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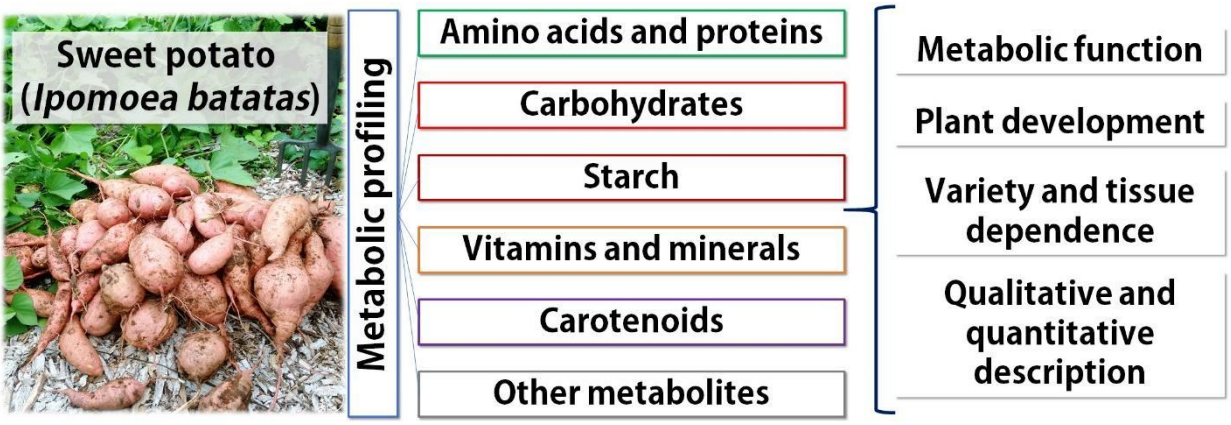
'Sweet potato, batata or camote' (*Ipomoea batatas*): Metabolomic characterization

Andrés Otálora [1,2], Daniel Palacios [2,3], Tulio A. Lerma [1,2], Natalia Afanasjeva [1], Manuel Palencia [1], Álvaro A. Arrieta [4]

[1] *Research Group in Science with Technological Applications (GI-CAT), Department of Chemistry, Faculty of Natural and Exact Sciences, Universidad del Valle, Cali - Colombia.*
[2] *Mindtech Research Group (Mindtech-RG), Mindtech s.a.s., Montería/Cali - Colombia.*
[3] *Departamento de Polímeros, Universidad de Concepción, Concepción - Chile.*
[4] *Department of Biology and Chemistry, Universidad de Sucre, Sincelejo-Colombia.*

Corresponding Author: Manuel Palencia. E-mail: manuel.palencia@correounivalle.edu.co

Graphical Abstract



Abstract. Sweet potato crop is one of the most relevant root crops in the world, occupying the seventh position among the most important food crops. The nutritional and economic importance of this crop in low-income regions of different developing countries, in addition to its limited productive and application development, has drawn attention to a more in-depth study of sweet potato plants to establish ideas for the improvement of traits, productivity, and utility of the crop. In this sense, understanding the plant at a metabolic level and identifying the relationship between its metabolome and its phenotypic characteristics or growth properties are important aspects to study. For this reason, this review sought to collect and present the works carried out so far focused on the determination and study of the metabolic profiling of sweet potato plants. Initially, a qualitative description of the plant metabolome was made based on these works, highlighting the most relevant results. Subsequently, a quantitative description of primary metabolites, such as proteins, amino acids, lipids, and carbohydrates, was carried out, including a brief physicochemical characterization of sweet potato starch. Finally, vitamins, minerals, and other important secondary metabolites, such as flavonoids and anthocyanins, were described quantitatively. Through this, it was possible to make a global approach to the metabolic behavior of sweet potato plants and their phytochemicals with greater relevance, which provides nutritional and medicinal value.

Keywords: Sweet potato, *Ipomoea batatas*, Metabolic profile, Starch, Carotenoids.

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Content

1. Introduction

Sweet potato, or more specifically *Ipomoea batatas*, is one of the root crops with the highest economic and nutritional relevance for many tropical and subtropical developing countries. Morphologically, sweet potato is a perennial herbaceous plant with vine characteristics. The ability of this plant to produce edible tuberous roots has allowed its productive growth as a crop since its domestication in the New World several centuries ago (Martínez et al., 2016). In turn, attention has been directed to determining the nutritional relevance of sweet potato plants, including leaves and roots. The roots have been found to have a high starch content as an energy reserve for the plant. Also, they can have high protein, vitamin, mineral, and pigment contents. The relatively high presence of species such as β-carotene, or provitamin A, anthocyanins, and flavonoids determines the nutritional content of each variety, its color, and its flavor (Bovell-Benjamin, 2007). At this point, the importance of sweet potatoes to treat vitamin A deficiency in children has been highlighted (Neela and Fanta, 2019). Thus, different sweet potato varieties are currently marketed and are classified mainly according to their color, from creamy-white to orange or violet. For its part, high protein and mineral contents have been reported in sweet potato leaves. The presence of anthocyanins and flavonoids in this part of the plant also gives it antioxidant and scavenging radical properties (Chandrasekara and Kumar, 2016).

Currently, the sweet potato crop is the sixth most important food crop after rice, wheat, potatoes, maize, and cassava. In 2018, world production of almost 92 million tons was reported, with a harvested area of more than 8 million tons and an average yield of 12.9 tons per hectare since 2000. Sweet potato production is concentrated in Asia. This continent participates in 66 % of world sweet potato production. Especially, China is the country with the highest production in Asia and the world, reporting close to 53 million tons in 2018, as illustrated in **Figure 1** (FAOSTAT, 2020). African countries like Malawi, Nigeria, Tanzania, Ethiopia, and Uganda also report high sweet potato production after China. Likewise, coun

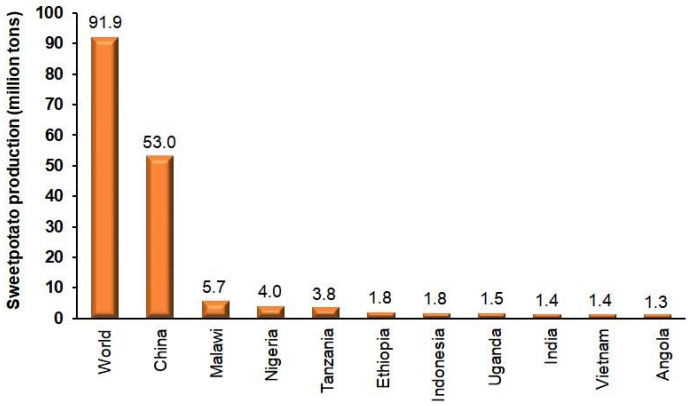

Figure 1. Sweet potato production in 2018 distributed in the 10 countries with the highest participation (FAOSTAT, 2020).

-tries in the Americas, such as the United States, Brazil, Haiti, Cuba, and Argentina, contribute a small part of world sweet potato production. Much of the sweet potato production is used to feed the local population of the producing countries, constituting an important source of food and income for farming families. Additionally, the adaptive properties of the sweet potato plant and its low nutritional requirements have allowed its exploitation as a crop in marginal soils (Ayeleso et al., 2016; Martínez et al., 2016). Despite this, sweet potato production has decreased since 2000 and in the last 10 years, it has been stagnant due to different factors, such as low technological implementation, production improvement, support from government policies, and product utility (Udemezue, 2019). Thus, several experts have ratified the importance of the continuous study of sweet potato cultivation to promote breeding projects, optimization of important traits, applicability, and nutritional relevance (Lareo and Ferrari, 2019). At this point, metabolomics is one of the most used tools to study plant metabolic profiles, through which it is possible to determine amounts of important metabolites, including nutrients; metabolic pathways involved in relevant processes, such as the synthesis of starch and β-carotene; and relationships between growing conditions, stress, or nutritional supplementation with plant metabolome (Drapal et al., 2019; Lebot et al., 2011; Ojong et al., 2008). Thus, it is possible to establish a sweet potato diversity at a metabolic level of utility in any productive improvement project. In this sense, this review sought to collect, expose and concisely discuss the research associated with the metabolic profile determination of the sweet potato plant, including a qualitative and quantitative description according to the most relevant parts of the plant and its metabolites.

2. Metabolic profile of sweet potato: Qualitative description

In recent times, the participation of different "omics" disciplines, e.g., genomics, transcriptomics, epigenomics, proteomics,

metabolomics, and phenomics, has increased markedly in the study of food crops at different levels. This is in order to determine important relationships between physical, molecular, genetic characteristics, among others, and the macroscopic development of each plant. In this way, the information obtained through this analysis would allow for establishing patterns, adjusting variables, differentiating between species, and proposing breeding programs that enhance the characteristics of each cultivar and promote optimal productive development. Especially, metabolomics is one of the most complex "omics" disciplines and has received recent attention in the study of different crops, particularly to map plant traits and selections at the metabolic level (Kumar et al., 2017).

Due to the nutritional and economic relevance of the sweet potato crop, several studies focused on the determination of its metabolites and important phytochemicals for human consumption, such as carbohydrates, proteins, vitamins, and minerals, have been carried out since the beginning of the last decade (Sharma et al., 2019; Wang et al., 2016). Carotenoids, flavonoids, phenolic acids, and anthocyanins determination has also been important, due to their properties of natural pigments, antioxidant activity, and scavenging of radicals (Ojong et al., 2008; Rodrigues de Albuquerque et al., 2019; Shekhar et al., 2015; Wang et al., 2018). Despite this, research focused on the qualitative and quantitative determination of the general metabolic profile of *Ipomoea batatas* is scarce. Some of these have focused on determining relationships between the metabolome and traits of different parts of the plant, especially leaves and roots, or different sweet potato varieties (Drapal et al., 2019; Park et al., 2016; Shekhar et al., 2016). Also, the establishment of relationships between the chemical components of sweet potato roots, their quality, and certain phenotypic characteristics has been addressed (Lebot et al., 2011).

Recently, Drapal et al. (2019) reported the metabolic profile determination of 27 sweet potato cultivars, including cultivars from Mexico, Ecuador, the United States, Colombia, Argentina, the Philippines, Peru, Taiwan, among others. In order to study the metabolic diversity of the leaves and roots of sweet potato plants. The analysis of polar and apolar extracts of the roots and leaves using Ultra Pressure Liquid Chromatography (UPLC) and Gas Chromatography coupled with Mass Spectrometry (GC-MS) allowed determining a total of 130 metabolites, of which 66 were common to both tissues, 47 exclusive of roots, and 17 exclusives of leaves. Two-thirds of the identified metabolites were classified into amino acids, sugars, tricarboxylic acid cycle intermediates (TCA), sterols, membrane precursors, and isoprenoids. The other third was classified as metabolites associated with phenylpropanoid metabolism, with spectral similarities to flavonoids. The relative content of sugars was higher, with about 85 % of the detected metabolites. While, amino acids, TCA intermediates, and phenylpropanoids were found between 2 and 5 %. Isoprenoids represented 4 % of the metabolites identified in leaves and less than 1 % in roots. The rest of the metabolites represented 1 % in both tissues. From this information, it was possible to establish some metabolic pathways of relevance for the correct development of the plant, as illustrated in **Figure 2**.

Similar results were reported by Shekhar et al. (2016) when analyzing polar and apolar extracts of the tuberous roots of two sweet potato cultivars, one white-fleshed cultivar, and another orange-fleshed cultivar. The analysis through LC-MS allowed them to identify 148 and 126 metabolites in orange-fleshed and white-fleshed cultivars, respectively. In this case, 40–45 % organic acid, 16–21 % sugars, and 6 % amino acids were reported. The rest were associated with other secondary metabolites. At this point, the presence of organic acids such as 9,12-octadecadienoic and 9-octadecenoic acid was highlighted, which are useful for the treatment of various medical illnesses (Chandrasekara and Kumar, 2016). Among the sugars, high content of glucose, fructose, maltose, turanose, and its variants were reported, which present important participation in tuber metabolism. Other identified metabolites were by-products and intermediates of important metabolic pathways, such as phytosterols, terpenes, phenols, nucleosides, and alcohol derivatives.

In this same sense, Park et al. (2016) evaluated the metabolic profile of three sweet potato varieties with differences in flesh color: white, orange, and purple. In this work, the polar extracts of sweet potato roots were analyzed using GC-MS. It was possible to identify at least 41 common metabolites in the varieties extracts, including 17 amino acids, 13 organic acids, 7 sugars, 3 sugar alcohols, and 1 amine. The comparison of their metabolic profile allowed determine that the purple-fleshed and orange-fleshed varieties have a higher content of sugars, sugar alcohols, and secondary metabolites, compared to the white-fleshed variety. This has been related to the fact that phenolic compounds content has a proportional relationship with sugar content in the varieties (El Far and Taie, 2009). Likewise, a positive correlation between metabolites involved in related pathways was determined, obtaining three groups of related metabolites. For example, in the first group, aspartic acid, asparagine, citric acid, quinic acid, threonine, glutamine, and fructose were related. Serine, zeaxanthin, mannose, and some phenolic compounds such as shikimic acid, quercetin, myristicin, ferulic acid, among others, were found in the second group. While, in the third group some sugars and alcohols were related, such as sucrose, mannitol, inositol, and trehalose; some acids, such as pyroglutamic acid, glycolic acid, and 4-aminobutyric acid; and some carotenoids such as β-carotene and its derivatives.

On the other hand, a quantitative analysis of the pigment content in leaves and roots of different sweet potato cultivars allowed Drapal et al. (2019) to obtain important results. The identified pigments corresponded mainly to carotenoids and anthocyanins. Generally, the former are responsible for the orange coloration of some sweet potato varieties, while the latter are associated with purple colora-

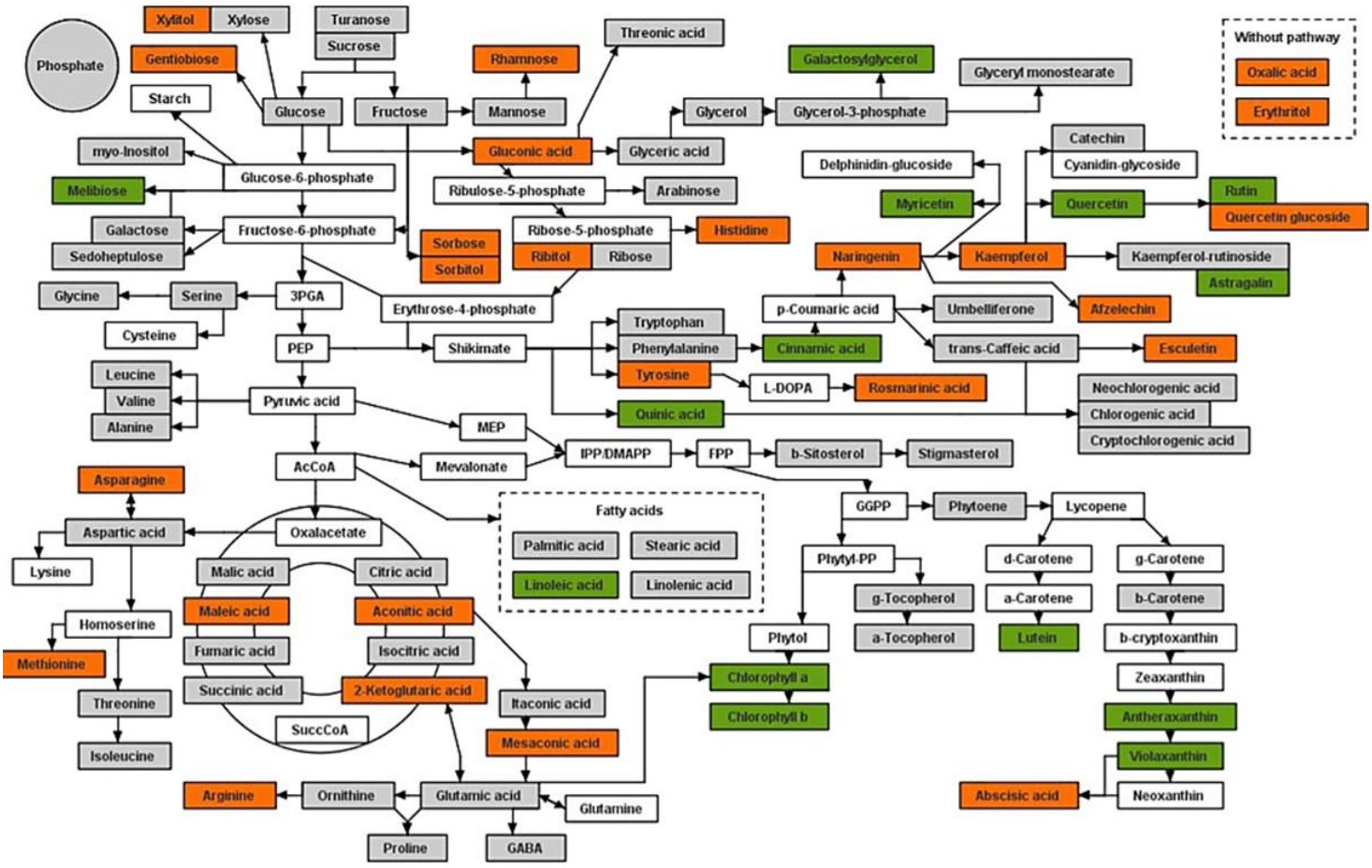

Figure 2. Display of metabolic pathways of the different metabolites detected in leaves (green), roots (orange), and both tissues (gray) of the sweet potato plant (Taken and edited from Drapal et al., 2019).

ration (Wang et al., 2016). Indeed, the results showed a higher carotenoid content in orange varieties and a higher anthocyanin content in purple varieties. Therefore, these purple varieties represent an important source of antioxidants and radical scavenger species (Bovell-Benjamin, 2007; Wang et al., 2016). On the other hand, the white-fleshed and yellow-fleshed cultivars presented low carotenoids and anthocyanins content. Among the carotenoids identified in the roots were phytoene, lutein, mutatochrome, and β-carotene (**Figure 3A**). While, in leaves, chlorophylls, violaxanthin, and anteraxanthin were mainly identified (**Figure 3B**), and to a lesser extent the aforementioned carotenoids.

Similar results were reported by Park et al. (2016). In this case, high content of carotenoids was reported in the orange-fleshed variety, about 90 times higher than the content of the white-fleshed and purple-fleshed varieties. The latter had a high content of flavonoids and anthocyanins. Quercetin, myricetin, kaempferol, and luteolin were found among the determined flavonoids (**Figure 4A**). While, among the identified anthocyanins, cyanidin and peonidin derivatives were found (**o**). Anthocyanins were exclusive to the purple-fleshed variety and were not detected in the white-fleshed and orange-fleshed varieties. Additionally, the phenolic acid content for the purple-fleshed variety was about 100 times higher than for the other varieties. On the other hand, high content of ferulic acid, *p*-hydroxybenzoic acid, and vanillic acid was identified. Specifically, the antioxidant potential of ferulic acid, its ability to improve vitamin C and E stability, and skin photoprotection have been highlighted (Shekhar et al., 2016).

The comparison of the metabolic profiles of leaves and roots of different sweet potato accessions carried out by Drapal et al. (2019) using principal component analysis (PCA) allowed determining that there is no significant metabolic diversity between leaves of different cultivars according to their genotype or phenotype, either using its overall metabolic composition or its primary metabolites. In the case of roots, it was found that there is a significant metabolic diversity according to their phenotype, comparing its overall metabolic composition. The varieties clustered according to their coloration (**Figure 5**) with the separation of three varieties with a high amount of certain metabolites, such as phenylpropanoids, some

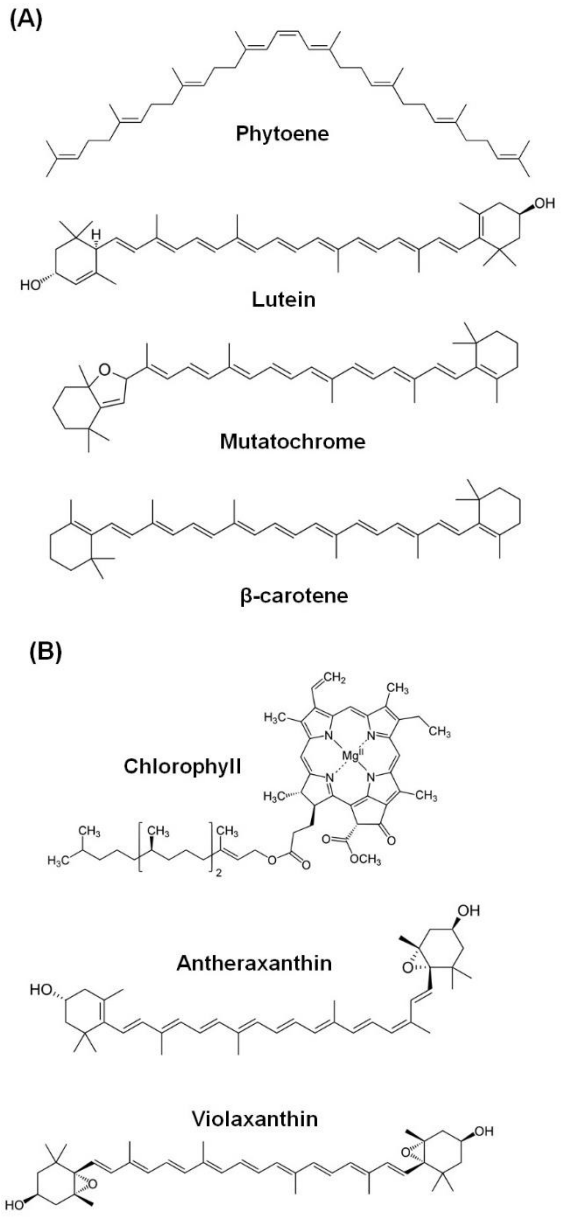

Figure 3. Chemical structures of the main pigments identified in (A) roots and (B) sweet potato leaves.

sugars, aspartic acid, cysteine, GABA, quinic acid, among others. Likewise, the PCA study confirmed that there is no relationship between sweet potato leaves and roots at the metabolic level, as it happens with other crops, e.g., potato and yam (Price et al., 2016). Through this, it was suggested that there is an independent genetic regulation between the two tissues of the same plant. Additionally, the absence of root differentiation according to their primary metabolites allowed considering low plant plasticity at the metabolic level due to multiple recombination events both in the New World and in Asia, Africa, and Oceania. Thus, the differentiation was limited to the carotenoids or root pigments contents.

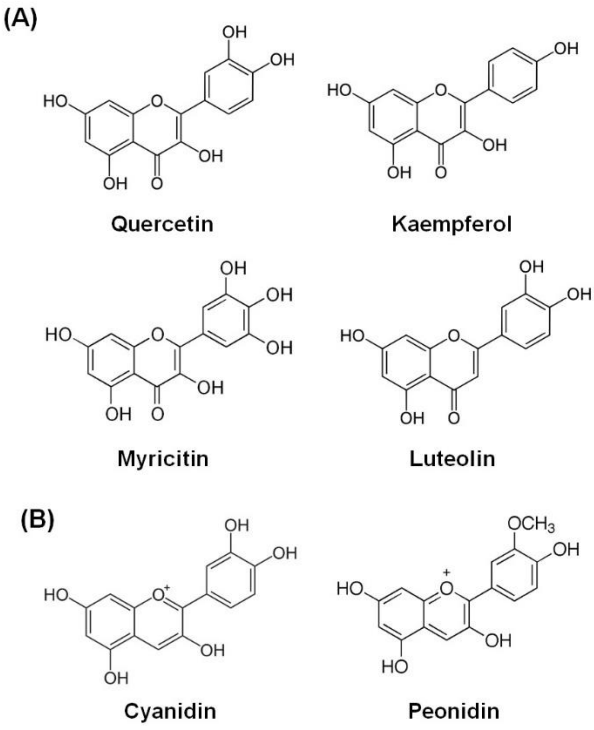

Figure 4. Chemical structures of (A) flavonoids and (B) anthocyanins identified in various sweet potato varieties.

Another important observation made in the same study was the relationship between the β-carotene and starch contents, determined using near-infrared reflectance spectroscopy. Through this technique, an inversely proportional relationship between the two metabolites was obtained, as previously reported (Cervantes-Flores et al., 2011). Drapal et al. (2019) highlighted that this finding supports the hypothesis that β-carotene and starch compete or interfere with the formation of macromolecular structures in the same organelles. This represents a drawback in breeding programs focused on obtaining a higher starch content, since the amount of β-carotene is affected, and vice-versa. On the other hand, no relationship was found between the amount of sucrose and β-carotene, indicating that the amount of provitamin A is not related to the root sweetness. This fact provides a benefit for consumers who prefer varieties with less sweetness.

3. Metabolic profile of sweet potato: Quantitative description

According to the previous discussion, the content of different metabolites can vary according to the tissue type, sweet potato variety, and even growing conditions. Thus, approximate values of the metabolite's contents of the sweet potato plant have been determined, highlighting its primary metabolites, such as amino

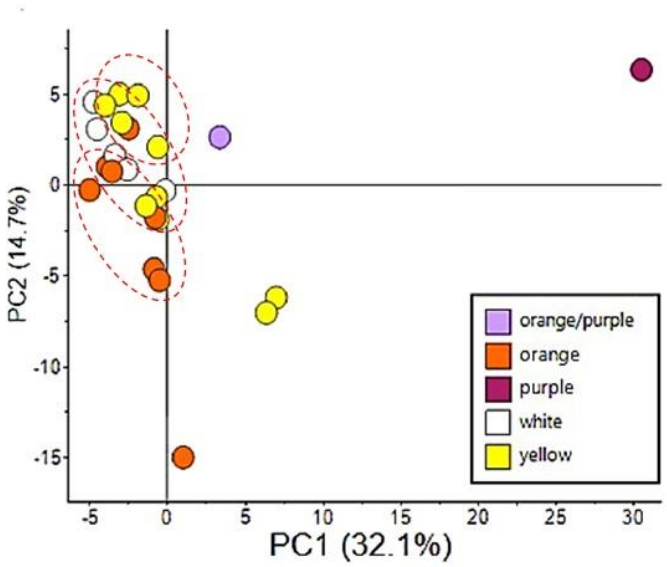

Figure 5. PCA plot for the global metabolic profile comparison of different sweet potato roots (Taken and edited from Drapal et al., 2019). The red dotted circles represent the main clusters formed according to the root phenotype.

acids, proteins, lipids, sugars, vitamins and minerals, and some secondary metabolites, such as anthocyanins and flavonoids, due to their nutritional and medicinal relevance.

3.1. Amino acids and proteins

The protein content in sweet potato roots ranges from ~1 to ~10 % on a dry weight basis. Generally, the content of these macromolecules is low, with some exceptions of improved varieties with a higher protein content (Mu et al., 2009). About 80 % of the total protein content in roots corresponds to storage proteins called sporamins, specifically classes A and B. In addition to their nitrogen storage function, sporamins also have antioxidant properties and participation in different metabolic processes (Wang et al., 2016). In a smaller proportion, but with a relevant function, proteins associated with glycolysis or gluconeogenesis have been found in the roots, such as sucrose synthase, ADP glucose phosphorylase, and β-amylase. Proteins such as catalases, peroxidases, enolases, aldolases, and lyases have also been identified, as participants in the metabolism of amino acids, sugars, and stress processes (Shekhar et al., 2016). In the case of the leaves, the protein content becomes higher, even with values close to ~ 20 %, due to the participation of a large number of enzymes in photosynthesis, CO_2 fixation, and generation of nutrients and energy (Wang et al., 2016). Sweet potato proteins are typically rich in aspartic and glutamic acids, as shown in **Table 1**, with values close to 10 mg per gram of dry weight in roots and greater than 20 mg per gram of dry weight in leaves. Additionally, high relative contents of leucine, valine, lysine, arginine, and phenylalanine have been reported. While sulfur amino acids are in low quantity (Chuang et al., 2011; Rodrigues de Albuquerque et al., 2019).

Table 1. The average composition of amino acids in sweet potato roots and leaves. Values in mg for each gram of dry weight.

Amino acid	Roots[a]	Leaves[b]
Glutamic acid	7.6	20.7
Aspartic acid	14.6	25.8
Serine	4.8	6.8
Threonine	5.4	7.5
Proline	3.9	7.6
Alanine	4.4	8.9
Glycine	4.0	7.6
Valine	6.7	9.3
Cysteine	0.4	1.9
Methionine	2.0	0.8
Isoleucine	4.5	7.0
Leucine	6.0	12.8
Tyrosine	4.8	5.5
Phenylalanine	6.9	9.8
Lysine	9.9	9.4
Histidine	3.2	4.0
Tryptophan	1.7	-
Arginine	10.1	9.2

[a] Purcell et al. (1978). The analysis comprised two cultivars.
[b] Chuang et al. (2011). The analysis comprised two cultivars.

3.2. Lipids

Lipid content is relatively low in sweet potato roots and leaves. In roots, lipids can be 0.2 to 3.0 % on a dry-weight basis, while leaves can contain 0.3 to ~ 5 % on a dry-weight basis (Lebot, 2009). Among the total lipid content in the roots, approximately 7–14 % correspond to phospholipids, and 30–50 % correspond to glyco- and galactolipids, which are structural components of cell membranes. On the other hand, approximately 45 to 60 % corresponds to neutral lipids, including acylglycerols and fatty acids, which participate in various metabolic processes, including hormonal regulation and starch storage. The presence of different fatty acids and their content in sweet potato roots has been highlighted. For example, palmitic acid and linoleic acid are between 35–43 % each, being the fatty acids with the highest presence in the roots. The presence of stearic acid, oleic acid, linolenic acid, and arachidic acid has also been reported, in approximate amounts of 2–4, 0.6–1.7, 14–18, and 0.2–0.4 %, respectively (Mu and Zhang, 2019; Wang et al., 2016). In

this same sense, various carotenoids have been determined within the unsaponifiable lipids, some of which have nutritional relevance, such as β-carotene. The β-carotene contents of up to 0.6 mg per g of dry weight have been reported in orange-fleshed varieties. Also, lipids such as lutein and phytoene (**Figure 3A**) can be found in ranges of 0.1–1.0 and 0–0.02 mg per gram of dry weight. In the leaves, considerable amounts of lipid pigments such as anteraxanthin and violaxanthin have been reported (**Figure 3B**) with concentration ranges of 0.07–0.1 and 0.1–0.3 mg per gram of dry weight (Price et al., 2020).

3.3. Sugars and carbohydrates: sweet potato starch

Simple and derivative sugars can be found in the sweet potato roots and leaves that participate in important metabolic processes, mainly in the production of energy and its storage as starch. Among these sugars, there are mainly glucose, fructose, sucrose, and maltose, which may be present between ~1 to ~500 mg per gram of dry weight in the roots, depending on variety (Price et al., 2020). The relative amount of these sugars determines the sweetness of each variety (Lebot, 2009). The high carbohydrate content in roots is a product of their energy storage function, which corresponds to 60–80 % of root dry weight (Rodrigues de Albuquerque et al., 2019). This biopolymer has been extensively studied due to its importance in food production, pharmaceutical applications, obtaining materials, and even biofuel generation (Lareo and Ferrari, 2019).

Sweet potato starch is stored in roots in granules of different sizes, depending on the cultivar, growing conditions, and plant physiology. Starch granules in sweet potatoes can have diameters between 2 and 45 μm, generally with a bimodal distribution (Ketnawa et al., 2019). The granules have a smooth surface and their shape can be round, polygonal, oval, or semi-oval, as illustrated in **Figure 6**. As a macromolecule, sweet potato starch is composed of 20 to 30 % amylose, a linear and slightly branched glucose polymer, and 70–80 % amylopectin, which has a high branching. The amylose content in sweet potato starch has been related to its granule size, such that higher amylose content induces greater granule size (Abegunde et al., 2013). In this sense, an important property of starch granules is their crystallinity. Experiments using X-ray diffraction have determined that sweet potato starch is made up of alternating amorphous and semi-crystalline sheets called "growth rings", their thickness is 100–400 nm with a separation of 9–10 nm (Ketnawa et al., 2019). A measure of the degree of starch crystallinity is its solubility and water absorption capacity, which have been reported with values of 7–18 % and 15–45 g of water per gram of starch (Iheagwara, 2013; Moorthy et al., 2010). Other physicochemical properties of sweet potato starch have been determined, such as the initial, peak, and conclusion temperature in its gelatinization process, reporting values of ~60, ~70, and ~80 ° C, respectively. Furthermore, the enthalpy associated with this process

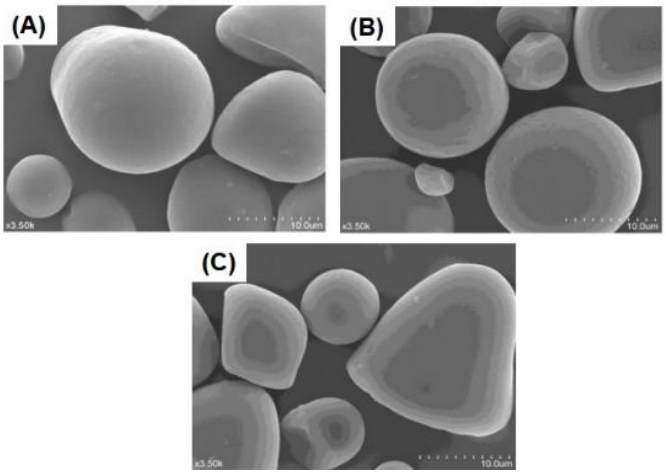

Figure 6. Scanning electron micrographs of sweet potato starch granules with (A) round, (B) oval, and (C) polygonal shapes (Taken and edited from Abegunde et al., 2013).

is between ~7 and ~12 J for each gram of starch (Abegunde et al., 2013).

Several studies have focused on elucidating the metabolic pathways associated with starch biosynthesis in sweet potato roots. Starch is known to be synthesized in plastids, which consist of chloroplasts and amyloplasts, in storage tissues and leaves. Synthesis occurs through three main mechanisms including the Calvin cycle, sucrose synthesis, and storage starch biosynthesis (Pfister and Zeeman, 2016). Specifically, in this last pathway, starch is obtained from adenosine diphosphoglucose and is a process catalyzed by multiple enzymes. Among these enzymes, granule-bound starch synthase I stand out, which is key in amylose synthesis. Whereas, enzymes such as soluble starch synthases and starch branching enzymes I and II participate in amylopectin production. In this sense, works have been carried out associated with the improvement of starch quality by regulation of the amylose/amylopectin ratio through genetic modification and modulation of enzymatic processes (Kitahara et al., 2017).

3.4. Vitamins and minerals

Vitamins and minerals contents of sweet potatoes have also been the subject of study in different works, due to its nutritional relevance associated with human consumption of sweet potatoes. **Table 2** summarizes the approximate content of minerals and vitamins in sweet potato roots and leaves. The minerals and vitamins contents are generally higher in leaves than in roots (Wang et al., 2016). This is a reflection of greater metabolic dynamism in the leaves than in the roots, which involves greater participation of vitamins and minerals within different enzymatic processes, regulation of metabolic pathways, transport processes, cell signaling, among others (Maathuis and Diatloff, 2012). Among the reported minerals,

Table 2. Approximate content of vitamins and minerals in sweet potato leaves and roots. Values per 100 grams of tissue dry weight.

Mineral or vitamin	Leaves[a]	Roots[b]
Calcium (mg)	1334–1407	68–73
Iron (mg)	11–20	1.6–2.3
Magnesium (mg)	455–513	26–27
Phosphorus (mg)	137–153	40–43
Potassium (mg)	1963–3340	235–502
Sodium (mg)	25–69	22–27
Zinc (µg)	3200–3300	249–389
Cooper (µg)	1400–1500	152–304
Vitamin C (mg)	22–104	63–81
Thiamine (µg)	490–620	53–128
Riboflavin (µg)	4400–6300	248–254
Niacin (µg)	450–540	856–1498
Vitamin E (mg)	3.2–5.8	1.4–2.8

[a] Suarez et al. (2020).
[b] Wang et al., (2016).

potassium content is much higher in both leaves and roots. Among the main functions of potassium in the plant are cell expansion, auxin homeostasis, cell signaling, and nutrient transport through the phloem (Sustr et al., 2019). Additionally, calcium, magnesium, and phosphorous contents are relatively moderate. While zinc and copper are found in low amounts. Furthermore, the vitamin C content is high in both leaves and roots. Additionally, they have a considerable content of riboflavin, niacin, thiamine, and vitamin E. It is important to highlight that depending on variety, provitamin A or β-carotene content can be high, as in previous sections. This suggests that from a nutritional point of view, sweet potato leaves and roots present an important option in the human diet, even for the treatment of nutrient deficiencies (Neela and Fanta, 2019).

3.5. Other important metabolites

There are other metabolites of importance for sweet potato plants that are of interest to human health. Among these, phenolic acids, flavonoids, and anthocyanins stand out. These species participate in different functions and metabolic pathways of the plant, such as tissue pigmentation, ultraviolet-light filtration, nitrogen fixation, cell cycle inhibition, protection against reactive oxygen species and oxidizing agents, and even cell signaling (Khoo et al., 2017; Mathesius, 2018).

There is a wide variety of phenolic acids in sweet potato roots and leaves. In the latter, caffeoylquinic acid and its derivatives have been reported, such as chlorogenic acid and other glycosylated structures. Purple-fleshed varieties have been found to contain the highest amount of caffeoylquinic acid, reaching 0.8 mg per gram of dry weight, while the total polyphenols content has been higher in orange-fleshed varieties (Rodrigues de Albuquerque et al., 2019). On the other hand, hydroxycinnamic acid and its derivatives, such as sinapic acid, have been found in the leaves, in addition to benzoic acid and *p*-anisic acids. The content of these acids is between ~50 and ~500 mg per gram of dry weight (Wang et al., 2016).

Flavonoids and anthocyanins contents vary markedly between varieties with different root colorations. Generally, the purple-fleshed varieties have a higher content of flavonoids and anthocyanins. Among the most identified flavonoids are quercetin, myricetin, kaempferol, and luteolin. Their structures are shown in **Figure 4A**. In purple-fleshed varieties, the flavonoid content can exceed 1000 µg per gram of dry weight, while in white-fleshed and orange-fleshed varieties values between 50 and 500 µg per g of dry weight can be found (Wang et al., 2018). In this same sense, anthocyanins, a specific group of flavonoids, have been quantified. Figure 4B shows the structures of two anthocyanins with the highest presence in sweet potato roots and leaves: cyanidin and peonidin. Additionally, there are numerous anthocyanins derived from these species. In quantitative terms, the anthocyanin content in roots can vary from 4.0 to 1.3 mg per g of fresh weight in purple-fleshed varieties. This content is relatively low in other varieties, with 0.02–0.05 mg per g of fresh weight (Wang et al., 2018). The presence of these species in the varieties, mainly those with purple flesh, provides them with nutritional and human health relevance due to their antioxidant and radical-scavenging activity (Rodrigues de Albuquerque et al., 2019; Wang et al., 2016).

7. Conclusions

The sweet potato crop is one of the most relevant root crops in different tropical countries. Sweet potato roots have contributed to the diet, economy, and subsistence mainly of low-income populations in these countries. Furthermore, the leaves have been used for food and medicinal purposes. The nutritional and economic importance of this crop has directed attention to the in-depth study of the plant, including a focus on its metabolic behavior, to obtain solid information for the establishment of breeding processes associated with productive improvement and important traits of sweet potato varieties. So far, some research focused on determining the metabolic profile of different sweet potato accessions has been carried out. Through these, hundreds of metabolites have been identified and it has been possible to establish important relationships between the content of metabolites and the phenotype or traits of each variety. An example of this is the proportional relationship between carotenoids and anthocyanins contents and the orange and purple coloration of root flesh, respectively. Likewise, an inverse relationship has been established between carotenoid

content and starch in the tuberous roots, a problem to be solved in methodologies for improving the content of these metabolites. In quantitative terms, different chemical species with relevance in plant metabolism have been determined, including proteins, amino acids, carbohydrates, lipids, vitamins, minerals, and other secondary metabolites, such as flavonoids, anthocyanins, and phenolic acids.

Conflict interest. Authors declare that there is no conflict of interest.

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