Biochemical Diversity of Sweetpotato Genotypes

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Abstract. A comprehensive analysis of the variation in sweetpotato [*Ipomoea batatas* (L.) Lam.] is essential for sound germplasm conservation and recommendation strategies for production and consumption. The study evaluated biochemical content of 68 sweetpotato genotypes grown at the Miyare Agriculture Training College and Kenya Agricultural and Livestock Research Organization, Embu, Kenya. Ten storage root and seven aerial traits were used in the characterization. Storage root dry matter, protein and total carotenoids contents were all higher at the Miyare Agriculture Training College site compared to the Embu site; storage root sucrose and total starch content were higher in Kenya Agricultural and Livestock Research Organization, Embu, compared to the Miyare Agriculture Training College. Dry matter content ranged from 22.9% to 41.7%, protein content ranged from 5.2% to 13.4%, total carotenoids content ranged from 5.9 $\mu\text{g}\cdot\text{g}^{-1}$ to 33.1 $\mu\text{g}\cdot\text{g}^{-1}$, sucrose content ranged from 11.0 mg kg^{-1} to 108.5 mg kg^{-1} , and total starch ranged from 9.1 mg kg^{-1} to 97.6 mg kg^{-1} . The study demonstrates varying biochemical characteristics in sweetpotato, depending on genotypes and location. Selecting and improving sweetpotato genotypes rich in biochemical contents could help to solve the problem of food security and nutrition, especially in developing countries.

Introduction

Most studies on phytochemicals in roots or leaves of sweetpotato [*Ipomoea batatas* (L.) Lam.] indicated that their health promoting and/or disease preventing benefits were related to the high level of polyphenols [1]. [2] demonstrated that sweetpotato extract offered activity levels of cancer prevention which was correlated with its level of phenolic content. Sweetpotato leaves are rich in proteins, iron, potassium, sodium, vitamin C, vitamin K, folates, minerals, fat, fibre, and carbohydrates. Leaves have low levels of toxicants, except for oxalate, which can be reduced by cooking [1]. Vitamin A deficiency is more severe in sub-Saharan Africa, where an estimated 32% of preschool aged children are affected and sweetpotato consumption has the potential of solving this problem [3, 4].

The concentration of nutrients in sweetpotato pulp depends on variety, and environment. Purple sweetpotatoes have high levels of anthocyanins, and consequently, high antioxidant capacity [5]. Conversely, orange sweetpotatoes are an excellent source of carotenoids [6]. The main characteristic of carotenoids in sweetpotatoes is their provitamin A activity [3]. The extent and distribution of nutritional variation in sweetpotato is essential for sound recommendation strategies for production and consumption to meet the demand for future food security [7]. Sweetpotato varieties can be identified based on their biochemical profiling [5]. Over time, natural hybridization and selection resulted in evolution of hundreds of native sweetpotato cultivars in Kenya [7]. Therefore, there is no distinct sweetpotato variety for commercial recommendation in Kenya. There is a need for evaluation of sweetpotato genotypes grown for their nutritional composition for recommendation to growers and consumers. The objective of the study was to determine the biochemical composition of selected sweetpotato genotypes.

Materials and Methods

The experiment was carried out at the Miyare Agriculture Training College (ATC) farm situated in Migori County and the Kenya Agricultural and Livestock Research Organization (KALRO) situated in Embu County. The KALRO-Embu is characterized by altitude of 1497 m above sea level, an average annual rainfall of 1252 mm, an average annual temperature of 19.5 °C and humic nitisols. The ATC-Miyare is characterized by altitude of 1300-1620 m above sea level, an average annual rainfall of 1600-1800 mm, an average annual temperature of 16-17 °C and humic acrisols.

Sixty-eight sweetpotato genotypes collected in 2013 (Table 1) as vine cuttings were used. The 68 genotypes included 57 local Kenyan landraces and 11 F₁ hybrids from a polycross carried out in the National Crops Resources Research Institute, Uganda (Table 1). The genotypes collected from Kenya were from the Western, Nyanza and Eastern regions. The criteria for genotype collection was based on genotypes commonly grown by farmers in the Western region of Kenya and those indicated to have some resistance to weevils (*Cylas* spp.). The sweetpotato genotypes were multiplied at KALRO-Embu.

The genotypes were planted in a randomized complete block design on 27 March 2014 and 28 April 2014 for ATC-Miyare and KALRO-Embu, respectively. Each plot size was 1.5 × 3.75 m; plant spacing was 30 × 75 cm giving 25 plants per plot. Sweetpotato vines, 30 cm long, from each genotype, were planted in 5 rows. No pesticides were applied during the course of the experiment. Weeding was carried out once at both sites 6 weeks after planting. The plants were rainfed at both sites. Harvesting was at 160 days after planting. Sweetpotato root samples in each plot were washed, packed and transported to KALRO (Njoro) biochemical laboratory for dry matter, protein, total carotenoids, total starch and sucrose.

Table 1. List of the sweetpotato genotypes used for the study.

Genotype	Origin ^a	Flesh color
Kenspot 1	Eastern (Kenya)	Yellow
Saly boro	Nyanza (Kenya)	Orange
91/2187	Western (Kenya)	Yellow
Oduogo jodongo	Nyanza (Kenya)	White
5 Nyandere	Western (Kenya)	Cream-Yellow
Odinga	Nyanza (Kenya)	Yellow
Naspot 1	Western (Kenya)	Yellow
Kenspot 3	Eastern (Kenya)	Orange
Naspot × New Kawogo 2	NaCCRI (Uganda)	Cream
Nyamuguta	Western (Kenya)	Cream-white
Nyautenge	Western (Kenya)	Cream
Ejumula × New Kawogo 4	NaCCRI (Uganda)	Yellow-orange
Nyarambe	Western (Kenya)	Cream
Nyakagwa	Western (Kenya)	Cream
Naspot × New Kawogo 3	NaCCRI (Uganda)	Yellow-orange
Ejumula × New Kawogo 2	NaCCRI (Uganda)	Cream
Nangili	Western (Kenya)	Yellow-orange
Kenspot 2	Eastern (Kenya)	White
SPK 013	Nyanza (Kenya)	White
Mugande × New Kawogo 4	NaCCRI (Uganda)	Yellow-orange
Alupe-or	Western (Kenya)	Orange
12 Marooko	Western (Kenya)	Cream
Kenspot 5	Eastern (Kenya)	Orange
36 Kalamb Nyerere	Nyanza (Kenya)	Cream-yellow
K/KA/2004/215	Western (Kenya)	Yellow
Ejumula × New Kawogo 3	NaCCRI (Uganda)	Yellow

292-H-12	Western (Kenya)	Yellow-cream
Mogesi Gikenja	Western (Kenya)	White
Lungabure	Western (Kenya)	Cream-white
Kenspot 4	Eastern (Kenya)	Orange
Vitaa	Nyanza (Kenya)	Cream
9 Nduma	Western (Kenya)	Purple-cream
24 Kampala	Western (Kenya)	Yellow-orange
Obugi	Western (Kenya)	Yellow-orange
56682-03	Western (Kenya)	Cream
Nyawo Nyathiodiewo	Nyanza (Kenya)	Orange
Gachaka	Western (Kenya)	Yellow-orange
Mugande	Western (Kenya)	White
Amina	Nyanza (Kenya)	Orange
Fumbara jikoni	Western (Kenya)	Cream
Ejumula	Western (Kenya)	Orange
Karunde	Nyanza (Kenya)	Cream
SPK 004	Nyanza (Kenya)	Orange
Kuny kibuonjo	Nyanza (Kenya)	Cream-white
K/KA/2002/12	Western (Kenya)	White
55 Nganyomba	Western (Kenya)	Cream
1 Ujili	Western (Kenya)	Yellow
Santo Amaro	Rift valley (Kenya)	Cream
Mugande × New kawogo 2	NaCCRI (Uganda)	Cream
Wera	Nyanza (Kenya)	Yellow
Kemb 10	Nyanza (Kenya)	Yellow
Mbita	Western (Kenya)	Yellow
Naspot × New Kawogo 1	NaCCRI (Uganda)	Cream
Kibuonjo	Nyanza (Kenya)	Cream-white
29 Kuny kibuonjo	Nyanza (Kenya)	Yellow
62 Odhiogo	Western (Kenya)	Yellow
52 Nyakisumu	Nyanza (Kenya)	Yellow-orange
Ejumula × New kawogo 1	NaCCRI (Uganda)	Cream
Bungoma	Nyanza (Kenya)	Cream
K117	Nyanza (Kenya)	White
Fundukhusia	Western (Kenya)	Yellow-orange
SPK 031	Western (Kenya)	Orange
Mugande × New kawogo 1	NaCCRI (Uganda)	Yellow
Mwavuli	Nyanza (Kenya)	Cream
Polo yiengo	Nyanza (Kenya)	Yellow
Mugande × New kawogo 3	NaCCRI (Uganda)	Cream
Sinia	Nyanza (Kenya)	Yellow
Tainung	Eastern (Kenya)	Orange

^a All crosses in the study are F₁ hybrids from a polycross obtained from the National Crops Resources Research Institute, Uganda.

Determination of dry matter content was conducted following the method of [8]. Pots were washed in distilled water, labelled and dried in oven at 80 °C. The pots were then sterilized by dry heat in the oven at 105°C for 30 min and placed in the desiccator for 30 min. The weight of the labeled pots was tared by use of the weighing scale. Fresh root samples of sweetpotato were chopped into small pieces of 1 cm³. A sample of 100 g of chopped fresh roots (from each genotype) were dried in an oven at 105°C for 48 h. Dry matter percent was determined.

Protein analysis was carried out based on standard procedures [9]. One-g catalyst (made up of 1000 g potassium sulphate, 5 g selenium and 25 g copper sulphate mixed together thoroughly) was weighed and put in numbered digestion tubes. One-g of sample was put in a digestion tube and 7.5 mL concentrated sulphuric acid (nitrogen free) added. This was placed in a digester (Tecator, Hoganas, Sweden) for 30 min at 398°C, or until the mix cleared. Samples were removed from the digestion block and left to cool for 20-30 min. After cooling, 25 mL of distilled water was added to the mix followed by slow addition of 25 mL NaOH, to avoid a vigorous reaction of the acid and base. Distillation followed after addition of a base, into a conical flask with 0.1 N boric acid for 4 min which contained bromophenol blue dye. Blue color in boric acid changed to green upon receiving nitrogen in a form of ammonia. This was then back-titrated using 0.1 N hydrochloric acid which changed color of the mix in the flask from green to blue. The titer volume was recorded and used in calculation of average percent protein. The conversion factor used was 6.25 which are specific for sweetpotato plant sample [9]. The whole process was replicated 3 times with a control consisting of all the reagents and conditions except the experimental samples.

Analysis of sucrose (free sugar) and starch were conducted following the method reported by [10]. About 0.05 g of flour was weighed into centrifuge tubes. The powder was moistened with 1.0 mL 95% ethanol. Afterwards, 2.0 mL of distilled water was added, and contents mixed. Then 10.0 mL of hot 95% ethanol was added and the mix vortexed. The products were centrifuged ($1000 \times g$) for 10 min. The supernatant was decanted into a 100 mL volumetric flask and made up to mark. An aliquot of 1.0 mL of the extract was transferred to a clean test tube then 0.5 mL 5% phenol added and mixed. Afterwards, 2.5 mL of concentrated H_2SO_4 (98%) was added and the mix vortexed. After cooling, absorbance at 490 nm was read and recorded. The 490 nm wavelength is at which sucrose absorbs the most light. The absorbance of the blank (distilled water) was read. A standard curve was made using $0-100 \mu g \cdot mL^{-1}$ using standard sucrose. Sugars (sucrose) obtained after hydrolysis of the residue was converted to starch by multiplying it by 0.9.

Carotenoids were extracted following the improved method of [11]. About 0.24 g of sweetpotato fresh tuber samples was weighed and cut into small pieces. The pieces were transferred to a clean test tube with a lid. Diethyl ether (3 mL) was pipetted and added to the test tube to help dissolve solutes in the sweetpotato. The test tube was wrapped with aluminum foil (to prevent exposure of diethyl to light for prevention of oxidation). The caps of the tubes were wrapped with parafilm to prevent spilling of the liquid. The liquid was taken to a shaker that revolves at 75 rpm to mix the contents. The products were centrifuged for 20 min at $1300 \times g$. The supernatant was transferred to a new glass tube (without disturbing the pellet). The UV/visible spectrophotometer were blanked with 1 mL diethyl ether at wavelengths 642, 660 and 470. Readings of each sample were recorded at 470 nm, 642 nm and 660 nm wavelengths and carotenoids concentration calculated according to the equation of [12].

Data were subjected to analysis of variance (ANOVA) in SAS (ver. 10, SAS Institute Inc, Cary, NC). Data were classified according to genotypes, locations, blocks and replications. Means were separated using Tukey's test at 5% level of significance. Cluster analysis was done on standardized nutrition data based on the Euclidian distance coefficient and UPGMA using NCSS-pc (ver. 11, Tarragona, Spain). A hierarchical program in NCSS was used to generate dendrograms. Data points with the smaller distances between them were grouped together.

Results

The ANOVA indicated the main effects of site and genotype affected all measured biochemical characteristics (Table 2); there was no significant interaction between sites and genotypes. Analysis of variance indicated differences in root dry matter content among the genotypes and sites (Table 3). Genotypes that had the highest dry matter content were Kenspot 3 and 9 Nduma. The genotype that had the lowest dry matter content was Tainung. Genotypes from ACT-Miyare had higher dry matter content than those from KALRO-Embu.

Similarly, there were differences in protein content among the genotypes and sites (Table 3). Genotypes with the highest protein content were Odinga, Nyamuguta, Santo Amaro, and Mbita. The genotype with the lowest protein content was 36 Kalamb Nyerere. Genotypes from ACT-Miyare had higher protein content compared with KALRO-Embu.

Differences in total carotenoids content of sweetpotato were significant for both genotypes and sites (Table 3). The genotype with the highest total carotenoids content was Kenspot 2. The genotype with the lowest total carotenoid content was Gachaka. Genotypes from ACT-Miyare had higher carotenoids content than genotypes from KALRO-Embu.

There were differences in sucrose content among the genotypes and sites (Table 3). The genotype with the highest sucrose content was Ejumula × New Kawogo 4. The genotypes with the lowest sucrose content were 292-H-12. Sweetpotato genotypes from KALRO-Embu had higher sucrose content compared with those from ACT-Miyare. Varieties that had high values in sucrose had high values in starch content. Differences in starch content were observed among the genotypes and sites (Table 3). The genotype with the highest starch content was Ejumula × New Kawogo 4. The genotype with the lowest starch content was 292-H-12. Sweetpotato genotypes from KALRO-Embu had higher starch content than those from ACT-Miyare.

Table 2. Analysis of variance for biochemical characteristics of sweetpotato genotypes at ATC-Miyare and KALRO Embu sites.

Source	Degree of freedom	Mean square				
		Root dry matter	Root protein	Root total carotenoids	Root sucrose	Root total starch
Site (S)	1	626.2*	620.5*	555.4*	2134.6*	2035.8*
Genotype (G)	67	69.7*	34.1*	31.1*	167.4*	164.2*
Interaction (S × G)	67	30.6ns	43.7ns	49.9ns	214.1ns	210.4ns
Error (E)	270	1.4	0.7	2.7	19.6	0.1

ns not significant or * significant at $p < 0.05$.

Table 3. Means for storage root dry matter, protein, total carotenoids, sucrose and total starch of the 68 sweetpotato genotypes.

Genotype	Dry matter (%)	Root protein (%)	Root total carotenoids ($\mu\text{g}\cdot\text{g}^{-1}$)	Root sucrose ($\text{mg}\cdot\text{kg}^{-1}$)	Root total starch ($\text{mg}\cdot\text{kg}^{-1}$)
Kenspot 1	36.5b ^a	11.8ab	13.2f	53.9cd	48.5g
Saly boro	36.7b	9.4cd	10.4g	44.6e	40.1h
91/2187	36.9b	9.3cd	10.6g	35.0g	32.2j
Oduogo jodongo	37.2b	12.9ab	26.4c	28.7h	25.3k
5 Nyandere	37.5b	10.3c	9.0h	16.0k	14.4m
Odinga	38.3ab	13.4a	8.0i	89.6b	80.6b
Naspot 1	37.2b	11.1b	7.3i	88.5b	79.6b
Kenspot 3	40.7a	8.0d	9.7gh	49.9de	45.6gh
Naspot × New Kawogo 2	36.8b	9.0cd	9.4gh	29.0h	26.1k
Nyamuguta	39.0ab	14.1a	6.1j	65.2c	58.6f
Nyautenge	36.2b	9.4cd	8.0i	28.6h	25.8k
Ejumula × New Kawogo 4	36.9b	7.4e	9.7gh	108.5a	97.6a
Nyarambe	37.4b	10.0c	9.6gh	56.9cd	51.2g
Nyakagwa	34.7b	7.7e	9.4gh	52.1cd	47.8gh
Naspot × New Kawogo 3	38.0ab	10.8b	28.4bc	33.6gh	30.3j
Ejumula × New Kawogo 2	35.4b	10.1c	8.4h	59.9cd	53.9g
Nangili	36.9b	9.8c	16.5e	42.1f	37.9i
Kenspot 2	39.7ab	5.9g	33.1a	36.0g	31.9j
SPK 013	34.0bc	9.9c	9.0h	53.2cd	47.9gh

Mugande × New Kawogo 4	32.6c	8.6d	13.4f	63.1c	56.8f
Alupe or	34.2bc	9.8c	21.9d	47.7e	43.0h
12 Marooko	37.2b	8.0d	17.1e	54.4cd	49.0g
Kenspot 5	33.0bc	5.2g	19.6d	81.5b	75.1c
36 Kalamb Nyerere	35.9b	4.2h	8.7h	56.2cd	50.6g
K/KA/2004/215	32.9c	11.0b	9.0h	52.7cd	47.4gh
Ejumula × New Kawogo 3	35.4b	8.6d	7.7i	43.3f	39.0i
292-H-12	35.8b	7.3e	6.6ij	11.0l	9.9n
Mogesi Gikenja	37.1b	10.1c	6.7ij	35.2g	31.7j
Lungabure	34.1bc	7.5e	15.5ef	29.2h	26.7k
Kenspot 4	33.8bc	11.4b	30.5b	22.6j	20.3l
Vitaa	34.5bc	9.8c	7.0ij	50.5de	49.1g
9 Nduma	41.4a	6.3f	6.3ij	56.8cd	52.6g
24 Kampala	35.8b	9.7c	7.8i	85.0b	76.5d
Obugi	37.4b	10.1c	11.4g	61.4c	60.8e
56682-03	33.9bc	10.8b	7.4i	49.0de	44.2h
Nyawo Nyathiodiewo	34.0bc	10.5bc	16.2e	42.3f	37.9i
Gachaka	34.2bc	11.9ab	5.9j	18.6k	24.0k
Mugande	35.8b	8.7d	7.3i	39.2fg	35.3i
Amina	36.1b	5.6g	7.8i	72.0c	64.8e
Fumbara jikoni	33.9bc	8.1d	8.4h	53.0cd	47.7gh
Ejumula	34.9bc	6.8ef	7.7i	38.0g	34.2i
Karunde	34.9bc	8.1d	16.4e	33.1gh	29.8k
SPK 004	34.2bc	10.8b	15.9ef	57.5cd	52.6g
Kunykibuonjo	33.3bc	10.9b	8.8h	78.9bc	71.0d
K/KA/2002/12	34.4bc	5.9g	8.6h	51.0d	45.9gh
55 Nganyomba	31.8cd	9.3cd	7.7i	47.2de	42.5h
1-Ujili	33.9bc	12.1ab	8.6h	37.8g	34.0i
Santo Amaro	34.1bc	13.8a	8.7h	53.6cd	48.3gh
Mugande × New Kawogo 2	30.4d	12.2ab	6.3j	26.6i	23.9k
Wera	33.3bc	11.4b	8.4h	27.6i	24.8k
Kemb 10	32.8c	5.9g	12.8fg	40.5fg	36.4i
Mbita	31.3cd	13.2a	18.0e	31.4h	28.2k
Naspot × New Kawogo 1	31.5cd	7.3e	7.0ij	39.1g	35.2i
Kibuonjo	32.9c	6.9ef	6.6ij	25.5i	23.0k
29 Kunykibuonjo	32.6c	6.9ef	11.3g	43.4f	39.6i
62 Odhiogo	29.4d	6.8ef	10.1g	35.1g	31.6j
52 Nyakisumu	32.3c	5.4g	12.1fg	43.6f	39.3i
Ejumula × New Kawogo 1	33.0bc	11.1b	6.1j	51.4d	46.2gh
Bungoma	32.9c	5.8g	11.0g	48.4de	44.1h
K 117	31.1cd	10.0c	7.9i	46.4e	41.8h
Fundukhusia	29.5d	10.9b	6.9ij	43.2f	39.7i
SPK 031	29.0d	11.2b	26.5c	56.6cd	51.0g
Mugande × New Kawogo 1	28.4de	10.9b	6.5ij	41.9f	37.7j
Mwavuli	29.6d	7.6e	7.4i	80.6b	72.6d
Polo yiengo	27.4e	9.9c	10.6g	23.4j	21.0l
Mugande × New Kawogo 3	26.6e	9.2cd	7.2ij	76.9bc	69.2d
Sinia	27.2e	9.3cd	7.4i	94.1b	84.7b
Tainung	22.9f	9.1cd	29.1b	55.0cd	49.5g

Location

ATC-Miyare	35.4a	12.9a	12.6a	44.0b	39.7b
KALRO-Embu	32.9b	5.7b	10.5b	54.0a	49.0a

^a values in columns followed by the same letter are not significantly different, Tukey's test, $p < 0.05$.

The dendrogram obtained using combined nutrition characters at both ACT-Miyare and KALRO-Embu, separated genotypes into 2 clusters (Fig. 1). Cluster A contained 2 genotypes (Naspot 1 and Naspot x New Kawango 3); cluster B contained the remaining 66 genotypes. Cluster A consisted of genotypes that had high sucrose, starch and dry matter content. Cluster B consisted of genotypes that had high total carotenoids content and moderately high contents of sucrose and starch.

Figure 1. The dendrogram (based on Euclidean distance coefficient) of sweetpotato genotypes generated from combined biochemical data at ACT-Miyare and KALRO-Embu. Genotypes connected by portions of the dendrogram are highly related. As the dendrogram couplets coalesce the genotypes are fit into groups that are related based on root protein, root total carotenoids, root sucrose, and root total starch. Letters (A and B) represent clusters.

Discussion

The sweetpotato genotypes were evaluated to determine their biochemical diversity. No single genotype was superior in all desirable attributes. Kenspot 3 and 9 Nduma had the highest dry matter content. [13] reported that among farmers' selection criteria for sweetpotato genotypes are high

yields, early maturity, tolerance to diseases and pests, high dry matter content and taste or sweetness. Therefore, sweetpotato genotypes with high dry matter content as observed in the study could be ideal for recommendation to farmers. Low biochemical content including low dry matter content is among attributes that have led to the abandonment of many varieties by farmers [14, 15]. Various studies have also reported high biochemical, dry matter content and storage root yield as important characteristics for good sweetpotato varieties [16, 17, 18]. Root dry matter content is influenced by genetic constituents, therefore, explaining the biochemical differences within the studied genotypes [19]. Biochemical content of sweetpotato varies with variety, location, climate, the incidence of pests and diseases, cultural practices and soil type [20, 21]. This could further explain the location differences in dry matter content. The results of this study agree with [1] and [18] who observed varying biochemical differences to be a common phenomenon to East African genotypes. Use of sweetpotato as a raw material for the biofuel and processing industries requires genotypes with a dry matter content that is above 35% of the fresh weight [19]. According to the results of this study, majority of genotypes are suitable to serve as effective raw material for processing. Genotype Kenspot 2 had the highest total carotenoids content, making it suitable for addressing vitamin A deficiency [3]. Genotypes rich in protein such as Odinga, Santo Amoro, and Mbita could be recommended for children and the sick. Genotype Ejumula × New Kawogo 4 was observed to have a high content of starch and sucrose. Sweetness is among farmer selection criteria for sweetpotato genotypes in Eastern and Southern Africa. Most farmers prefer genotypes that are sweet (contain high contents of sucrose); some prefer genotypes that are less sweet. Genotypes with high sucrose content can enhance carbohydrate uptake by individuals while less sweet genotypes can be used to fortify cereal products.

The dendrogram indicated that genotypes did not cluster together uniformly in all trees. The trees could only give the general germplasm relatedness and diversity. The probable reason as to why clustering was not uniform is that expressions of biochemical characters are environmentally dependent [19, 22]. High ploidy level in sweetpotato may be responsible for variability in nutritional composition due to increased mutation associated with polyploidy [23].

Conclusions

The findings demonstrate that sweetpotato genotypes have varying biochemical characteristics depending on the growing location, attributed to environmental influence and growing conditions. Selecting and improving sweetpotato genotypes rich in biochemical contents could help to solve the problem of food security and nutrition, especially in developing countries.

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Conflict of Interest

The author declares that there is no conflict of interest.

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