GENETIC DIVERSITY OF SWEET POTATO REVEALED BY DESCRIPTORS MULTICATEGORICAL BINARIES

Elsayed, A. Y.
Breeding Res. Dept. Of Vegetable Crops, Hort. Res. Inst., Egypt.
Postdoctoral at UFVJM Uni., Brazil between 2011 - 2013.

ABSTRACT

This work aimed to study the genetic diversity of a collection of sweet potato that was collected between 2010 and 2012 from different regions of Brasil. Furthermore, to identify duplicate clones, as well as, identify useful sources of germplasm as a pre - breeding process. The work was conducted in the Department of Horticulture, Federal University of Jequitinhonha and Mucuri (UFVJM), Diamantina-MG during 2012 and 2013. Randomized complete block design was the experimental design used in this study comprised of 77 clones and 4 replications. Twenty four morphological descriptors multi-categorical binaries were applied in the characterization. The cluster analysis of Tocher and Hierarchical was used in the clones grouping. By the dissimilarity matrix between multi-categorical variables, the clones were divided into nine groups demonstrating great variability. The cluster methods Tocher and Hierarchical agreed with the first group formed, where remained the assembled clones in both methods with an increment of five clones in Hierarchical method. The clones varied in skin and flesh colors like white, cream, orange, pink, purple-red and dark purple. It was not possible to observe duplicate clones by the analysis of genetic similarity. The clones UFVJM-17, UFVJM-27, UFVJM-31 and UFVJM-42 were more similar with minimum similarity of 0.8. A high degree of variability was detected in the total tuber yield, between 47.13 to 4.26 tonne/hectare. It can be concluded that the existence of genetic variability among the clones conserved at Germplasm Bank of UFVJM can be used as a gene sources for developmental of high - quality value in sweet potato clones.
Keywords: Characterization, germplasm,genetic variability, *Ipomoea batatas*.

INTRODUCTION

Sweet potato is one of the seven crops in the world produce over 105 hundred million metric tonnes of edible food products in the world annually FAO (2011). Sweet potato is a hexaploid with a basic chromosome number (n) of 15 and a double chromosome number (2n) of 90 (Jones, 1965). It is a dicotyledonous plant belonging to the family Convolvulaceae. The family includes about 45 genera and 1,000 species, of which only *Ipomoea batatas* (L.) Lam. is of economic importance (Onwueme, 1978). A very large number of sweet potato clones have arisen through systematic breeding efforts, but an appreciable number of them have also arisen through natural hybridization and mutation (Onwueme, 1978).

Sweet potato clones fall into three categories on the basis of tuber texture after cooking as follows; a) those with firm, dry, mealy flesh after cooking, b) those with soft, moist, gelatinous flesh after cooking, c) those with very coarse tubers which are suitable only for animal feed or for industrial uses. Sweet potato clones also differ from one another in the colour of tuber skin (white, brown, yellow or reddish-purple), colour of the tuber flesh (white

or yellow), the shape of the tuber, shape of leaves, depth of rooting, time of maturity, resistance to disease and several other vegetative characteristics. Some of the clones recommended for various parts of the world include Centennial and Nema gold in the U.S.A.; Cambraia, Brazlândia Branca e Brazlândia Rosada in Brasil; Tucumana Morada and Brasilera Blanca in Argentina; Onokeo in Hawaii; Accessions 2342, 2291 and 2292 in Nigeria; La Catemaco and Dulce in Venezuela; A26/7 and T25 in the West Indies.

The characterization of germplasm, diversity and genetic relationships among cultivars are critical for clonal maintenance and improvement programs. Over 8000 accessions, cultivars and lines of sweet potato and about 26000 accessions of other species of Ipomoea are maintained at 83 gene banks in the world (Rao *et al*., 1994). The gradual loss of accessions in the field gene banks is a common problem in most countries that maintain sweet potato collections due to the use of very small plots with few plants. Another important problem is the high level of mixtures between accessions in national sweet potato collections. Mixtures occur because of the lack of enough space between plots which favors the obtrusion of accessions with very disperse growth habit. Other mixtures can also occur when the field gene bank does not have an adequate crop rotation system.

Morphological characterization of collections of sweet potato is not an easy task due to the great diversity in morphological and phenotypic characteristics. In this context, multi-categorical descriptors have a very important application in the management of genetic resources due to the ease of data collection, economic and less time consuming compared to quantitative and molecular data.

This study aimed to characterize a collection of 77 clones, identify the genetic variability among the sweet potato germplasm maintained in the UFVJM germplasm bank and investigate useful sources of germplasm as a pre breeding process.

MATERIALS AND METHODS

The field experiment was carried out in the Department of Horticulture, Federal University of Jequitinhonha and Mucuri (UFVJM), Diamantina-MG (altitude 1387m, 18°12'01'' S and 43º34'20'' W). On the 13th of November, 2012, cuttings of 77 clones was taken (40 cuttings/clone) and planted in trays of 128 cells, previously disinfected with active chlorine. At 35^{th}-days of rooting, the cuttings were transplanted to the field. The experimental design was randomized complete block design comprising 77 clones and four replications. Plots consisted of 2.4 m row length, 1.0 m between rows and 0.30 m between plants and 8 plants per plot with total area approximately 1000 m^2. Based on the IBPGR descriptors developed by Huamán (1999), 24 morphological descriptors (Table 1) were used to be characterize of sweet potato used in this study.

Table 1. Morphological descriptors were used in the characterization of 77 clones of sweet potato (Ipomoea batatas), vegetative part (stem and leaf) and tuberous roots.

The trait	Categories
1. Plant type	3 Erect (<75 cm); 5 Semi-compact (75 – 150 cm); 7 Spreading (151 – 250 cm); 9 Extremely spreading (>250 cm).
2. Vine internode diameter	1 Very thin (< 4mm); 3 Thin (4 - 6 mm); 5 Intermediate (7 – 9 mm); 7 Thick (10 – 12 mm); 9 Very thick (>12 mm).
3. Vine internode length	1 Very short (<3 cm); 3 Short (3 – 5 cm); 5 Intermediate (6 – 9 cm); 7 Long (10 – 12 cm); 9 Very long (> 12 cm).
4. Predominant color of vine	1 Green; 3 Green with few purple spots; 4 Green with many purple spots; 5 Green with many dark purple spots; 6 Mostly purple; 7 Mostly dark purple; 8 Totally purple; 9 Totally dark purple.
5. Secondary color of vine	0 Absent; 1 Green base; 2 Green tip; 3 Green nodes; 4 Purple base; 5 Purple tip; 6 Purple nodes; 7 Other.
6. Vine tip pubescence	Degree of hairiness of immature leaves recorded from the apex of the vines. 0 None; 3 Sparse; 5 Moderate; 7 Heavy; 9 Very heavy.
7. General leaf outline	1 Rounded; 2 Reniform (kidney-shaped); 3 Cordate (heart-shaped); 4 Triangular; 5 Hastate (Trilobular, spear-shaped, with the basal; lobes more or less divergent); 6 Lobed; 7 Almost divided.
8. Type of leaf lobes	0 No lateral lobes (entire); 1 Very slight (teeth); 3 Slight; 5 Moderate; 7 Deep; 9 Very deep.
9. Number of leaf lobes	1, 3, 5, 7 and 9 lobes.
10. Shape of central leaf lobe	0 Absent; 1 Teeth; 2 Triangular; 3 Semi-circular; 4 Semi-elliptic; 5 Elliptic; 6 Lanceolate; 7 Oblanceolate; 8 Linear (broad); 9 Linear (narrow).
11. Mature leaf size	3 Small (<8 cm); 5 Medium (8 – 15 cm); 7 Large (16 – 25 cm); 9 Very large (>25 cm).
12. Abaxial leaf vein pigmentation	1 Yellow; 2 Green; 3 Purple spot at base of main rib; 4 Purple spots in several veins; 5 Main rib partially purple; 6 Main rib mostly or totally purple; 7 All veins partially purple; 8 All veins mostly or totally purple; 9 Lower surface and veins totally purple.
13. Mature leaf color 14. Immature leaf color	1 Yellow-green; 2 Green; 3 Green with purple edge; 4 Greyish (due to heavy pubescence); 5 Green with purple veins on upper surface; 6 Slightly purple; 7 Mostly purple; 8 Green upper, purple lower; 9 Purple both surfaces.
15.Petiole pigmentation	1 Green; 2 Green with purple near stem; 3 Green with purple near leaf; 4 Green with purple at both ends; 5 Green with purple spots throughout petiole; 6 Green with purple stripes; 7 Purple with green near leaf; 8 Some, petioles purple, others green; 9 Totally or mostly purple.
16. Petiole length	1 Very short (<10 cm); 3 Short (10 – 20 cm); 5 Intermediate (21 – 30 cm); 7 Long (31 – 40 cm); 9 Very long (>40 cm).

Table 1. Continued.

The trait	Categories
17. Storage root shape	1 Round – almost a circular outline with a length to breadth (L/B) ration of about 1 to 1; 2 Round elliptic – a slightly circular outline with acute ends L/B ration not more than 2 to 1; 3 Elliptic – outline with about the maximum breadth at equal distance from both ends which are slightly acute. L/B ratio not more than 3 to 1; 4 Obovate – outline resembling the longitudinal section of an egg; 5 Ovate – inversely ovate outline. The broadest part is at the proximal end; 6 Oblong – almost rectangular outline with sides nearly parallel and corners rounded. L/B ratio about 2 to 1; 7 Long oblong – oblong outline with an L/B ratio of more than 3 to 1; 8 Long elliptic – elliptic outline with a L/B ratio of more than 3 to 1; 9 Long irregular or curved.
18. Storage root defects	0 Absent; 1 Alligator's like skin; 2 Veins; 3 Shallow horizontal; constrictions; 4 Deep horizontal constrictions; 5 Shallow longitudinal grooves; 6 Deep longitudinal grooves; 7 Deep constrictions and deep grooves; 8 Other.
19. Predominant skin color	1 White; 2 Cream; 3 Yellow; 4 Orange; 5 Brownish orange; 6 Pink; 7 Red; 8 Purple red; 9 Dark purple.
20. Intensity of predominant color	1 Pale; 2 Intermediate; 3 Dark.
21. Secondary skin color	0 Absent; 1 White; 2 Cream; 3 Yellow; 4 Orange; 5 Brownish orange; 6 Pink; 7 Red; 8 Purple-red; 9 Dark purple.
22. Predominant flesh color	1 White; 2 Cream; 3 Dark cream; 4 Pale yellow; 5 Dark yellow; 6 Pale orange; 7 Intermediate orange; 8 Dark orange; 9 Strongly pigmented with anthocyanins.
23. Secondary flesh color	0 Absent; 1 White; 2 Cream; 3 Yellow; 4 Orange; 5 Pink; 6 Red; 7 Purple-red; 8 Purple; 9 Dark purple.
24. Distribution of secondary flesh color	0 Absent; 1 Narrow ring in cortex; 2 Broad ring in cortex; 3 Scattered spots; 4 Narrow ring in flesh; 5 Broad ring in flesh; 6 Ring and other areas in flesh; 7 In longitudinal sections; 8 Covering most of the flesh; 9 Covering all flesh.

The dissimilarity between two clones 1 and 2 was calculated by:
$D = \{Root\ [sum\ (D^2/ni)]\ /v\}$ where
n_i: number of categories within the $_i$*th* variable,
V: total number of variables
D^2: square of the difference between the two clones.

The matrix of dissimilarity based on the complement of the coefficient of coincidence was generated. Based on the dissimilarity matrix, groups were formed by the Tocher method. Cluster analysis based on Tocher method forming groups in which the values of the intra-group distances are less than any intergroup distances (Cruz and Carneiro, 2003). The dissimilarity matrix was also used for grouping the clones by hierarchical method UPGMA (Unweighted Pair Group Mean Average). Mean comparisons were done in agreement with Scott-Knott test at 5%. Statistical analyses were performed using GENES program (Cruz, 2006) version 2009.7.0 and Office Excel application.

RESULTS AND DISCUSSION

Based on the dissimilarity matrix between variables multi-categorical through the Tocher method, the clones were divided into 9 groups (Table 2), which demonstrates the large variability in these clones. The characteristics of the leaves were those that showed more variability, especially the shape, size, color and length of the petiole. In a similar study, Moulin *et al*., (2012) noted that the morphological characterization was efficient to detect genetic variability among 46 accessions of sweet potato. The first group consisted of 50 clones (65 % of the clones), the majority of clones in this group has the same color of green mature leaf, petiole length between 10 and 30 cm, green secondary color and mature leaf size between 8 and 15 cm.

The second group consisted of 7 clones present green color of immature leaves with purple veins on the upper surface and erect plant type (<75 cm). While the UFVJM-40 and UFVJM-55 clones were separated into two groups. This classification probably attributed to the color of the mid rib (partially purple) and petiole length (31-40 cm) for UFVJM-40 and the predominant purple color of stem and large mature leaf size (16-25 cm) for UFVJM-55.

Table 2. Grouping formed by Tocher method using the matrix of dissimilarity of 77 sweet potato clones based on multi-categorical descriptors.

Group	Individuals
1	Arruba, UFVJM-01, UFVJM-02, UFVJM-03, UFVJM-04, UFVJM-05, UFVJM-06, UFVJM-07, UFVJM-09, UFVJM-10, UFVJM-12, UFVJM-13, UFVJM-14, UFVJM-15, UFVJM-16, UFVJM-17, UFVJM-18, UFVJM-19, UFVJM-20, UFVJM-22, UFVJM-23, UFVJM-24, UFVJM-25, UFVJM-26, UFVJM-27, UFVJM-29, UFVJM-30, UFVJM-31, UFVJM-32, UFVJM-33, UFVJM-34, UFVJM-35, UFVJM-36, UFVJM-37, UFVJM-38, UFVJM-39, UFVJM-42, UFVJM-43, UFVJM-44, UFVJM-45, UFVJM-46, UFVJM-49, Batata mandioca, Espanhola, Marmel, Palmas, T Carro 2, Coquinha, UFVJM-51, UFVJM-56.
2	UFVJM-47, UFVJM-50, UFVJM-54, UFVJM-53, UFVJM-57, UFVJM-59, UFVJM-60.
3	UFVJM-28, UFVJM-41, Brazlândia-Branca, Brazlândia-Rosada, Beaugard, UFVJM-48, UFVJM-58, UFVJM-61.
4	Cariru vermelha, Cambraia, Licuri.
5	UFVJM-08, Brazlândia-Roxa, UFVJM-62.
6	UFVJM-21, T Carro 1.
7	Princesa, UFVJM-52.
8	UFVJM-40
9	UFVJM-55.

Considering cutting point as the average dissimilarity of clones (the axis x at 81.8% of the relative distance between the clones) resulting in formation of 8 groups (Fig. 1). Both clustering methods Tocher and Hierarchical (UPGMA) agreed with the first formed group, where they remained the clones assembled in both methods with increment of five clones

in hierarchical (UFVJM-53, T Carro 1, UFVJM-51, Licuri and Cariru vermelha). However, with the other clones, some were grouped distinctly. The major differences were observed in the number of groups formed in both clusters where the first established more groups (nine) compared to hierarchical method (eight) groups.

The morphological characterization of tuberous roots

Eight morphological descriptors were used to be characterize clones of sweet potato. A noticeable genetic variability among the sweet potato clones revealed by the morphological descriptors roots as the skin color, flesh color, shape and defects of the tuberous roots were detected (Table 3). The root shape is quite important for human consumption. About 15% of the clones demonstrated elliptic and round elliptic roots that are considered the most desirable for the fresh consumption. While the rest of clones had the curved roots, very elliptical, ovate and oboval shapes (Table 3).

In relation to the root defects, in general, most clones demonstrated notes from 0.0 to 4.0 where 0.0 represents free of any defects while the note 4.0 represents deep horizontal constrictions. Fourty one clones showed none defects, since they were free from any type of defects. Two clones (UFVJM-20 and UFVJM-43) demonstrated deep horizontal constrictions deep. Twenty clones showed alligator-like skin, four clones (UFVJM-13, 24, 26 and 41) demonstrated veins defects while four clones (UFVJM-30, 51, 55 and 56) demonstrated shallow horizontal constrictions.

Considering the part of the x axis section, the average dissimilarity of clones, at the point of 12.64 % of the relative distance between the clones, 5 groups were formed. The cluster methods Tocher and Hierarchical (UPGMA) were convenient regarding to the first group formed with the same clones, but less nine clones for the hierarchical method that were moved to the second group. The groups 3, 4 and 5 remained the same in both methods (Figure 2).

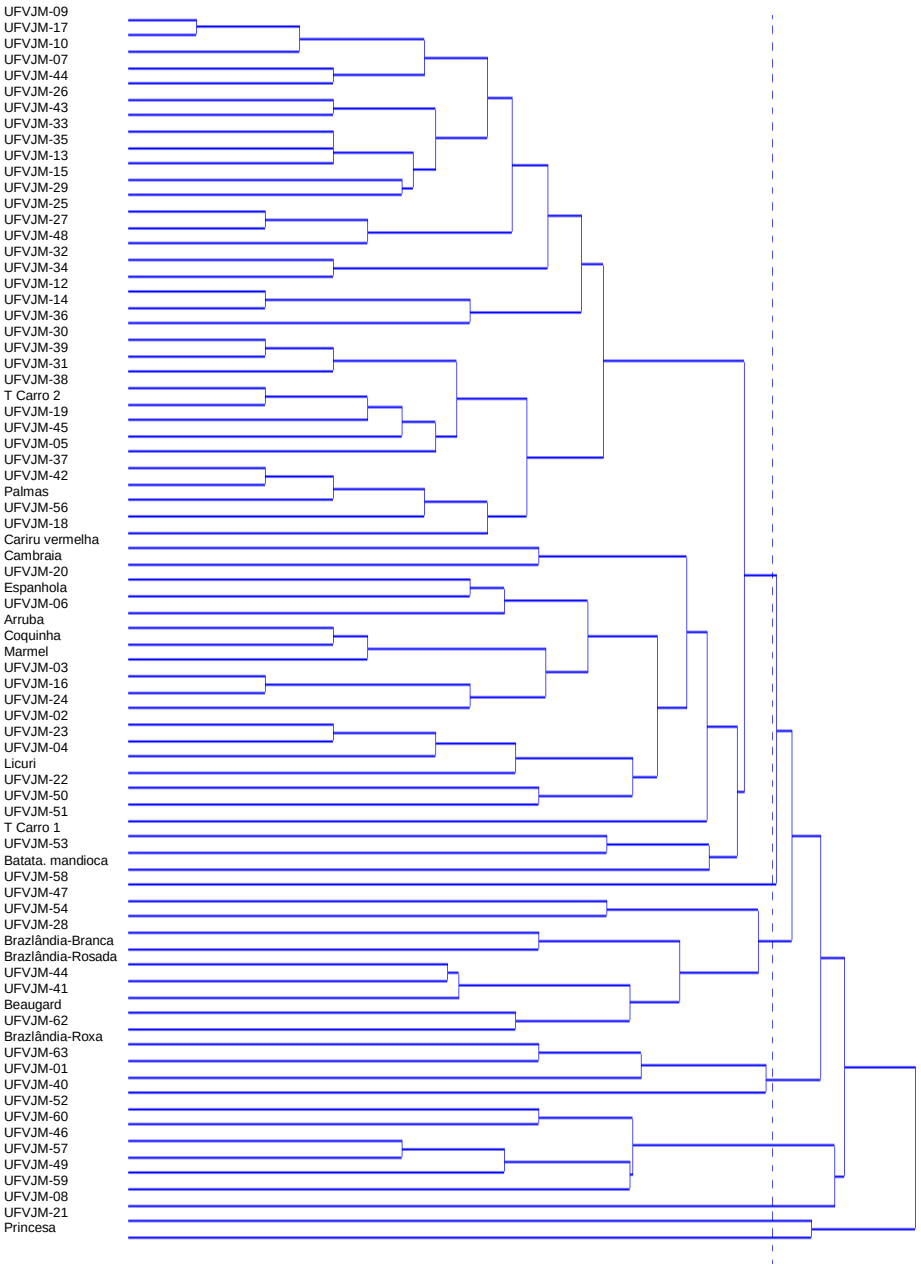

Figure 1. Dendrogram of genetic similarity among 77 clones of sweet potato, obtained by the UPGMA method based on the dissimilarity matrix of 18 morphological descriptor's data .

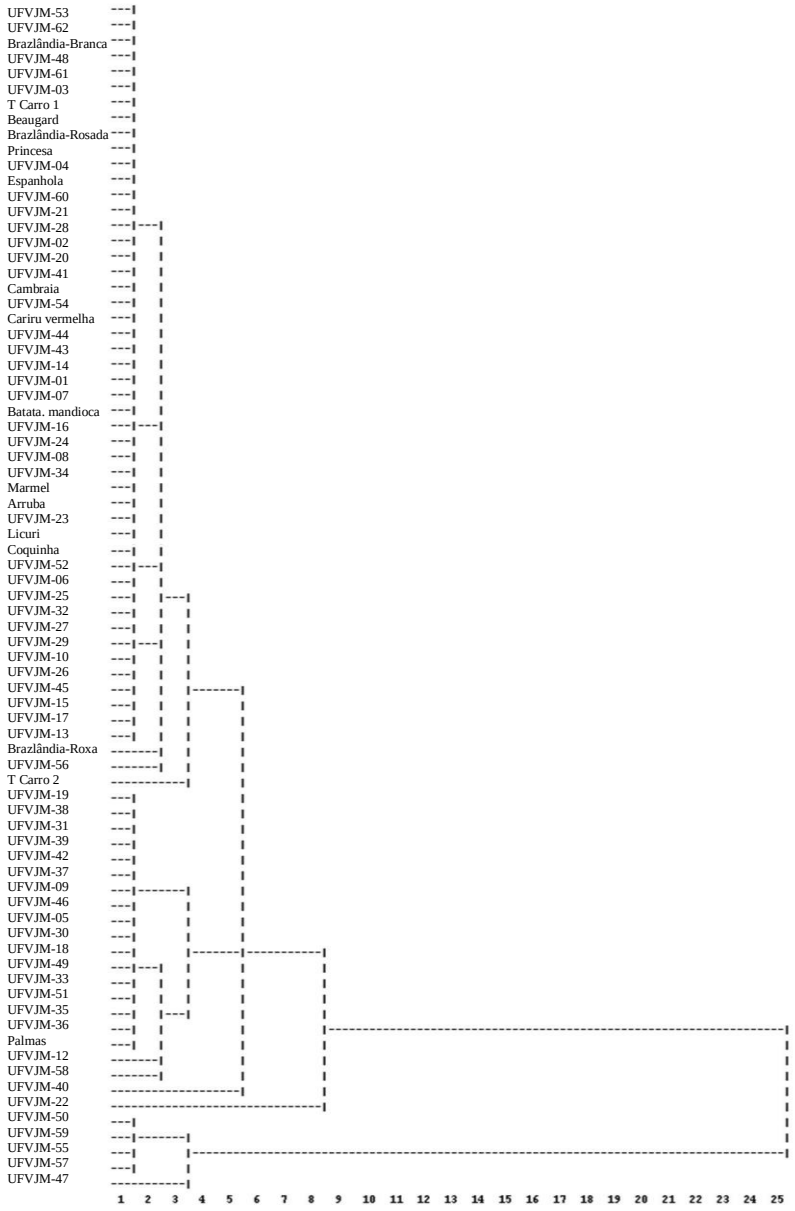

Figure 2. Dendrogram of genetic dissimilarity of 77 clones of sweet potato (*Ipomoea batatas*) established by the method of average linkage between groups using the Mahalanobis distance obtained from eight morphological descriptors of roots.

T3

Total root yield

Significant differences among clones were observed by *F*-test for the total root yield. The clone T Carro 1 ranked first, followed by UFVJM-61 and UFVJM-21 (Table 4). While the clone Batata mandioca was the fourth rank. Eighteen clones (about 23% of total clones) have higher total production compared to commercial check Brazlândia Rosada. The overall average was 24.79 t / ha, while the maximum and minimum values of total production were 47.12 and 4.26 t / ha, respectively. Despite its high potential as a producer of food and biomass (above 40 t / ha in 6-month cycle), the culture of sweet potato is still characterized by low average productivity (less than 12 t / ha), caused by lack of proper cultural practices and the use of genetic material (cultivars) obsolete, susceptible to pests and diseases, mainly chrysomelids insects and root-knot nematode. The average productivity is well below the potential for the crop, which can exceed 40 t / ha, where the levels of 25 to 30 t / ha can be easily obtained in 4 to 5 months with minimally appropriate technology (Andrade Junior *et al.,* 2009). Experimental yields of 69 t / ha as obtained by Brito *et al*., (2004) are uncommon.

In general, the clones of white flesh and cream skin colors have the highest productivity, but there is not enough evidence to ensure the relationship between the color and the productivity or other important traits like dry weight or starch content in these clones. Further studies are required to investigate this point and how the indirect selection can be exploited for the development of high-value sweet potato clones. The large tubers contributed more to the total tuber yield than the small tubers. Selection for maximum tuber yield could, therefore, be aimed at clones that produce large tubers.

The leaf area index, leaf area duration, crop growth rate, net assimilation rate, harvest index, tuber bulking rate, final, number of tubers per plant and mean tuberous root weight are the major factors that influence yield in the sweet potato (Forbes and Watson, 1992). Therefore, the great variability in productivity among the clones could be explained by the fact that genetic diversity existing in the morphological traits for the evaluated clones. The high-yielding genotypes generally partitioned more photosynthates to the tuberous root than the low-yielding ones. Therefore, selection of clones with large sink capacities and ideal degrees of response of sink to source is possible.

Compared to other crops such as corn and sorghum, sweet potato is more efficient in the amount of net energy produced per unit area and per unit time. This is because it produces large volume of roots in a relatively short cycle at low cost during the whole year. The root of the sweet potato has about 30% of dry weight that contains on average 85% carbohydrate, which the main component is starch (Lu and Sheng, 1990).

Table 4. Mean values of total yield (tonne/ hectare) of 77 sweet potato clones evaluated in a randomized complete block design.

Clones	Mean	Group	Clones	Mean	Group
T Carro 1	47.13	a	UFVJM-36	24.18	c
UFVJM-61	45.95	a	UFVJM-38	24.03	c
UFVJM-21	44.05	a	UFVJM-58	23.73	c
Batata. mandioca	43.52	a	UFVJM-19	23.50	c
UFVJM-28	43.08	a	UFVJM-59	23.32	c
Cariru vermelha	42.30	a	UFVJM-48	23.10	c
Beaugard	42.17	a	UFVJM-51	22.59	c
UFVJM-01	40.99	a	UFVJM-53	22.53	c
UFVJM-23	38.93	a	UFVJM-03	22.26	c
UFVJM-06	38.01	a	UFVJM-42	21.58	c
Licuri	35.90	a	UFVJM-44	21.01	c
Princesa	33.48	b	UFVJM-46	20.98	c
UFVJM-56	33.40	b	UFVJM-39	20.08	c
UFVJM-40	32.91	b	UFVJM-50	19.15	c
UFVJM-20	32.19	b	UFVJM-52	18.81	c
UFVJM-16	31.22	b	UFVJM-62	18.72	c
Marmel	30.73	b	UFVJM-32	18.66	c
Cambraia	30.69	b	UFVJM-07	18.36	c
Brazlândia-Rosada	30.21	b	UFVJM-02	18.13	c
UFVJM-24	30.20	b	UFVJM-26	17.90	c
UFVJM-49	29.86	b	UFVJM-05	17.65	c
UFVJM-47	29.61	b	UFVJM-37	17.39	c
UFVJM-14	29.14	b	UFVJM-55	16.68	c
Palmas	28.87	b	UFVJM-60	15.79	d
UFVJM-04	28.43	b	UFVJM-13	15.21	d
UFVJM-57	27.52	b	T Carro 2	15.11	d
UFVJM-08	27.44	b	UFVJM-33	15.02	d
Arruba	27.42	b	UFVJM-15	14.39	d
Brazlândia-Roxa	27.10	b	UFVJM-17	14.02	d
UFVJM-41	26.53	b	UFVJM-45	13.55	d
UFVJM-10	26.51	b	UFVJM-29	11.25	d
UFVJM-12	26.34	b	UFVJM-09	11.15	d
Espanhola	25.90	b	UFVJM-27	10.99	d
UFVJM-31	25.79	b	UFVJM-43	10.32	d
UFVJM-25	25.60	b	UFVJM-22	9.52	d
Brazlândia-Branca	25.45	b	UFVJM-34	7.45	d
UFVJM-18	25.35	b	Coquinha	7.34	d
UFVJM-35	24.77	c	UFVJM-54	4.26	d
UFVJM-30	24.65	c			

Response of sweet potato to environmental changes is very high (Bacusmo *et al.,* 1988;. Carpena *et al.,* 1980). Grüneberg *et al.,* (2005) observed variations in yield and stability in multi-environment testing of different genotypes of sweet potato. A significant interaction G × E was reported for the average weight of root and root yield. However, the major contribution to the overall genotype effect has a greater variability than the environment and the effect of G × E interaction (Caliskan *et al.,* 2007). Although the significant interactions G × E for yield stability and quality of sweet potato was reported (Caliskan *et al*,. 2007 ; Manrique and Hermann, 2000), it is difficult to obtain a variety possess great stability along with high yield and good performance (Affleck *et al.,* 2008).

Sweet potato is asexually propagated via stem cuttings and adventitious buds arising from storage roots, which may result in the accumulation of random mutations. Therefore, this variability may be related to the high somatic mutation reported in this crop (Hernandez *et al.,* 1964). This variation can be identified by the farmer and depends on their local knowledge and experience with the plants. Identification by the local farmers of vegetatively propagated crop species could be considered a special human selection model, known as ``selection for perceptual distinctiveness`` where the maintenance of a variety depends on morphological variations that can distinguish it from others (Boster, 1985). Intravarietal polymorphism related to vegetative crop species has also been reported for potato (*Solanum tuberosum*) by Quiroz *et al.,* (1990) and cassava (*Manihot esculenta*) by Colombo *et al.,* (2000) and Sambatti *et al*., (2001). The exchange of plants among the farmers and the chances of new genotypes emerging from seed banks arising from other plantings in the past, were probably the most important factors in the maintenance and amplification of the genetic diversity for this crop.

In conclusion, this study supports the existence of high genetic variability between sweet potato clones with a higher proportion of this variation occurring possibly due to factors such as mating system or somatic mutations but mainly to management and the exchange system between farmers. This genetic variability among the clones of sweet potato could be used as a source of genes of interest in sweet potato breeding programs. For example, the nutritional quality content in sweet potatoes can be enhanced by developing new varieties from available germplasm. Furthermore, natural colourant and antioxidant present in purple and red-flesh potatoes can be used for developing high-efficient foods.

REFERENCES

Affleck, I.; Sullivan, J. A.; Tarn, R.; Falk, D.; (2008). Genotype by environment interaction effect on yield and quality of potatoes. Can. J. Plant Sci. 88: 1099-1107.

ANDRADE JÚNIOR, V.C.; VIANA, D.J.S.; FERNANDES, J.S.C.; FIGUEIREDO, J.A.; NUNES, U.R.; NEIVA ,I.P. (2009). Selection of sweet potato clones for the region Alto Vale do Jequitinhonha. Horticultura Brasileira 27: 389-393

Bacusmo, J.; Collins, W.; Jones, A. (1988) Comparison of methods of determining stability and adaptation of sweetpotato. Theor Appl Genet. 75: 492-497

Boster, J.S. (1985) Selection for perceptual distinctiveness: Evidence from Aguaruna cultivars of *Manihot esculenta*. Econ Bot 39:310-325.

Brito, J.F.; Momenté, V.G.; Silveira, M.A.; Silva, L.M.A.; Dias Neto, J.J.; Ribeiro, P.A.A.; Brito, D.R.; Santos, G.F. (2004) Avaliações de clones de batata-doce nas condições de Gurupi-TO. Horticultura brasileira, V.22, N.2.

Caliskan, M.E.; Erturk, E.; Sogut, T.; Boydak, E.; Arioglu, H. (2007). Genotype x environment interaction and stability analysis of sweet potato (*Ipomoea batatas*) genotypes. New Zealalnd J Crop Hort. 35: 87-99.

Carpena, A.; Rebancos, J. R. E.; Manguiat, P.; Zalameda, M.; Sajise, J. R. G.; Pedro, J. (1980). Stability of yield performance of some sweet potato culttvars. Philipp J Crop Sci. 5: 30-33.

Colombo, C.; Second, G. and Charrier, A. (2000). Diversity within American cassava germplasm based on RAPD markers. Genet Mol Biol 23:189-199.

Cruz, C.D. (2006). Programa Genes – Estatística experimental e matrizes. Viçosa, MG: Editora da Universidade Federal de Viçosa,140p.

Cruz, C.D. and Carneiro, P.C.S.(2003). Modelos biométricos aplicados ao melhoramento genético. Viçosa: UFV, v. 2, 585p.

FAO (2011). Statistical database. http://faostat.fao.org/site/567/DesktopDefault.aspx?PageID=567#ancor (accessed November 9, 2013).

Forbes, J.C. and Watson, R.D. (1992). Plants in Agriculture Cambridge University Press, The Pitt. Building, Trumpington Street, Cambridge. 355pp.

Grüneberg W. J.; Zhang, D.; Manrique, K.; Hermann, M. (2005). Genotype x environment interactions for a diverse set of sweet potato clones evaluated across varying ecogeographic conditions in Peru. Crop Sci. 45: 2160-2171

Hernandez, T.P.; Hernandez, T. and Miller, J.C. (1964). Frequency of somatic mutations in several sweet potato varieties. Proc. Am. Soc Hortic. Sci. 85:430-434.

Huamán, Z. (1999). Descriptor for sweet potato.(ed.), CIP/AVRDC/IBPGR. International Potato Board for Plant Genetic Resources, Rome, Italy.

Jones, A. (1965). A proposed breeding procedure for sweet potato. Crop. Sci. 5: 191-192.

Lu, G. Q. and Sheng, J. L. (1990). Application of near infrared reflectance spectroscopy (NIRS) in sweet potato quality breeding. Scientia Agricultura Sinica, 23, 76-81.

Manrique, K. and Hermann, M. (2000). Effect of G x E interaction on root yield and beta carotene content of selected sweetpotato (*Ipomoea batatas* (L) Lam.) varieties and breeding clones CIP, Lima.

Moulin, M.M.; Rodrigues, R.; Gonçalves, L.S.A.; Sudré, C.P; Santos, M.H.; Silva, J.R.P. (2012). Collection and morphological characterization of sweet potato landraces in north of Rio de Janeiro state. Horticultura Brasileira 30:286-292.

Onwueme, I. C. (1978). The Tropical Tuber Crops. Yams, cassava, sweet potato, and cocoyams. Wiley, New York, 234pp.

Quiroz, C.F.; Brush, S.B.; Douches, D.S.; Zimmerer, K.S. and Huestis, G. (1990) Biochemical and folk assessment of variability of Andean cultivated potatoes. Econ Bot 44:254-266.

Rao, V.R.; Debouck, T. and Iwanga, M. (1994). The role of international organizations in root and tuber crop conservation. In ``The First Ministry of Agriculture, Forestry and Fisheries, Japan International Workshop on Genetic Resources Root and Tuber Crops`` 15-17 March 1994, Tsukuba, MAFF, Japan, P.7-22.

Sambatti, J.B.M.; Martins, P.S. and Ando, A. (2001). Folk taxonomy and evolutionary dynamics of cassava: A case study in Ubatuba-Brazil. Econ Bot 55:93-105.

إظهار التنوع الوراثى في البطاطا السكرية باستخدام الواصفات الثنائية متعدده الأشكال

أحمد يوسف عبدالنبى

قسم تربية الخضر- معهد بحوث البساتين- مركز البحوث الزراعية - مصر

يهدف هذا البحث إلى دراسة التنوع الوراثي لمجموعة من سلالات البطاطا السكرية التي تم تجميعها بين عامي ٢٠١٠ و ٢٠١٢ من مناطق مختلفة من البرازيل . علاوة على ذلك، فقد تم تحديد السلالات المكررة وكذلك تحديد مصادر مفيدة للأصول الوراثية كعملية ما قبل التربية. تم تنفيذ هذا البحث في قسم البساتين - جامعة UFVJM بالبرازيل خلال عامى ٢٠١٢ ، ٢٠١٣. إحتوت التجربة على ٧٧ سلالة من البطاطا تم زراعتها في أربع مكررات بإستخدام تصميم القطاعات الكاملة العشوائية. تم قياس 24 من الصفات المورفولوجية متعددة الاشكال في التوصيف. تم استخدام التحليل العنقودى لـ Tocher ، Hierarchical في دراسة التنوع الوراثى للسلالات. و عن طريق تقدير مصفوفة الإختلاف بين المتغيرات متعددة الأشكال ، تم تقسيم السلالات الى ٩ مجموعات تحتية والتى أظهرت مدى واسعاً من التباين. كانت كلتا الطريقتين Tocher، Hierarchical متوافقتين بالنسبة لمكونات المجموعة الأولى حيث ظلت السلالات المقسمة في كلا الطريقتين كما هى مع زياده ٥ سلالات فى الحالة الأخيرة. احتوت السلالات على ألوان متنوعة سواء لون الجلد الخارجى أو لون اللحم مثل الأبيض ، الكريمى ، البرتقالي ، الوردي ، الأرجواني ، الأرجواني الداكن. لم يكن هناك سلالات متطابقة كلياً من خلال تحليل التشابه الوراثي. أظهرت السلالات UFVJM-17، UFVJM-27 ، UFVJM-31 ، UFVJM-42 تماثل أعلى بحد أدنى من التشابه 0.80. وعليه فإن هذه النتائج تشير إلى إمكانية إستخدام التنوع الجينى بين السلالات المحفوظة في بنك الأصول الوراثية فى جامعة UFVJM كمصدر للجينات لتطوير اصناف عالية القيمة من البطاطا السكرية.

قام بتحكيم البحث

أ.د / خليفة عبد المقصود زايد — **كلية الزراعة – جامعة المنصورة**

أ.د / محمد سعد حمادة — **كلية الزراعة – جامعة دمياط**

Table 3. List of the main root morphology traits (color, shape and defects) of sweet potato (*Ipomoea batatas*) collections based on the descriptors of IBPGR developed by Huamán (1999).

Clone	Shape	Defects[1]	Root color[2]		Clone	Shape	Defects	Root color	
			Skin	Flesh				Skin	Flesh
Arruba	Curved	1	Brownish orange	White	UFVJM-39	Obovate	1	Cream	Dark purple
UFVJM-01	long elliptic	1	Brownish orange	White	UFVJM-40	long elliptic	0	Dark purple	Dark purple
UFVJM-02	Curved	0	Cream	White	UFVJM-41	Oblong	2	Cream	White
UFVJM-03	long elliptic	0	Cream	White	UFVJM-42	Obovate	0	Cream	Dark purple
UFVJM-04	long elliptic	1	Cream	White	UFVJM-43	Elliptic	4	Pink	White
UFVJM-05	long elliptic	1	Cream	Dark purple	Brazlândia-Branca	Long oblong	1	Cream	White
UFVJM-06	Ovate	1	Orange	Cream	Brazlândia-Rosada	long elliptic	1	Cream	White
UFVJM-07	long elliptic	0	Brownish orange	White	UFVJM-44	Elliptic	0	Cream	White
UFVJM-08	Obovate	1	Brownish orange	White	UFVJM-45	Round elliptic	1	Pink	Cream
UFVJM-09	long elliptic	0	Cream	Dark purple	UFVJM-46	long elliptic	1	Cream	Dark purple
Cariru vermelha	Elliptic	1	Cream	White	Brazlândia-Roxa	Round elliptic	1	Brownish orange	Orange
UFVJM-10	Obovate	1	Pink	Cream	Batata. mandioca	long elliptic	0	Brownish orange	Purple
UFVJM-12	Ovate	0	Cream	Yellow	Cambraia	Elliptic	0	Cream	White
UFVJM-13	Elliptic	2	Pink	Cream	Espanhola	Obovate	0	Cream	White
UFVJM-14	Elliptic	1	Cream	Orange	Licuri	Long oblong	0	Brownish orange	White
UFVJM-15	Long oblong	0	Pink	Cream	Marmel	Elliptic	0	Brownish orange	White
UFVJM-16	Obovate	1	Brownish orange	White	Palmas	Long oblong	0	Pink	Cream
UFVJM-17	Ovate	0	Pink	Cream	Princesa	long elliptic	0	Cream	White
UFVJM-18	Curved	0	Pink	Cream	T Carro 1	long elliptic	0	Cream	White
UFVJM-19	Ovate	0	Cream	Dark purple	T Carro 2	Oblong	1	Cream	Dark purple
UFVJM-20	Curved	4	Cream	White	Coquinha	Ovate	0	Brownish orange	Cream
UFVJM-21	Curved	0	Cream	White	Beaugard	long elliptic	0	Cream	White
UFVJM-22	Ovate	1	Cream	Orange	UFVJM-47	long elliptic	0	Purple-red	Cream
UFVJM-23	Curved	1	Brownish orange	White	UFVJM-48	long elliptic	0	Cream	White
UFVJM-24	Obovate	2	Brownish orange	White	UFVJM-49	Curved	1	Pink	White
UFVJM-25	Curved	0	Pink	Cream	UFVJM-50	long elliptic	1	Purple-red	Dark purple
UFVJM-26	Obovate	2	Pink	Cream	UFVJM-51	long elliptic	3	Pink	White
UFVJM-27	long elliptic	0	Pink	Cream	UFVJM-52	Ovate	1	Cream	Cream
UFVJM-28	Curved	0	Cream	White	UFVJM-53	Long oblong	0	Cream	White
UFVJM-29	long elliptic	0	Pink	Cream	UFVJM-54	Elliptic	1	Cream	White

UFVJM-30	Elliptic	3	Cream	Dark purple	UFVJM-55	Obovate	3	Purple-red	Dark purple
UFVJM-31	Long oblong	0	Cream	Dark purple	UFVJM-56	Long oblong	3	Brownish orange	Orange
UFVJM-32	Curved	1	Pink	Cream	UFVJM-57	Curved	0	Purple-red	Dark purple
UFVJM-33	long elliptic	0	Pink	White	UFVJM-58	Long oblong	1	Cream	Purole-red
UFVJM-34	Elliptic	0	Brownish orange	White	UFVJM-59	long elliptic	1	Purple-red	Dark purple
UFVJM-35	long elliptic	0	Pink	Cream	UFVJM-60	Obovate	0	Cream	White
UFVJM-36	long elliptic	0	Pink	Cream	UFVJM-61	long elliptic	0	Cream	White
UFVJM-37	Obovate	0	Cream	Dark purple	UFVJM-62	Long oblong	0	Cream	White
UFVJM-38	Ovate	0	Cream	Dark purple					

[1]Storage root defects: (0)None; (1)Alligator-like skin; (2)Veins; (3)Shallow horizontal constrictions; (4)Deep horizontal constrictions.
[2]Predominant color