by the Shapiro-Wilks

In compensation, the smallest variations were detected for the number of roots (NR) (0,54 to 7,65), with an average of 2,63; number of braches (NB)(1,29 to 6,86) presenting an average of 2,35; internode distance (ID)(5,41 to 12,25), with an average of 8,33root diameter (RD) (9,70 to 35,20), presenting an average of 21,94; root length (RL) (15,20 to 62,60), with an average of 30,44 (Table 1).

In relation to the standard deviation, it was verified values of 40,89 for the plant height (PH), 26,09 shoot yield (SY), 24,51 root yield (RY) indicating that these were the variables that more presented dispersion in relation to the average while to the number of braches (NB) and the number of roots (NR) with respective values of 0,71 and 1,29, they were the variables that presented smaller variations in relation to the average (Table 1).

In agreement with the descriptive statistics, for the test of normality of Shapiro-Wilk, significant to 5% of probability (Table 1), it is known that the variables don't follow normal distribution, for that, the correlation of Pearson was used (Table 2).

Most of the correlations was no significant and positive, to the exception of the correlations among the number of braches (NB) with the stem diameter (SD), the medium number of braches (NB) with height of the first branch (HFB), plant height (PH) with , stem diameter (SD), plant height (PH) with internode distance (ID), later, among the plant height (PH) and height of the first branch (HFB) and finally, among stem diameter (SD) with internode distance (ID) that were significant and positive (Table 2).

It was noticed that of the significant and positive correlations just one is high, in other words, among the number of roots (NR) with the root yield (RY) they obtained a value of 0.71 *. Also high positive correlations were observed among the stem diameter (SD) with the root diameter (RD), later among the root diameter (RD) with the root yield (RY). Therefore, those that presented high significant and negative correlations were, among the height of the first branch (HFB) with the root length (RL) and for end among the stem diameter (SD) with the root length (RL), (Table 2).

Table 2. Coefficient of correlation of Pearson for the quantitative variables, in the which follows the order: number of braches (NB), plant height (PH), stem diameter (SD), internode distance (ID), height of the first branch (HFB),number of roots (NR),root diameter (RD), root length (RL), shoot yield (SY), root yield (RY).

NB	PH	SD	ID	HFB	NR	RD	RL	SY	RY
NB	-0.03^{ns}	0.26**	-0.03^{ns}	0.27**	-0.05^{ns}	0.11^{ns}	-0.04^{ns}	-0.04^{ns}	0.01^{ns}
PH		0.55**	0.64**	0.45**	-0.03^{ns}	0.07^{ns}	0.02^{ns}	0.06^{ns}	0.03^{ns}
SD			0.35**	-0.06^{ns}	0.12^{ns}	0.17*	0.03^{ns}	0.03^{ns}	0.08^{ns}
ID				0.11^{ns}	-0.06^{ns}	-0.12^{ns}	-0.15*	0.11^{ns}	0.03^{ns}
HFB					-0.05^{ns}	0.07^{ns}	0.10^{ns}	-0.05^{ns}	-0.08^{ns}
NR						0.11^{ns}	0.03^{ns}	0.05^{ns}	0.71*
RD							-0.16*	0.05^{ns}	0.16*
RL								-0.01^{ns}	-0.04^{ns}
SY									0.12^{ns}

* * and * significant to 1% and 5%, respectively, for the test t ns no significant to 5% of significant.

Leaning on in the coefficient of diversity of Singh [20], we noticed that the variable root yield (RY) presented as the character of larger importance among the ten appraised descriptors, for presenting the largest contribution percentage as for the genetic divergence (16,31%) being responsible for the largest percentage of all variability of the data (Table 3). the characteristic that less it contributed to the diversity was the stem diameter (SD).

Table 3. Relative contribution of the characters for diversity according to Singh (1981).

Descriptors	**S.j**	**S.j (%)**
Number of braches	276,10	5,95
Plant height	611,24	13,17
Stem diameter	232,17	5,00
Internode distance	373,47	8,05
Height of the first branch	428,07	9,22
Number of roots	489,55	10,55
Root diameter	556,18	11,98
Root length	478,16	10,30
Shoot yield	440,34	9,49
Root yield	757,01	16,31

With base in the 10 descriptors, seeking to study the behavior of 40 cassava varieties was obtained a dendrogram through the hierarchical method UPGMA (Figura1), submitted the a cut point based on the grouping analysis suggested by the method proposed by the package NbClust of the program computational R [5], where it was used five groups formed the Table 4 accordingly. Among the five different groups formed in

the 10 quantitative descriptorswas verified that the number that presented larger proportion among the five proposals was it of a group.

As criterion for definition of the number optimumof groups the index was used Pseudo-T^2, with this, it was possible the formation of 5 groups for the method UPGMA for all of the evaluation methodologies and analyses of groupings used (Table 4).

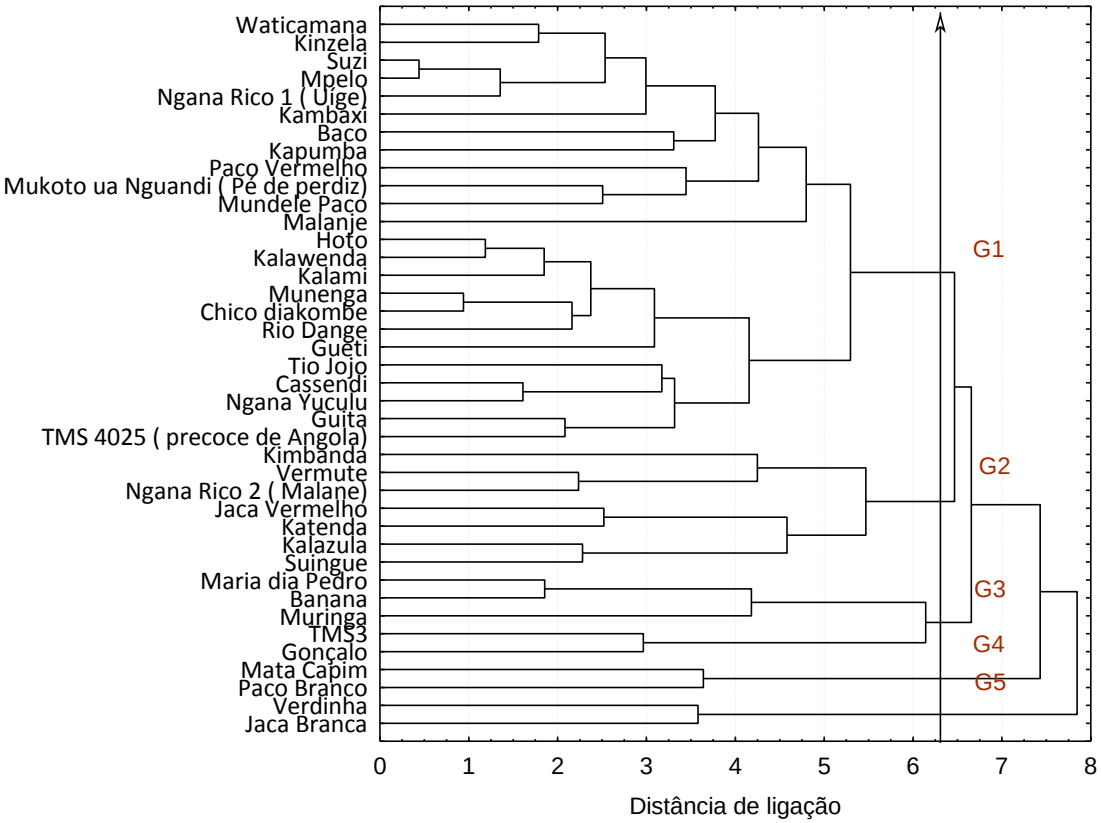

Figure 1. Dissimilarity dendrogram based on Mahalanobis distance and UPGMA grouping method from 10 quantitative descriptors of 40 cassava varieties.

Table 4. Relationship of varieties within groups in the cluster analysis based on the quantitative descriptors used in the evaluation of 40 varieties of the cassava germplasm bank of the Malanje Agronomic Research Institute and the Malanje Food Company.

[1] Pseudo-T^2criterion.

Grupos[1]	Variedades
1	Waticamana, Kinzela, Suzi, Mpelo, Ngana Rico 1 (Uíge), Kambaxi, Baco, Kapumba, Paco vermelho, MukotouaNguandi (Pé de perdiz), Mundele Paco, Malanje, Hoto, Kalawenda, Kalami, Munenga, Chico diakombe, Rio Dange, Gueti, Tio Jojo, Cassendi, NganaYuculu, Guita, TMS 4025 (precoce de Angola).
2	Kimbanda, Vermute, Ngana Rico 2 (Malanje), Jaca Vermelha, Katenda, Kalazula, Suingue.
3	Maria dia Pedro, Banana, Muringa, TMS3, Gonçalo.
4	Mata Capim, Paco Branco.
5	Verdinha, Jaca Branca.

IV. Discussion

The descriptive statistics of the appraised quantitative descriptors in this research, an oscillation is observed in the variation coefficient (CV) from 16, 21 % to 80, 87 %. These results are inside of the acceptable patterns for the cassava culture, once Afonso et al. [1], they obtained results of CV 5, 57% to 42, 37%, when evaluating some morphologic descriptors of cassava genotypes. The same authors affirm us that, these results can be considered medium, when compared with other similar works with the cassava culture. Result also attested by VIEIRA et al., [23].

According to Pimentel-Gomes [15], the variation coefficients give an idea of precision of the experiment and, when found in agricultural experiments of field, they can be considered low, when inferior to 10%, medium, when of 10 to the 20%, high, when of 20 to the 30%, and very high, when superior to 30%.

It was noticed that of the significant and positive correlations just one is high, in other words, among the number of roots (NR) with the root yield (RY) they obtained a value of 0.71 *, what was of waiting, however, that demonstrates that the increment of the selection of morphologic descriptors is directly associated to the number of roots (NR) and the root yield (RY). Although the height of the first branch (HFB) represents an important component in the number of roots (NR), it was not possible to observe significant correlation among root diameter (RD).

The descriptors selection based on the coefficient of diversity of Singh [20], which was taken in consideration to the relative contribution of each characteristic for the genetic divergence revealed that the variable root yield (RY) came as the characteristic of larger importance among the ten appraised descriptors for presenting the largest contribution percentage as for the genetic divergence (16, 31%), it answers for the largest percentage of all variability of the data. This information evidence that those characteristics possess great importance in the differentiation of the cassava varieties, being of great importance in studies of genetic diversity of the culture.

However, this dendrogram comes to attest that, the methodologies of clustering analyses were effective in emphasizing the existence of genetic divergence among the 40 varieties of Angolan cassava studied (for the used methodology), dividing them in five groups and they show for other, the importance of the combination of statistical methods, once they were able to optimize, in a considerable way, the interpretation of the results for larger knowledge of the varieties of Angola cassava studies.

This result doesn't corroborate with the result found by Zuin[21], studying the genetic divergence among 43 cassava varieties in the Municipal district of Cianorte - PR, using 12 descriptorsmorphoagronomic, for analysis multivariate with the same grouping method, which obtained as result the formation of 6 groups.

In an additional way, the use of the techniques of grouping analysis comes as a solution to contain and/or to describe a group of individuals. Tends in view that they consider, simultaneously, the whole group of appraised descriptors[1]. The analyses multivariate were efficient for the separation of the cassava accesses with base in appraised morphologic characters. The separation of the accesses in only five groups, however, it informs that, for the appraised characters in the accesses, great genetic variability was detected.

V. Conclusions

Wide genetic variability exists in the characteristics appraised morphoagronomic in the 40 cassava varieties. The method of hierarchical grouping UPGMA was what best explained the genetic divergence of the varieties in that work, where five groups were created by the package NbClust.

The observed genetic divergence identified varieties of different cassava amongst themselves, making possible the selection of genotypes for the programs of genetic improvement and conservation of the species seeking to the obtaining of you cultivate resistant the biotic factors and abiotic.

Acknowledgment

Thank the Company ofFoods of Malanje (CAM), for having allowed the accomplishment of the rehearsal in his/her experimental field and especially, in the person of Fernando Correia,Francisco Marques, the Mrs. Sónia Pinga. My special gratitude my advisor, Sandra Domingos João Afonso and not forgetting about teacher Isabel Felizardo Chambingo, for they accept to work with me and for the support in the several tasks developed in the elaboration of this work.

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Sandra Domingos João Afonso "Morphoagronomic Evaluation And Clustering Analysis In cassava (*ManihotEsculenta* Crantz) Varieties In The Agro-Ecological Conditions of Malanje In Angola"IOSR Journal of Agriculture and Veterinary Science (IOSR-JAVS) 11.11 (2018): 01-07.