

Genomic-Assisted Nutritional and Quality Breeding Efforts in Sweetpotato

7

Reuben Tendo Ssali, Bonny Michael Oloka,
Victor A. Amankwaah, Benard Yada,
Edward Carey, and G. Craig Yencho

Abstract

Sweetpotato, *Ipomoea Batatas* L., is widely considered as a staple food in many developing countries especially in sub-Saharan Africa (SSA). It has storage roots that are rich in starch, micronutrients (especially Fe and Zn), and vitamins A and C. Partly due to its polyploidy, heterogeneity and outcrossing nature, it can be cultivated in a wide range of environments. Sweetpotato additionally comes in a variety textures, colors, flavors, and nutritional

profiles thus appealing to many different groups of people. Conventional breeding of sweetpotato to improve nutritional and quality traits has only been moderately successful over the years due to several factors. This is mainly true in areas like SSA which are characterized by low adoption of high β -carotene orange-flesh types. The biggest challenge has been to understand, measure and combine cultural preferences for taste and quality with nutritional components. In this work, we look at efforts to measure quality preferences, and accelerate the breeding process of sweetpotato by tapping into new breeding technologies and genomic-assisted breeding approaches.

R. T. Ssali (✉)

International Potato Center (CIP), Kampala, Uganda
e-mail: R.Ssali@cgiar.org

B. M. Oloka · G. C. Yencho

Department of Horticultural Science, North Carolina State University, Raleigh, NC 27695, USA
e-mail: boloka@ncsu.edu

G. C. Yencho

e-mail: craig_yencho@ncsu.edu

V. A. Amankwaah

CSIR-Crops Research Institute, Kumasi, Ghana
e-mail: va.amankwaah@gmail.com

B. Yada

National Crops Resources Research Institute,
National Agricultural Research Organization,
Kampala, Uganda
e-mail: yadabenard21@gmail.com

E. Carey

International Potato Center (CIP), Kumasi, Ghana
e-mail: tcarey@ksu.edu

Keywords

Sweetpotato nutrition · Cooking quality ·
Sensory evaluation · Textural characteristics

7.1 Introduction

Sweetpotato (*I. batatas* L.) is a widely grown staple crop in the tropical and subtropical developing world. It ranks seventh in global food production and fifth in production within developing countries. In 2022, world production of sweetpotato was 86.4 million metric tons, from a total harvested area of 7.4 million hectares

(FAOSTAT 2022). The developing countries account for 95% of this production. Sweetpotato is often considered a crop for low-income farmers because it is relatively easy to produce with minimal inputs and is known for its ability to produce high yields in marginal environments. It is grown in diverse agroecological areas from the desert edges of lowland tropics to the highlands of the humid tropics. This adaptability to diverse environmental conditions is due to the inherent plasticity of the crop and the range of genotypes grown. The crop is ideal for subsistence farmers because maintaining planting material is straight forward. Although sweetpotato is primarily used as a source of carbohydrates from the tuberous roots, there is growing awareness of the additional health benefits that come from the consumption of these storage roots. It is considered as a staple food in many developing countries due to its starch-rich storage roots (da Silva Pereira et al. 2023).

Generally, the roots have a high moisture content with an average dry matter content of 25–30% (Truong et al. 2018). Starch is the major carbohydrate in sweetpotato storage roots, making up approximately 80–90% of the dry matter (Tumwegamire et al. 2011a, b). Sugars make up about 15–20% of the dry matter and are mostly in the form of sucrose, glucose, fructose, and maltose, with the latter being undetectable in raw roots but predominant in cooked roots due to β -amylolysis of starch (Kitahara et al. 2017; Truong et al. 2018; Amankwaah 2019; Amankwaah et al. 2023). It is also rich in mineral content with potassium, manganese, copper, iron and zinc. Potassium is the most abundant mineral, available at concentrations as high as 300 mg/100 g of fresh roots. This can contribute about a fifth of the recommended dietary allowance for children (Sanoussi et al. 2016). The mineral content is not only dependent on the variety and cooking conditions but also on agricultural practices, particularly the use of fertilizers. Sweetpotato also contains high-quality proteins (Truong et al. 2018), rich in methionine, threonine, valine,

and tryptophan (de Albuquerque et al. 2019). The protein content is low in comparison with cereal crops (Neela and Fanta 2019). It has been observed that baking sweetpotato roots reduces their protein content whereas boiling helps retain it. Sweetpotato provides twice the amount of dietary fiber of potato and cassava (Neela and Fanta 2019) thus aiding in satiety and digestive health. Some genotypes are rich in pro-vitamin A (β -carotene) and vitamins B1, B3, C, and E (Woolfe 1992; Truong et al. 2018; Neela and Fanta 2019). Therefore, sweetpotato can be exploited through targeted breeding to increase nutrient content for the world's food needs (Mwanga et al. 2021a, b). This nutrient density underscores its importance as a staple food and an ally in addressing hunger, malnutrition, and poverty in sub-Saharan Africa. Specifically, sweetpotato diversifies diets, provides sustenance to vulnerable populations, and offers income opportunities for smallholder farmers.

The nutritional value of a food crop depends largely on its beneficial nutrients, organoleptic properties, and any undesirable elements. Conversely, nutritional quality is determined by its impact on the nutritional status and health of those who consume it. Therefore, a crop can be nutritionally valuable but not necessarily of high nutritional quality if it's not accessible or preferred by the community. This distinction is crucial for enhancing sweetpotato varieties. Sweetpotato varieties with high nutritional value that are easy to grow and more affordable offer significant benefits. However, to boost the nutritional quality of sweetpotato, breeding efforts should also prioritize traits like taste, ease of preparation, and yield. It's important to note that high nutritional value and quality can coexist, and improving both could positively affect the health and livelihoods of subsistence farmers who rely on sweetpotato. Nonetheless, it is essential to identify the nutritional traits that need enhancement and to understand and quantify the genetic factors influencing these traits. Historically, these aspects have not been the primary focus in the sweetpotato variety development.

Although sweetpotato is an important food crop in the tropics and sub-tropics, it often faces significant challenges from pests and diseases. This affects its production and availability of planting materials, especially for high-yielding and nutritionally rich varieties. Breeding for pest and disease resistance along with improved yield and nutritional quality, is essential for enhancing the livelihoods of sweetpotato farmers and consumers. The success of new sweetpotato varieties relies on their production characteristics, but most importantly on their sensory and utilization qualities for the consumers (Tomlins et al. 2007). Consequently, prioritizing the preferred characteristics of sweetpotato roots for the end users is a key objective in sweetpotato breeding. Furthermore, the sweetpotato food chain is characterized by different actors with different preferences of choice due to factors such as socio-economic and gender dynamics (Mudege et al. 2019). Therefore, it is crucial to define preferences for quality characteristics by market segments and gender to meet the diverse needs of end users. For instance, Ugandan consumers of boiled and/or steamed sweetpotato prefer varieties that are aromatic, sweet, mealy, firm, and non-fibrous (Mwanga et al. 2021a, b). However, these desirable qualities must be linked to the biophysical and functional properties of the food to develop laboratory methods for quantitative evaluation. Typically, sweetpotato breeding programs assess these nutritional, physical, dietary and cooking attributes only in the final stages of diversity testing and release when 90–99% of breeding lines have already been discarded (Kays and Wang 2002; Grüneberg et al. 2015). This is due to the cost and complexity of these analyses and the lack of high-throughput phenotyping protocols and equipment (Kays and Wang 2002). Therefore developing high-throughput phenotyping protocols for user-approved quality and nutritional traits will facilitate their integration into breeding and selection of sweetpotato.

Genomic-assisted breeding is a promising approach for developing sweetpotato varieties

with improved nutritional, eating, and processing qualities right from the early breeding stages. This approach involves using genomic information to identify genetic markers associated with desirable traits. The chapter describes progress towards the application of genomic assisted breeding to develop new varieties with improved eating quality, processing suitability and nutrition value of sweetpotato. In contrast to conventional breeding, which depends on the visual assessment of traits to choose preferred characteristics, genomic-assisted breeding employs a more precise strategy.

7.2 Importance of Nutritional Value in Sweetpotato

Billions of people in developing countries suffer from chronic deficiencies in essential nutrients. Scientists have been working towards designing crops with improved essential nutrient content through either agricultural practices also known as “agronomic biofortification” or breeding (Bouis and Welch 2010). Micronutrient deficiencies are widespread, and diet-based strategies are the most sustainable solutions. These deficiencies affect particularly significant proportions of populations in developing countries and are especially high in pregnant women and pre-school children. In the developing world, an estimated 122 countries have populations deficient in Vitamin A. Sub-Saharan Africa has the highest percentage, with 48% of children under 5 affected. Each year, between 250,000 to 500,000 malnourished children go, with about half of them dying within a year of losing their sight. In 24 countries across Africa and Southeast Asia, over 20% of pregnant women suffer from night blindness and severe vitamin A deficiency is a major cause of maternal mortality in these regions. Incorporating sweetpotato into the diet is a practical solution for vitamin A deficiency. Since sweetpotato is commonly grown in the developing world, introducing pro-Vitamin A rich varieties would

be an effective and low-cost strategy to combat vitamin A deficiency. All plants have high levels of carotenoids in their leaves, primarily in thylakoid membranes. Sweetpotato leaves specifically contain four carotenoids: lutein (47.6% of total carotenoids), β -carotene (25.2%), violaxanthin (13.9%) and neoxanthin (9.6%) (Chen and Chen 1993). Khan et al. (2022) suggested that use of molecular genetic and genomic methods to understand and manipulate carotenoid biosynthesis in sweetpotato might provide the fastest and most effective means to generate increased pro-vitamin A sweetpotato cultivars.

Biofortification is a health-based strategy that aims to reduce micronutrient deficiencies and improve public health through the development of staple food crops that are rich in essential vitamins and minerals. The approach is to either enrich or increase the accumulation of micronutrients in the storage organs of the crop through plant breeding, using traditional methods or genetic engineering. Biofortification is generally perceived as a more sustainable, cost-effective, and efficient means to alleviate malnutrition than providing nutrient supplements or commercially fortified foods (Bouis and Welch 2010; Haas et al. 2005) and molecular genetics and genomic information presents new opportunities to expedite biofortification of crops (Bouis and Saltzman 2017; Welch and Graham 2004).

Although sweetpotato is primarily grown for its storage root, the young leaves and shoots are also consumed in many countries in sub-Saharan Africa, the Pacific, Asia, and the Caribbean. Sweetpotato is widely regarded as a healthy food and ranks high in nutritional value among root and tuber crops and as a staple food. It is a rich source of carbohydrates, dietary fiber, vitamins A, C, and several B-vitamins. The roots are fat-free and contain a moderate source of complex starch, which makes it an ideal food for diabetics. However, the most significant nutritional attribute of sweetpotato is the high beta-carotene content found in orange-fleshed varieties, which is a dietary source of vitamin A.

7.3 Genetic Basis for Nutritional Value in Sweetpotato

A crucial first step to conduct biofortification of crops is to gain a better understanding of the genetic and physiological factors affecting variation in nutrient content. Until relatively recently most plant breeders have employed a “phenotypic” approach to enhance nutrient content, which essentially involves identifying plants with desirable nutrient content based on visual observation of proxy traits like flesh color or laboratory analysis and using these plants as a source of genes for nutrient enhancement. This approach is limited by low heritabilities of many nutritional traits, difficulties in accurate and rapid phenotypic assessment of nutrient content, and problems with obtaining desirable levels of nutrient content in combination with other traits of agronomic importance (Bouis and Saltzman 2017).

The exploration of the genetic underpinnings that contribute to the nutritional value of sweetpotato is both intricate and intriguing. Sweetpotato is characterized by its autohexaploid nature, possessing 90 somatic chromosomes ($2n=6x=90$), and a substantial genome size estimated at approximately 4.4 Gb. The genetic structure of sweetpotato is a determinant of its nutritional profile, which includes mineral content (like Fe and Zn), vitamins (such as A and C), and nutraceutical components such as β -carotene and anthocyanins, especially notable in varieties with orange and purple flesh (da Silva Pereira et al. 2023). These elements are vital for human well-being and contribute to the agricultural value of the crop. The recent progress in developing molecular tools has enabled genetic mapping of significant quantitative trait loci (QTLs) and a genome-wide characterization of population structure, paving the way for genomics-assisted breeding. This approach is designed to develop new varieties that not only yield abundantly in adverse conditions but also exhibit resistance to pests and diseases, alongside enhanced nutritional properties.

The great biological variation in the genus *Ipomoea*, its complex genetic structure, and its high ploidy levels make the study of the inheritance of specific traits and the gene mapping difficult. Although great improvement was achieved in the last decade for studying and understanding the molecular composition of the sweetpotato genome (analysis of DNA content, construction of genetic maps, and development of genomic and expressed sequenced tags resources), the complex inheritance of the nutritional traits in sweetpotato (vitamin A, vitamin C, E, dietary fiber, glycemic index, and anthocyanin content) demands new strategies for dissecting them. Whatever the trait, due to the complexity of the root's genotype and the environmental interactions, the understanding of the regulatory or structural genes and the allelic polymorphisms that control them is not enough for the development of a functional marker and an effective regulatory system for improvement, but it is certainly an essential step in the right direction. At this point, a thorough understanding of the gene functions and biochemical pathways by which the nutrient synthesis and accumulation are controlled is lacking for sweetpotato. Such information is a prerequisite for devising strategies to increase the nutritional quality. Since each nutritional trait can be affected by many different factors, it is not feasible to discuss all of them in this context. A more general view of where we stand and where we should go for the better understanding of the genetic regulation of sweetpotato nutritional traits would be explained in the following paragraphs. Despite the great nutritional potential of sweetpotato, its genetic background and the regulatory mechanisms that control the nutritional trait composition are still poorly understood. The recent accomplishment of gene interrogations and functional genomics approaches in the model plants and the development of the high-throughput methods including the transcriptomics and metabolomics has heightened the momentum to study the nutritional traits of sweetpotato at the molecular level. The information gleaned will aid in the breeding approaches mentioned in the other papers of this publication and be a platform to

describe the desirable nutrient-dense sweetpotato of the future.

As the nutritional value of sweetpotato is directly related to human consumption and directly influences the livelihood of developing nations, there has been interest in determining the genetic markers to the nutritional value. Through identification of such markers, breeders could select for higher nutritional value sweetpotato, and farmers could grow sweetpotato specifically suited for certain nutritional needs. However, determining the nutritional value of storage roots is time consuming and expensive because chemical analyses must be run on large sample sizes to produce accurate results. There have been efforts of using near-infrared reflectance spectroscopy (NIRS) to predict storage root nutritional value because it is a rapid, nondestructive, inexpensive method of analysis and NIRS has been successful in predicting various traits in other crops. Ash of the storage root, which is the mineral content, has been the most successful in terms of accurate and precise prediction of nutritional value using NIRS compared to other nutritional factors. It was demonstrated by Tumwegamire et al. (2011a; b) that NIRS could be used to reliably predict dry matter, starch, and beta-carotene content in sweetpotato storage roots. Ash prediction equations could then be used to see if there are quantitative trait loci (QTL) affecting this nutritional factor. Development of genetic markers for nutritional value will allow breeders to breed for high nutritional value sweetpotatoes more efficiently.

As mentioned earlier, it is very difficult to define a superior sweetpotato genotype for nutritional value since high nutritional value is largely dependent on having a good balance between various nutritional components. However, it is possible to breed sweetpotato to have a specific nutritional composition if this is desired. It is basically a matter of setting levels for specific nutritional parameters and then selecting progeny that meet the desired nutritional profile. This is easily achieved for Pro-vitamin A since various flesh colors can be attributed with specific carotenoid content levels; hence, the only requirement is to select progeny that have a

specific flesh color. However, selecting progeny based on sensory data to ensure acceptability of nutritious varieties is problematic since sensory data will always have a large environmental effect but an understanding of which genes are affected by the environment will enable the development of genotypes that have a specific nutritional profile under defined storage conditions. Since it is genes that control nutritional composition, determining specific genes for each nutritional parameter will be the ultimate way to modify sweetpotato nutritional composition. This can be done using a QTL analysis or by using a transgenic approach. While transgenics will give an instant result, the development of a transgenic approach is not feasible for sweetpotato breeding in developing countries, and a transgenic approach also has social and ethical issues. A QTL analysis, while being a long process, will enable the development of genotypes with specific nutritional profiles without many of the negative issues of transgenics. So both of these methods have their advantages, and it is fortuitous that both can be employed to determine the specific genes for each nutritional parameter, with the knowledge of a QTL analysis being transferable to a marker-assisted selection (MAS) program.

A number of key genes responsible for different nutritional components of sweetpotato have been identified, including (1) **Su α -branching enzyme gene** responsible for amylose content (Takiko et al. 2006); **sporamin gene** involving storage root formation and it is rich in methionine content (Ravi et al. 2014); **β -amylase gene** controlling sugar and starch content in the roots (Nakamura et al. 2014); **IbVIN1** encoding a vacuolar invertase that limits sucrose accumulation in the roots at low temperature (Ru et al. 2021). The knowledge of these genes enables better understanding of effect on nutritional traits, provides directions for selection or breeding of sweetpotato with improved nutritional quality.

It is recognized that the nutritional quality and health benefit of any crop will depend on the various bioactive constituents and anti-nutritional factors, as well as the inherent diversity in human nutritive and health needs. A

detailed understanding of the genes encoding the enzymes and other proteins that dictate the nutritional and health status of a crop is a prerequisite for crop improvement. The successful development of nutritionally improved crops will require a comprehensive understanding of the genetic control of the target nutritional traits. Over the past two decades, significant research efforts have been directed at understanding the genetic basis for nutritional quality in several crops. Although this research has been fragmented, a relatively coherent and detailed picture has emerged in some cases. This has largely been due to the advent and application of genomics and other bioinformatic tools. While the application of these tools to sweetpotato lags far behind other major crops, there have been some notable research initiatives on the genetic basis for nutritional quality in sweetpotato. In some cases, findings from research on other crops has been fortuitously useful to sweetpotato researchers. For example, knowledge of the genes encoding the enzymes of starch biosynthesis is fairly advanced in several major crops. This has allowed sweetpotato researchers, on occasion, to glean useful information relevant to sweetpotato without actually doing the research. A case in point is a study aimed at understanding the genetic control of starch quantity and quality in sweetpotato (Gemenet et al. 2020b). The aim of the study was to identify genes encoding enzyme of starch biosynthesis which are differentially expressed in storage root of a high versus low starch line. The study exploited the fact that sequence information and PCR primers for such genes were available from similar studies in other crops, notably maize and potato. Using these, the researchers were able to identify the sweetpotato counterpart genes and address the research aims. Future research efforts on the genetic basis for nutritional quality of sweetpotato would be greatly facilitated by access to information on genes and gene families of other crops, and the development of sweetpotato genomics and bioinformatics.

The final level of a biological system involved in the expression of phenotype, from

both genetic and environmental impacts, is the accumulation of specific gene products and their interactions to form the unique attributes of a defined cell type or tissue. Gene expression and its regulation represent the process by which a gene's DNA sequence is transcribed into RNA and the RNA transcript is then translated into a protein. Changes in the dynamics of gene regulation, including changes in mRNA levels, and changes in protein function, can greatly influence phenotype. Changes in gene expression can have both direct and indirect effects on phenotype. Currently, gene regulation is assumed to represent the most frequent form of natural variation within a species, and the easiest means by which complex phenotypic variation can occur. This assumes importance as genotyping efforts begin to identify genes and QTL which control specific nutritional traits, particularly in centers of crop diversity where landraces may have high nutritional value but lack the needed consumer preferred traits. Ultimately, these genes or QTL must be identified in breeding material, and fully characterized, in order to exploit them for crop improvement.

7.4 Phenotyping Tools for Nutritional and Cooking Quality Traits

Phenotyping tools are essential for characterizing and measuring the nutritional and cooking quality traits of sweetpotato. Here are some commonly used phenotyping tools for these traits:

1. **Dry Matter Content:** Dry matter content refers to the amount of solid material in sweetpotato. This is an important trait for assessing cooking quality, as it can affect the texture and flavor of the cooked sweetpotato. Dry matter content can be measured using techniques like oven-drying or freeze-drying (Twegamire et al. 2011a; b; Gruneberg et al. 2019).
2. **Starch Content:** Starch content is an important determinant of cooking quality, as it

affects the texture and flavor of the cooked sweetpotato. Starch content can be measured using techniques like HPLC (High-Performance Liquid Chromatography) or a simple iodine test (Twegamire et al. 2011a; b).

3. **Sugar Content:** Sweetpotato are known for their sweetness, which is due to their high sugar content. Sugar content can be measured using techniques like HPLC or refractometry or NIRS (Twegamire et al. 2011a; b).
4. **Antioxidant Content:** Sweetpotato are rich in antioxidants, which can protect against chronic diseases like cancer and heart disease. Antioxidant activity can be measured using techniques like DPPH (2,2-diphenyl-1-picrylhydrazyl) assay or spectrophotometry (Shimamura et al. 2014).
5. **Vitamin and Mineral Content:** Sweetpotato are a rich source of vitamins and minerals like vitamin A, vitamin C, potassium, and iron. These can be measured using techniques like HPLC or spectrophotometry (Twegamire et al. 2011a; b).
6. **Color:** The color of sweetpotato can be an indicator of their nutritional value, with darker varieties containing more antioxidants. Color can be measured using techniques like colorimetry and image analysis (Nakatumba-Nabende et al. 2023).
7. **Texture:** Texture is an important determinant of cooking quality, as it affects the mouthfeel of the cooked sweetpotato. Texture can be measured using techniques like texture profile analysis or sensory evaluation or image analysis (Nakitto et al. 2022; Nakatumba-Nabende et al. 2023).

Sensory characteristics of sweetpotato roots are critical to consumer choice and acceptability with potential to drive the adoption of improved varieties (Jenkins et al. 2018; Mwangi et al. 2021a, b). Sensory evaluation has been defined by the Institute of Food Technologists as a scientific method used to evoke, measure, analyze, and interpret responses to products as perceived through the senses of sight, hearing, touch, smell, and taste (IFT 2007). It can either

be objective or subjective; objective evaluation (also known as descriptive sensory evaluation) makes use of trained sensory panelists to rate eating quality differences whereas in subjective evaluation (hedonic) consumers' reactions to the sensory properties of products are measured (Kemp et al. 2018). Consumer testing provides invaluable information regarding potential acceptance or rejection, and the reasons for rejection by consumers. While descriptive sensory analysis gives detailed and reliable information about the intensity of the quality attributes of a product, thus providing a basis for understanding acceptability (Joanna et al. 2019).

Recently, a systematic deployment of descriptive sensory evaluation for sweetpotato breeding was described in Uganda (Nakitto et al. 2022). This involved (1) lexicon development, (2) panel training and (3) evaluation of genotypes. A lexicon was developed for sweetpotato comprising 27 sensory attributes for characterization and differentiation of genotypes by sensory profiles (Table 7.1).

7.5 Improving Bioavailability of Nutrients

Bioavailability is a measure of the degree and rate at which a nutrient is absorbed from the diet and used for normal body functions (Jackson 1997). It is an intricate concept with the possibility of multiple nutrients interacting within the body to influence the absorption of each other. The rate of metabolism can also influence the availability of a given nutrient. Transitory complexes of starch, which are not directly correlated to yield of a storage root, can provide a readily mobilized source of energy and increase the bioavailability of other nutrients by sparing them from being used as an energy source. The identification of key enzymes and transporters in synthesis and accumulation of the targeted nutrient can lead to transgenic approaches specifically aimed at increasing the nutritive value of the crop (Shahzad et al. 2021). An example from sweetpotato would be the conversion of a portion of the storage root anthocyanin pigments

into proanthocyanidins, effectively transferring some of the antioxidant nutrient value from the skin to the flesh of the root.

7.6 Genomic Tools for Nutritional and Cooking Quality Traits

Genomic tools are essential for identifying the genes and genetic variations that underlie nutritional quality traits in sweetpotato. These tools can help breeders to develop new varieties with improved nutritional and cooking quality and can also help researchers to better understand the biology of sweetpotato and the mechanisms that underlie these traits.

Reference Genome: Breeding for desired quality attributes in sweetpotato is challenging since traits that are of economic importance are often positively and negatively correlated. The possibility of pleiotropy in set of economic traits is inevitable. Identifying haplotypes which control traits of economic importance will help in facilitating selection decisions both at the phenotypic and molecular levels. Sequencing of the sweetpotato genome to identify genes associated with specific nutritional traits like beta-carotene (vitamin A precursor), starch and sugar content, iron uptake, and zinc accumulation is crucial. Genomic tools like a reference genome for cultivated sweetpotato is now available to facilitate genome enabled breeding for nutritional traits. Two diploid wild relatives of cultivated sweetpotato, *Ipomoea trifida* and *Ipomoea triloba*, have been sequenced and released now widely used as reference sequences in whole-genome studies (Wu et al. 2018). Comparative and phylogenetic analyses using these reference genomes provide insights into the ancient whole-genome triplication history of the genus *Ipomoea*. Researchers can now explore evolutionary relationships within the Batatas complex, which includes sweetpotato. By resequencing data from 16 genotypes widely used in African breeding programs, genes and alleles associated with carotenoid biosynthesis in sweetpotato storage roots have been identified. Genome browser for this haplotype-resolved chromosome-scale genome

Table 7.1 An example of sensory attributes constituting the lexicon for evaluation of cooked sweetpotato by a trained descriptive sensory panel

Assessment method	Descriptors	Simplified definition	Scale range
<i>Aroma</i>			
Once sample is received, slightly unwrap it, observe aroma with a single short whiff, close the foil, and mark your scores on the aroma scales	Sweetpotato	Smell of cooked sweetpotato	0 = none to 10 = very strong
	Caramel	Smell of burnt sugar or molasses (<i>sukaali gula</i>)	0 = none to 10 = very strong
	Pumpkin	Smell of cooked pumpkin	0 = none to 10 = very strong
	Off-odor	“Unusual smells in sweetpotato including potato, boiled beans, amaranth, herbal, floral, and pungent/acidic/rotting sweetpotato”	0 = none to 10 = very strong
<i>Appearance</i>			
Visually assess the outer surface of the sweetpotato for orange color intensity	Orange color intensity	Intensity of orange color across the surface of the sample	0 = white, 1 = cream, 3 = yellow, 5 = yellow orange, 8 = orange, 10 = deep orange
			0 = highly variable to 10 = consistent throughout
Observe the cross-sectional cut for uniformity of color, degree of translucency and fibrousness	Uniformity of color	Evenness of color distribution across sample surface	0 = 100% chalky/opaque to 10 = 100% translucent
	Translucency	Quality of an object to allow light to pass through it but does not allow images to be distinguished such as a slice of steamed cucumber	0 = none to 10 = extremely fibrous
	Fibrous appearance	Presence of visible strings within sample mass	0 = none to 10 = extremely fibrous
<i>Flavor</i>			
Take a portion of the sample and chew slowly to score the intensity of the flavors	Sweetpotato	Intensity of the flavor of cooked sweetpotato	0 = none to 10 = very strong
	Pumpkin	Intensity of the flavor of cooked pumpkin	0 = none to 10 = very strong
	Cooked carrot	Intensity of the flavor of cooked carrot	0 = none to 10 = very strong
	Floral	Intensity of the flavor of flowers	0 = none to 10 = very strong
Take a portion of the sample and chew slowly to score the intensity of the basic tastes that you observe	Sweet	Taste of sugar	0 = not at all sweet to 10 = extremely sweet
	Bitter	Taste of quinine, strong coffee, <i>katunkuma</i> (<i>Solanum anguivi</i>), <i>nakati</i> (<i>Solanum aethiopicum</i>)	0 = not bitter 10 = extremely bitter
<i>Texture in mouth</i>			
Take a portion of sample and bite using front teeth (incisors) and assess fracturability	Fracturability	Ease with which sample breaks into distinct pieces when bitten between incisors	0 = easily deforms to 10 = easily fractures
	Hardness in mouth	Amount of force required to compress product between molars	0 = extremely soft to 10 = hard

(continued)

Table 7.1 (continued)

Assessment method	Descriptors	Simplified definition	Scale range
While chewing (chew down), assess crunchiness and moisture in mass (3 chews)	Crunchiness	Production of low-pitched sound while chewing certain foods such as cooked carrot, cucumber	0 = not crunchy to 10 = extremely crunchy
	Moisture (in the mass)	Amount of moisture present in sample mass	0 = dry to 10 = extremely moist
	Crumbliness in mouth	Extent of powder like particles in sample mass	0 = not mealy to 10 = extremely mealy
	Adhesiveness	Amount of sample that adheres to oral surfaces	0 = none to 10 = very high
After chewing 3 times, place sample between tongue and palate and assess crumbliness in mouth, adhesiveness, fibrousness, and smoothness	Fibrousness	Presence of string like structures in mouth after chewing	0 = none to 10 = very high
	Smoothness	Degree of absence of grainy particles in mass	0 = grainy to 10 = very smooth
	Rate of breakdown	Number of chews required to masticate a sample until you can swallow it	0 = very slow to 10 = very fast
	Texture by hand		
Press down the center of the sample to evaluate the force required to compress sample	Hardness by hand	Amount of force required to compress sample	0 = very soft, 5 = firm, 10 = very hard
Take a portion of sample and press between fore finger and thumb to assess moisture release	Moisture release	Attribute of food products to release moisture when pressure is applied such as cooked cucumber and French beans	0 = none to 10 = extremely moist
Attempt to make a ball from the sample to evaluate cohesiveness (moldability)	Cohesiveness (moldability)	Ease with which a ball like shape can be molded from sample	0 = falls apart to 10 = moldable
Rub a portion of sample between fingers to evaluate mealiness	Crumbliness (mealiness)	Ease with which sample breaks into small particles upon rubbing	0 = not mealy to 10 = extremely mealy

Source Nakitto et al. (2022)

assembly and annotation for different varieties of sweetpotato has been made available. It includes a set of search and query tools such as a BLAST server, genome browsers for two reference genomes, and gene report pages for all annotated genes in the species. This resource has bolstered efficient breeding of varieties with high provitamin A content.

Marker Development: Mapping complex traits genetically is by far the most expensive but also an important approach to identifying functional variants (Wallace et al. 2018). A number of quantitative trait loci have been identified for some of the nutritional quality traits using the Tanzania by Beauregard mapping population and its reciprocal cross in different environments in West Africa and United States of America. These two mapping populations are segregating for important quality attributes such as storage root dry matter, starch, β -carotene and sugar contents. Associating the phenotype and genotypes of clones in these two mapping populations in different environments enabled scientist to better understand the genetic architecture of quality attributes (Amankwaah 2019). Gemenet et al. 2020b using a biparental mapping population generated from a cross between an orange-fleshed and a non-orange-fleshed sweetpotato variety, identified two major QTLs located on linkage group (LG) three (LG3) and twelve (LG12) affecting starch, β -carotene, and their correlated traits, dry matter and flesh color. (Gemenet et al. 2020b). Some of the QTL discovered for nutritional quality have been hypothesized to be associated with important candidate genes in sweetpotato which could be targeted in improving cell wall structure, texture and flavor aside nutritional quality attributes. Based on the identified genes, scientists develop DNA markers. These markers function as flags, indicating the presence of genes linked to desired nutritional qualities. QTLs identified mentioned earlier were differentially expressed in Beauregard and Tanzania storage roots. It was reported that the two QTLs detected acted in a cis and trans manner to inhibit starch biosynthesis in amyloplasts and enhance chromoplast biogenesis, carotenoid biosynthesis,

and accumulation in OFSP. Breeders use these markers to screen large numbers of sweetpotato seedlings. Plants with the desired genetic markers are more likely to have improved nutritional content, allowing for faster selection and breeding.

Genomic Selection (GS): Genomic selection is a promising approach to enhance the nutritional quality of sweetpotato. It involves developing models to predict genotypes with desirable traits, such as higher protein content, essential amino acids, vitamins, and minerals, through genetic markers. This method can significantly accelerate the breeding process for developing nutrient-rich sweetpotato varieties. Genomic selection is a promising approach to enhance the nutritional quality of sweetpotato. It involves developing identifying and selecting desirable traits, such as higher protein content, essential amino acids, vitamins, and minerals, through genetic markers. This method can significantly accelerate the breeding process for developing nutrient-rich crop varieties. Predicting the genetic value of the sweetpotato germinated seedlings with the help of genome-wide marker data to identify individuals of high nutritional quality prior to phenotypic assessment. Functional genomics: Understanding the functions of genes involved in nutrient biosynthesis and metabolism, which facilitate the manipulation of these pathways to improve nutrient content.

7.7 Challenges and Future Directions

Efforts to increase nutrition must be balanced with other traits, emphasizing the need for nutritional genomics to influence overall crop genotyping strategies. This raises difficulties because nutritional traits often associated with consumer benefits have quantitative inheritance and multifactorial genetic causation. The enormous genetic diversity in sweetpotato also presents challenges. Gaining access to genotypes representing the full range of nutritional phenotypes can be difficult, but the main challenge is

to understand and develop crops with increased nutrition that are suited to the full range of environments where sweetpotato is grown in the developing world. This will need extensive research on genotype by environment by management interaction, and increased nutrition must be accompanied by maintenance or enhancement of productivity (Low et al. 2020). One of the enabling technologies for genetic enhancement of complex traits, including nutrition, is transgenesis, which often acts as a genetic “proof” of the identity of genes and their function. But transgenesis in many food crops, including sweetpotato, does not lead to commercialization and its adoption for crop improvement has been variable, despite offering significant benefits over alternative technologies such as marker-assisted selection. This is because regulatory, biosafety, and consumer acceptance barriers are high for transgenesis. Alternative strategies such as MAS must be used as a bridge to commercial biotech, and there is concern that misinterpretation of transgenesis will lead to rejection of all biotechnology, negating the potential benefits of genomics on nutritional enhancement. Efforts in genomics-assisted breeding are anticipated to promote increased nutritional quality of sweetpotato. Success would heighten the profile of sweetpotato as a health-promoting food and support the crop’s contribution to food security in the developing world. However, success is not assured and there are a number of technical and commercialization challenges to be overcome.

References

- Amankwaah VA (2019) Phenotyping and genetic studies of storage root chemistry traits in sweetpotato. North Carolina State University, Raleigh
- Amankwaah VA, Williamson S, Reynolds R et al (2023) Development of NIRS calibration curves for sugars in baked sweetpotato. *J Sci Food Agric* 104:4801–4807. <https://doi.org/10.1002/jsfa.12800>
- Bouis HE, Saltzman A (2017) Improving nutrition through biofortification: a review of evidence from HarvestPlus, 2003 through 2016. *Glob Food Sec* 12:49–58. <https://doi.org/10.1016/j.gfs.2017.01.009>
- Bouis HE, Welch RM (2010) Biofortification: a sustainable agricultural strategy for reducing micronutrient malnutrition in the global south. *Crop Sci* 50:20–32
- Chen BH, Chen YY (1993) Stability of chlorophylls and carotenoids in sweetpotato leaves during microwave cooking. *J Agric Food Chem* 41:1315–1320
- Da Silva Pereira GS, Amankwaah VA, Ketavi M et al (2023) Sweetpotato: nutritional constituents and genetic composition. *Compendium of crop genome designing for nutraceuticals*. Springer, Singapore, pp 1–43
- de Albuquerque TMR, Sampaio KB, de Souza EL (2019) Sweetpotato roots: unrevealing an old food as a source of health promoting bioactive compounds—a review. *Trends Food Sci Technol* 85:277–286. <https://doi.org/10.1016/j.tifs.2018.11.006>
- FAOSTAT (2022) World food and agriculture: statistical yearbook 2022. FAO, New York
- Gemenet DC, da Silva PG, De Boeck B et al (2020a) Quantitative trait loci and differential gene expression analyses reveal the genetic basis for negatively associated β -carotene and starch content in hexaploid sweetpotato [*I. batatas* (L.) Lam.]. *Theor Appl Genet* 133:23–36. <https://doi.org/10.1007/s00122-019-03437-7>
- Gemenet DC, Kitavi MN, David M, Ndege D, Ssali RT, Swankaert J, Makunde G, Yencho GC, Gruneberg W, Carey E, Mwanga RO, Andrade MI, Heck S, Campos H (2020b) Development of diagnostic SNP markers for quality assurance and control in sweetpotato [*Ipomoea batatas* (L.) Lam.] breeding programs. *PLOS ONE* 15(4):e0232173. <https://doi.org/10.1371/journal.pone.0232173>
- Grüneberg WJ, Ma D, Mwanga ROM et al (2015) Advances in sweetpotato breeding from 1992 to 2012. Potato and sweetpotato in Africa: transforming the value chains for food and nutrition security. CABI, New York, pp 3–68
- Gruneberg WJ, Eyzaguirre R, Diaz F, De Boeck B, Espinoza J, Mwanga ROM, Swankaert J, Dapaah H, Andrade M, Makunde G, Tumwegamire S, Agili S, Ndingo-Chipungu FP, Attaluri S, Kapinga R, Nguyen T, Kaiyung X, Tjintokohadi K, Ssali RT, Carey T, Low J (2019) Procedures for the evaluation of sweetpotato trials. Manual. Lima (Peru). International Potato Center (CIP), p 86
- Haas JD, Beard JL, Murray-Kolb LE, del Mundo AM, Felix A, Gregorio GB (2005) Iron-biofortified rice improves the iron stores of nonanemic filipino women. *J Nutr* 135(12):2823–2830. <https://doi.org/10.1093/jn/135.12.2823>
- IFT (Institute of Food Technologists) (2007) Sensory evaluation methods. The Society for the Food Technologists, Chicago, IL
- Jackson MJ (1997) The assessment of bioavailability of micronutrients: introduction. *Eur J Clin Nutr* 51:S1–S2
- Jenkins M, Shanks CB, Brouwer R, Houghtaling B (2018) Factors affecting farmers’ willingness and ability to adopt and retain vitamin A-rich varieties of orange-fleshed sweetpotato in Mozambique. *Food Sec* 10:1501–1519. <https://doi.org/10.1007/s12571-018-0845-9>

- Joanna L, Inés MA, Esteban V, Gustavo R, Patricia A, Mariana R et al (2019) Integration of sensory analysis into plant breeding: a review. *Agrociencia Uruguay* 23:1–15
- Kays SJ, Wang Y (2002) Sweetpotato quality: its importance, assessment and selection in breeding programs. *Acta Hort* 187–193. <https://doi.org/10.17660/ActaHortic.2002.583.21>
- Kemp SE, IFST PFSG Committee (2008) Application of sensory evaluation in food research. *Int J Food Sci Technol* 43:1507–1511
- Kemp SE, Ng M, Hollowood T, Hort J (2018) Introduction to descriptive analysis. In: Kemp SE, Hort J, Hollowood T (eds) *Descriptive analysis in sensory evaluation*. Wiley, Hoboken, pp 3–39
- Khan Z, Takemura M, Maoka M, Hattan T, Otani M, Misawa N (2022) Molecular breeding of sweetpotato carotenoids. *IntechOpen*. <https://doi.org/10.5772/intechopen.101849>
- Kitahara K, Nakamura Y, Otani M et al (2017) Carbohydrate components in sweetpotato storage roots: their diversities and genetic improvement. *Breed Sci* 67:62–72. <https://doi.org/10.1270/jsbbs.16135>
- Low JW, Ortiz R, Vandamme E, Andrade M, Biazin B, Grüneberg WJ (2020) Nutrient-dense orange-fleshed sweetpotato: advances in drought-tolerance breeding and understanding of management practices for sustainable next-generation cropping systems in Sub-Saharan Africa. *Front Sustain Food Syst* 4. <https://doi.org/10.3389/fsufs.2020.00050>
- Mudege NN, Kebaara K, Mukewa E (2019) Effects of commercialization of sweetpotato on gender relations and wellbeing among smallholder farmers: technical workshop to review study findings and develop recommendations for improved programming
- Mwanga ROM, Swanckaert J, da Silva PG et al (2021a) Breeding progress for vitamin A, iron and zinc biofortification, drought tolerance, and sweetpotato virus disease resistance in sweetpotato. *Front Sustain Food Syst* 5:6674. <https://doi.org/10.3389/fsufs.2021.616674>
- Mwanga ROM, Mayanja S, Swanckaert J, Nakitto M, Felde T, Gruneberg W et al (2021b) Development of a food product profile for boiled and steamed sweetpotato in Uganda for effective breeding. *Int J Food Sci* 56:1385–1398
- Nakamura Y, Ohara-Takada A, Kuranouchi T, Masuda R, Katayama K (2014) Mechanism for maltose generation by heating in the storage roots of sweetpotato cultivar “Quick Sweet” containing starch with a low pasting temperature. *Nippon Shokuhin Kagaku Kogaku Kaishi* 61:577–585
- Nakatumba-Nabende J, Babirye C, Tusubira JF, Mutegeki H, Nabiryo AL, Murindanyi S, Katumba A, Nantongo J, Sserunkuma E, Nakitto M, Ssali R, Makunde G, Moyo M, Campos H (2023) Using machine learning for image-based analysis of sweetpotato root sensory attributes. *Smart Agricult Technol* 16:291. <https://doi.org/10.1016/j.atech.2023.100291>
- Nakitto M, Johanningsmeier SD, Moyo M, Bugaud C, de Kock H, Dahdouh L, Forestier-Chiron N, Ricci J, Khakasa E, Ssali RT, Mestres C (2022) Sensory guided selection criteria for breeding consumer-preferred sweetpotatoes in Uganda. *Food Qual Prefer* 101:104628. <https://doi.org/10.1016/j.foodqual.2022.104628>
- Neela S, Fanta SW (2019) Review on nutritional composition of orange-fleshed sweetpotato and its role in management of vitamin A deficiency. *Food Sci Nutr* 7:1920–1945. <https://doi.org/10.1002/fsn3.1063>
- Ravi V, Chakrabarti SK, Makesh Kumar T, Saravanan R (2014) Molecular regulation of storage root formation and development in sweetpotato. *Hortic Rev Am Soc Hortic Sci* 42:157–208. <https://doi.org/10.1002/9781118916827.ch03>
- Ru L, Chen B, Li Y, Wills RBH, Lv Z, Lu G, Yang H (2021) Role of sucrose phosphate synthase and vacuolar invertase in postharvest sweetening of immature sweetpotato tuberous roots (*I. batatas* (L.) Lam Cv ‘Xinxiang’). *Sci Hortic* 282:110007
- Sanoussi AF, Adjatin A, Dansi A, Adebowale A, Sanni LO, Sanni A (2016) Mineral composition of ten elites sweetpotato (*I. batatas* [L.] Lam.) Landraces of Benin. *Int J Curr Microbiol Appl Sci* 5(1):103–115
- Shahzad R, Jamil S, Ahmad S et al (2021) Biofortification of cereals and pulses using new breeding techniques: current and future perspectives. *Front Nutr* 8:721728. <https://doi.org/10.3389/fnut.2021.721728>
- Shimamura T, Sumikura Y, Yamazaki T, Tada A, Kashiwagi T, Ishikawa H, Ukeda H (2014) Applicability of the DPPH Assay for evaluating the antioxidant capacity of food additives: inter-laboratory evaluation study. *Anal Sci* 30:717–721
- Takiko S, Motoyasu O, Tatsuro H, Sun-Hyung K (2006) Increase of amylose content of sweetpotato starch by RNA interference of the starch branching enzyme II gene (IbSBEII). *Plant Biotechnol* 23(1):85–90. <https://doi.org/10.5511/plantbiotechnology.23.85>
- Tomlins K, Ndunguru G, Stambuli K et al (2007) Sensory evaluation and consumer acceptability of pale-fleshed and orange-fleshed sweetpotato by school children and mothers with preschool children. *J Sci Food Agric* 87:2436–2446. <https://doi.org/10.1002/jsfa.2931>
- Truong VD, Avula RY, Pecota KV, Yencho GC (2018) Sweetpotato production, processing, and nutritional quality. *Handbook of vegetables and vegetable processing*. Wiley, Amsterdam, pp 811–838
- Tumwegamire S, Rubaihayo PR, LaBonte DR et al (2011a) Genetic diversity in white- and orange-fleshed sweetpotato farmer varieties from east Africa evaluated by simple sequence repeat markers. *Crop Sci* 51:1132–1142. <https://doi.org/10.2135/cropsci2010.07.0407>
- Tumwegamire S, Kapinda R, Rubaihayo PR, LaBonte DR, Grüneberg WJ, Burgos G, Felde TZ, Carpio R, Pawelzik E, Mwanga RO (2011b) Evaluation of dry matter, protein, starch, sucrose, β -carotene, iron, zinc, calcium, and magnesium in east African sweetpotato [*I. batatas* (L.)

- Lam] germplasm. *HortScience Horts* 46(3):348–357. <https://doi.org/10.21273/HORTSCI.46.3.348>
- Wallace JG, Rodgers-Melnick E, Buckler ES (2018) On the road to breeding 4.0: unravelling the good, the bad and the boring of crop quantitative genomics. *Annu Rev Genet* 52:421–444
- Welch RM, Graham RD (2004) Breeding for micronutrients in staple food crops from a human nutrition perspective. *J Exp Bot* 55:353–364
- Woolfe J (1992) Sweetpotato: an untapped food resource. Cambridge University Press and the International Potato Center (CIP), Cambridge
- Wu S, Lau KH, Cao Q, Hamilton JP, Sun H, Zhou C, Eserman L, Gemenet DC, Olukolu BA, Wang H, Crisovan E, Godden GT, Jiao C, Wang X, Kitavi M, Manrique-Carpintero N, Vaillancourt B, Wiegert-Rininger K, Yang X, Bao K, Schaff J, Kreuze J, Gruneberg W, Khan A, Fei Z (2018) Genome sequences of two diploid wild relatives of cultivated sweetpotato reveal targets for genetic improvement. *Abstr Nat Commun* 9(1). <https://doi.org/10.1038/s41467-018-06983-8>

Open Access This chapter is licensed under the terms of the Creative Commons Attribution 4.0 International License (<http://creativecommons.org/licenses/by/4.0/>), which permits use, sharing, adaptation, distribution and reproduction in any medium or format, as long as you give appropriate credit to the original author(s) and the source, provide a link to the Creative Commons license and indicate if changes were made.

The images or other third party material in this chapter are included in the chapter's Creative Commons license, unless indicated otherwise in a credit line to the material. If material is not included in the chapter's Creative Commons license and your intended use is not permitted by statutory regulation or exceeds the permitted use, you will need to obtain permission directly from the copyright holder.

