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origin, DISTRIBUTION, TAXONOMY, BOTANICAL DESCRIPTION, GENETICS AND CYTOGENETICS, GENETIC DIVERSITY AND BREEDING OF SWEET POTATO (*IPOMOEA BATATAS* (L.) LAM.)

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ABSTRACT

Sweet potato belongs to the family Convolvulaceae, genus *Ipomoea* and species *Ipomoea batatas.* The English word *potato* is from the word *batata* (sweet potato) of the Taino Indians of the West Indies by way of the Spanish word *patata.* The English word originally referred to the sweet potato, but was later applied to the common potato, which is called *papa* in Spanish. The word *yam* is probably from *nyami* in the language of the West African Wolof people. It is likely that when African people were brought to the New World as slaves that they used the word that they knew for the native sweet potato. Sweet potatoes are often called *yams* in the United States. Sometimes a distinction is made with the darker fleshed roots called "yams" and the lighter "sweet potatoes." Another Spanish word for sweet potato is *camote,* which is sometimes used in the southwestern United States. In New Zealand, sweet potatoes are called by their Maori name, *kumara.* The cultivated species *I. batatas* includes plants that are very variable in their morphology. Thousands of cultivars have been selected and cultivated in Latin America since ancient times. At the present time, it is cultivated throughout the tropics. However. the largest plantings of sweet potatoes are found in China and other countries of Asia. Sweet potato from the family Convolvulaceae, is an important food crop, which is widely grown in tropical, subtropical and warm temperate regions. Asian countries, particularly China, are the main producers with 113.6 Mt in 2004, representing 88.9% of the world production. The storage roots of sweet potato are used as staple food, raw material for alcohol production and animal feed. In this review article on Origin, Domestication, Taxonomy, Botanical Description, Genetics and Cytogenetics, Genetic Diversity, Breeding of Sweet potato are discussed.

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INTRODUCTION

Sweet potato belongs to the family Convolvulaceae, genus *Ipomoea* and species *Ipomoea batatas* (Wikipedia, 2024).

Family: Convolvulaceae- Commonly referred to as the morning glory family of flowering plants. This family includes members that are found in both temperate and tropical environments. Many members are erect and twining herbs but some are trees, shrubs or woody vines.

Genus: *Ipomoea*- This genus contains over 500 members making it one of the largest genera that fall under Convolvulaceae. Members are mostly found in warm climates and include herbaceous plants, shrubs and trees. Members of this genus feature flowers that are funnel shaped.

Species: *Ipomoea batatas*- This species is a widely cultivated food plant native to tropical America. *Ipomoea batatas* is a herbaceous perennial vine that has purplish flowers, large nutritious tuberous roots and heart-shaped lobed leaves (Bioweb, 2024).

The most common names for this plant in Latin America are batata, camote, bonlato, batata doce, aplchu, and kumara (Huaman, 1992). The botanical name for the sweet potato is *Ipomoea batatas* [L.] (Lam). The most common indigenous names for the sweet potato tuber in Central and South America include *batata*, *boniato*, *camote*, *batata doce*, and *apichu*. From Peru, Hawaii, and Samoa to the Philippines, sweet potato is known by a broad range of cognates: *kumar*, *uala*, *umala*, and *kamote*, respectively. The sweet potato is called *kumara* in New Zealand. Eastern Africans know the sweet potato as *cileraabana*, "protector of the children," and it is called *ubhatata* in South Africa. It is known as *kara-imo*, "Chinese potato" in southern Kyushu, and in most other parts of Japan, it is known as *satsuma-imo*, "Japanese potato" (EGA, 2020). The English word *potato* is from the word *batata* (sweet potato) of the Taino Indians of the West Indies by way of the Spanish word *patata.* The English word originally referred to the sweet potato, but was later applied to the common potato, which is called *papa* in Spanish. The word *yam* is probably from *nyami* in the language of the West African Wolof people. It is likely that when African people were brought to the New World as slaves that they used the word that they knew for the native sweet potato. Sweet potatoes are often called *yams* in the United States. Sometimes a distinction is made with the darker fleshed roots called "yams" and the lighter "sweet potatoes." Another Spanish word for sweet potato is *camote,* which is sometimes used in the southwestern United States. In New Zealand, sweet potatoes are called by their Maori name, *kumara* (Wikipedia, 2024).

Though the sweet potato is also called *batata* in Hebrew, this is not a direct loan of the Taino word. Rather, the Spanish *patata* was loaned into Arabic as *batata* , owing to the lack of a /p/ sound in Arabic, while the sweet potato was called *batata ḥilwa* ; literally ('sweet potato'). The Arabic *batata* was loaned into Hebrew as designating the sweet potato only, as Hebrew had its own word for the common potato, (*tapuakh adama*, literally 'earth apple'; compare French *pomme de terre*) (Wikipedia, 2024). In Argentina, Colombia, Venezuela, Puerto Rico, and the Dominican Republic, the sweet potato is called *batata*. In Brazil, the sweet potato is called *batata doce*. In Mexico, Bolivia, Peru, Chile, Central America, and the Philippines, the sweet potato is known as *camote* (alternatively spelled *kamote* in the Philippines), derived from the Nahuatl word *camotli* (Wikipedia, 2024). In Peru and Bolivia, the general word in Quechua for the sweet potato is *apichu*, but there are variants used such as *khumara*, *kumar* (Ayacucho Quechua), and *kumara* (Bolivian Quechua), strikingly similar to the Polynesian name *kumara* and its regional Oceanic cognates (*kumala*, *umala*, *uala*, etc.), which has led some scholars to suspect an instance of pre-Columbian trans-oceanic contact. This theory is also supported by genetic evidence (Wikipedia, 2024). In Australia, about 90% of production is devoted to the orange cultivar 'Beauregard', which was originally developed by the Louisiana Agricultural Experiment Station in 1981. In New Zealand, the Māori varieties bore elongated tubers with white skin and a whitish flesh, which points to pre-European cross-Pacific travel. Known as *kumara* (from the Māori language *kūmara*), the most common cultivar now is the red 'Owairaka', but orange ('Beauregard'), gold, purple and other cultivars are also grown (Wikipedia, 2024).

The cultivated species I. batatas includes plants that are very variable in their morphology. Thousands of cultivars have been selected and cultivated in Latin America since ancient times. At the present time, it is cultivated throughout the tropics. However. the largest plantings of sweet potatoes are found in China and other countries of Asia (Huaman, 1992). Sweet potato from the family Convolvulaceae, is an important food crop, which is widely grown in tropical, subtropical and warm temperate regions. Asian countries, particularly China, are the main producers with 113.6 Mt in 2004, representing 88.9% of the world production. The storage roots of sweet potato are used as staple food, raw material for alcohol production and animal feed (Srisuwan *et al*., 2006). Although sweet potato skin color varies fairly extensively among cultivars, flesh color is either white or dark orange. The white-fleshed types usually are drier in consistency and originally were favored in northern areas of our country. Orange-fleshed types, favored in the South, typically have moist flesh and often (erroneously) are referred to as "yams" (Trinklein, 2009). As an interesting aside, sweet potato has been the subject of a considerable amount of developmental research over the years. African-American agricultural scientist and Missouri native George Washington Carver (best known for his work with peanut) also worked with sweet potato. From the latter he is credited with developing over 125 diverse products including dyes, wood fillers, candies, pastes, breakfast foods, starches, flours, and molasses (Trinklein, 2009).

Sweet potato is a common subsidiary component in many cropping systems of Asia, Africa and America. Its ability to produce stable yields within a short growing season, multiple uses as human food, livestock feed and raw material for starch based industries and its comparatively lower input requirements make this crop very attractive for resource poor farmers (Nedunchezhiyan *et al.,* 2012). It has the ability to produce higher dry matter per unit area per unit time. In cropping systems its role varies from place to place. In certain cropping systems it is a fallow or catch crop. In some others it may serve as an erosion control crop or livestock feed or even as green manure crop. Sweet potato is grown in a wide range of environmental conditions and is associated with a number of annual and perennial crops (Nedunchezhiyan *et al*., 2012). Further, most of the subsistence and semi-commercial farmers follow multiple cropping (intermixed or relay) in one form or the other. In some of the semi commercial enterprises sequential cropping with wet season cereals is in vogue. Monocropping is the ruling practice under commercial farming of sweet potato (Nedunchezhiyan *et al.,* 2012). Yields are related to rainfall and number of cropping seasons, followed by nutrient availability, nematode and weevil infestation (Hartemink *et al*. 2000). In Orissa, India, sweet potato is rotated with rice and fallow in upland ecosystem to regain soil fertility and suppress weeds and weevil (Nedunchezhiyan *et al*. 2006). Hartemink *et al*. (2000) observed nematode and weevil population buildup when sweet potato was cultivated continuously for three seasons. Hence development of sustainable intensified cropping system is needed to overcome biophysical constraints and to feed ever increasing population (Nedunchezhiyan *et al.,* 2012).

Sweet potato is an important root crop in tropical and sub tropical countries like China, USA, India, Japan, Indonesia, Philippines, Thailand, Vietnam, Nigeria etc. Among the root and tuber crops grown in the world, sweet potato ranks second after cassava. The carbohydrate rich root is used as a subsidiary food after boiling/ baking. In some countries, the vine tips are used as vegetables. Vines form an excellent source of green fodder for cattle. Development of varieties having high dry matter, starch, carotene and anthocyanin has opened up new vistas in industrial applications apart from traditional usage as food and feed. Industrial products like starch, liquid glucose, citric acid, mono sodium glutamate and ethanol are produced from sweet potato roots in various countries (Nedunchezhiyan *et al.,* 2012a). Sweet potato yields high amount of energy per unit areaper unit time and is expected to bridge the food shortages and malnutrition. The comparative short duration coupled with its innate power for tremendous dry matter production has enabled sweet potato to rank as the foremost root crop in respect of calorie value. It has the potential as a feedstock for bio-ethanol production. However, varieties with high yields and dry matter content termed industrial sweet potatoes (ISP) have to be developed to exploit as bio fuel crop (Nedunchezhiyan *et al*., 2012a).

Two fundamental questions related to the origin and dispersal of the sweet potato remain unanswered. First, did the sweet potato evolve once or multiple times, and what species were involved in its origin? Second, how did the sweet potato, a crop of American origin, come to be widespread in Polynesia before the arrival of the Europeans? Answering the first question requires knowledge of evolutionary relationships between the sweet potato and the species that are most closely related to it, often termed crop wild relatives (Muñoz-Rodríguez *et al*., 2018). Understanding this relationship is the key to unraveling the origin of this crop and has implications for food security because these CWRs constitute potential sources of genetic variation for future crop improvement. In the case of the sweet potato, knowledge of these relationships is especially poor, even though it is a widely consumed crop and an important resource for combating vitamin A deficiencies, estimated to affect over 190 million children worldwide. Answering the second question (how did the sweet potato come to be present in Polynesia before the Europeans first arrived?) requires the consideration of two additional questions. First, what is the possibility of the sweet potato dispersing from its native range in America to Polynesia by natural means (*i.e*., wind, water, or birds)? Second, when did the sweet potato colonize Polynesia? (Muñoz-Rodríguez *et al*., 2018).

Sweet potato is both a staple and a vegetable crop, containing a significant amount of proteins, provitamin A, B, and C and minerals such as Ca, Fe and Na. Both tuber and shoot can serve for human consumption, livestock feed and for the prevention of skin cancer, indicating the importance of this crop. The tuber is also used for the industrial production of starch, sugar and alcohol (Belay, 2018). Good quality sweet potatoes should be smooth and firm, with uniform shape and size, be free from mechanical damage, and have a uniform peel color typical of the variety (Belay, 2018). In most Ethiopia, Kenya, Tanzania, Madagascar, Angola, and southern Africa, the diet is based on grains, primarily maize. Sweet potato is an important secondary food crop. It plays critical roles in rural diets in certain areas during shortage of grain crops like maize, when drought occurs. Most African households plant sweet potatoes as a food security or famine prevention crop. Sweet potatoes are viewed in this instance as a form of insurance in the event of drought, political turmoil, or other food supply-threatening events (Belay, 2018).

Plant genetic resource, one of the most essential natural resources, has been a research topic resulting in major advancement in the field. Gene banks are concerned with the maintenance of crop resource genetic variations, and plant genetic resource conservation is now receiving greater attention. In order to establish effective and efficient conservation practices for plant genetic resources, understanding the genetic diversity between and within population is important (Lee *et al*., 2019). Sweet potato is a vegetative propagation crop that belongs to the family Convolvulaceae. The origin of sweet potato is either the Central or South America. Sweet potato is attractive to resource-poor farmers because they have the highest rate of production per unit area/time. It also has a short growth period and is easily propagated and grown with good production in various climates and farming systems. Previous studies have explained the genetic diversity and origin of sweet potato landraces in Mexico, Peru, and New Guinea using chloroplast and nuclear SSR (Lee *et al.,* 2019). Sweet potato is regarded as the world's seventh most important food crop and can be used as a staple food, animal feed, industrial raw material to extract starch as well as in alcohol and biofuel. In addition, orange-fleshed sweet potato has a high level of β-carotene, which could be used to prevent vitamin A deficiency-related blindness and maternal mortality in many developing countries. Due to its high productivity and adaptability to a wide range of environmental conditions, sweet potato is cultivated in more than 100 countries worldwide, particularly in the developing countries of Sub-Saharan Africa and South Asia. China is the largest producer of sweet potato, where several cultivars have been developed over 100 years of cultivation. However, information regarding the genetic diversity of Chinese sweet potato germplasm remains limited due to the complicated genome of this species, which limits the process of developing improved cultivars (Yusha Meng *et al*., 2021). To establish effective breeding strategies, it is necessary to analyze the genetic diversity, evaluate the genetic structure and understand the genetic background among sweet potato accessions. In recent years, several morphological and molecular markers have been developed to assess the genetic diversity of sweet potato germplasm, including random amplified polymorphic DNAs (RAPDs), amplified fragment length polymorphisms (AFLPs), simple sequence repeats (SSRs), and single nucleotide polymorphisms (SNPs). However, for the massive genome sequences of sweet potato, these published markers are not sufficient to construct a high-density genetic map that could be highly useful for genetic studies. Thus, there is a great need for the exploration of new molecular markers (Yusha Meng *et al*., 2021).

The notion of sweet potato being a poor-man's crop is rapidly being replaced with a more positive consideration of a diverse food crop for health and wealth. The diversity of potential sweet potato products opens new markets where consumers are learning the positive health benefits of sweet potato consumption. The introduction and promotion of orange-fleshed sweet potato in Sub-Saharan Africa is just one example of how sweet potato is improving livelihoods. However, the high diversity of sweet potato can also present a challenge. People consuming sweet potato as a staple crop, have their preference regarding color, texture and taste. Deviations from this preference generally lead to low adoption rates of newly-released varieties even though they have selective advantages such as high yield and resistances to pests and diseases (Swanckaert *et al.,* 2021). Understanding the high variability in quality traits is necessary to target new varieties for specific market segments. After identifying traits of interest, molecular breeding will allow for mapping genomic regions responsible for these traits and identifying the position of important causative genes. Despite many efforts, a huge task remains to unravel a reference genome supporting the development of high quality integrated genetic maps for the hexaploid sweet potato. Furthermore, the role of biotechnology is becoming more important as breeding programs work towards a hybrid exploiting breeding scheme. Facing challenges due to increased pressure on land, climate change and more mouths to feed, the adaptability of sweet potato will allow for food security during difficult times. In this chapter, we present an overview of the economic importance, cultivation and traditional breeding, germplasm diversity and conservation, molecular breeding and hybridization (Swanckaert *et al.,* 2021). Sweet potato is an important crop globally as a versatile food source in that both the roots and the leaves can be consumed. The crop is also utilized in the manufacturing of industrial and food products such as starch, flour, noodles, colorants, candy, chips, and alcohol, in addition to fodder and fish food. In 2018, over 91 million tons of sweet potato were produced worldwide on over eight million hectares of land with China being the largest producer (Anglin *et al*., 2021). Sweet potato is also widely cultivated in many developing countries where the yields are well below the average, compared with developed countries. Sweet potato is also an important source of income for women compared with men in developing countries, such as Nigeria, due to its low input requirements and short maturity time relative to other crops. Sweet potato also grows well on marginal soils with limited inputs and is tolerant to a wide range of climatic conditions making production improvements feasible. Sweet potato is a versatile food source that is nutritionally beneficial for human health and serves a medicinal role in many parts of the world. Leaves, stems, or raw roots are consumed for the treatment of type 2 diabetes in Ghana, inflammatory and oral infections in Brazil, anemia, and hypertension in Japan, and prostatis in Cameroon (Anglin *et al*., 2021).

Sweet potato is one of the most important root crops cultivated worldwide. Because of its adaptability, high yield potential, and nutritional value, sweet potato has become an important food crop, particularly in developing countries. To ensure adequate crop yields to meet increasing demand, it is essential to enhance the tolerance of sweet potato to environmental stresses and other yield-limiting factors. The highly heterozygous hexaploid genome of *I. batatas* complicates genetic studies and limits improvement of sweet potato through traditional breeding. However, application of next-generation sequencing and high-throughput genotyping and phenotyping technologies to sweet potato genetics and genomics research has provided new tools and resources for crop improvement (Yan *et al*., 2022). Sweet potato is one of the most economically important crops for addressing global food security and climate change issues, especially under conditions of extensive agriculture, such as those found in developing countries. However, osmotic stress negatively impacts the agronomic and economic productivity of sweet potato cultivation by inducing several morphological, physiological, and biochemical changes. Plants employ many signaling pathways to respond to water stress by modifying their growth patterns, activating antioxidants, accumulating suitable solutes and chaperones, and making stress proteins. These physiological, metabolic, and genetic modifications can be employed as the best indicators for choosing drought-tolerant genotypes. The main objective of sweet potato breeding in many regions of the world, especially those affected by drought, is to obtain varieties that combine drought tolerance with high yields (Sapakhova *et al.,* 2023). Rising global temperature levels as a result of climate change represent a significant challenge. Agricultural production is highly influenced by climatic factors, so it may be seriously affected in the near future if no actions are taken to accommodate and reduce the effects of abiotic stress on crops. Thus, there is an urgent need for the cultivation of crops that use water resources the most effectively. Sweet potato is considered to be one such crop, although its productivity is reduced under abiotic stress conditions. However, sweet potato has several advantages over other economically important crops that enable it to better address global food security and climate change issues, especially under the conditions of extensive agriculture seen in developing countries (Sapakhova *et al.,* 2023).

Sweet potato is a basic foodstuff, fodder, and horticultural crop grown in tropical countries. It ranks seventh in the world in terms of production. It is a root vegetable crop of the Convolvulaceae family. Ipomoea batatas is the main staple crop. A few other Convolvulaceae species are localized, but many of them are noxious (Sapakhova *et al.,* 2023). I. batatas is a herbaceous liana plant with alternating leaves and tubular flowers. Its edible tuberous roots may vary in shape and color depending on its variety and environmental conditions. These root tubers are usually long, and their skin color varies from white to purple. **I. batatas** has a high WUE (water-use efficiency) and causes limited soil erosion during the rainy season, so it can be used as a cover crop as well as in the frost-free period of at least four months long. Because of its high nutritional content and broad suitability for poor terrain, sweet potato is a prospective crop for preventing food shortages and enhancing food safety. It also holds great promise for inclusion as part of a healthy diet in developing countries. Less chemical pesticide and fertilizer are required for sweet potato cultivation in comparison to other crops (Sapakhova *et al*., 2023). Sweet potato is a universal and hardly crop that grows best in warm, tropical climates with average temperatures of 24 °C. It is also an adaptable crop that produces large amounts of food per unit area and per unit time during short rainy periods, giving it an advantage over other staple foods. Sweet potato has flexible planting and harvesting times, a short growing season, and a tolerance to high-temperature soils with low fertility, and it is not severely affected by pests or diseases. In addition, growing sweet potato requires fewer labor resources compared to other crops, making it particularly suitable for small farms. It can be used as a fast-rotating crop as a result of its wide ecological adaptation, drought resistance, and maturation period of three-to-five months (Sapakhova *et al*., 2023).

FAO's innovative sweet potato breeding and conservation in Papua New Guinea is a beacon of 'Better Production.' It not only addresses immediate challenges but also lays the foundation for a more resilient and sustainable agrifood system in the country. In fact, I'm proud enough to call it a model that shows how targeted interventions, backed by scientific research and community engagement, can transform the face of agriculture, not just in Papua New Guinea but globally (FAO, 2023). Together, FAO in Papua New Guinea, the government, local communities and our resources partners, are working hand in hand to improve this production. But we are going beyond that. Our intention is to creative a better holistic situation for everyone. To do that, we follow FAO's 'four betters' approach – Better Production, Better Nutrition, Better Environment and a Better Life for all. Ultimately, our goal is to leave no one behind (FAO, 2023). Because sweet potato can be planted throughout the year and there is a large range in maturity dates, farmers can manage the supply period and ensure continual yield, both for home consumption and for the local market. In most countries in SSA roots are available 4-8 months out of a year and in countries with two rainy seasons (*i.e.,* Rwanda, Burundi, and Uganda) roots are available 11 months of the year. In most SSA countries except South Africa sweet potato is grown primarily by smallholder producers who often plant a mix of different varieties in the same field, which is typically rainfed (Barb and Mahama, 2023).

The sweet potato is a member of the Convolvulaceae family of flowering plants, which includes the morning glory, chokeweed, and water spinach. The sweet potato has been cultivated for thousands of years for its tuberous roots. It is one of the most nutritious vegetables and is grown and eaten in many countries around the world. It is also used as animal feed and as the source of many other products (Wikipedia, 2024). Sweet potatoes offer both a physical value, and an inner or spiritual value for humans. Physically, they are one of the most nutritional vegetables available, and likewise are an important commercial crop. Beyond this, however, they also provide aesthetic value through the beauty of their flowers and the color and texture of their skin (which can be red, purple, brown, and white) and their flesh (which can range between white, yellow, orange, and purple). Likewise, the stimulating taste provides a joy beyond that of merely the nutrients received (Wikipedia, 2024). The sweet potato (*Ipomoea batatas*) is a dicotyledonous plant that belongs to the bindweed or morning glory family, Convolvulaceae. Its large, starchy, sweet-tasting tuberous roots are used as a root vegetable.[2][3] The young shoots and leaves are sometimes eaten as greens. Cultivars of the sweet potato have been bred to bear tubers with flesh and skin of various colors (Wikipedia, 2024). The sweet potato is native to the tropical regions of South America in what is present-day Ecuador. Of the approximately 50 genera and more than 1,000 species of Convolvulaceae, *I. batatas* is the only crop plant of major importance —some others are used locally (*e.g., I. aquatica* "kangkong" as a green vegetable), but many are poisonous. The genus *Ipomoea* that contains the sweet potato also includes several garden flowers called morning glories, but that term is not usually extended to *I. batatas*. Some cultivars of *I. batatas* are grown as ornamental plants under the name *tuberous morning glory,* and used in a horticultural context. Sweet potatoes can also be called yams in North America. When soft varieties were first grown commercially there, there was a need to differentiate between the two. Enslaved Africans had already been calling the 'soft' sweet potatoes 'yams' because they resembled the unrelated yams in Africa.[7] Thus, 'soft' sweet potatoes were referred to as 'yams' to distinguish them from the 'firm' varieties (Wikipedia, 2024).

Sweet potato, food plant of the morning glory family (Convolvulaceae), native to tropical America. The sweet potato is widely cultivated in tropical and warm temperate climates and is an important food crop in the southern United States, tropical America and the Caribbean, the warmer islands of the Pacific, Japan, and parts of Russia. The fleshy roots are served as a cooked vegetable, in whole or mashed form, and are used as pie filling. In Japan the crop has long been grown for drying and for manufacture of starch and alcohol (EEB, 2024). Sweet potato, a herbaceous perennial vine belonging to the Convolvulaceae family, is cherished for its versatile, edible storage roots or tubers. Native to Central America, this plant has now established itself across the globe. These robust vines, known for their heart-shaped lobed leaves and charming white or lavender flowers, can stretch up to 4m in a single growing season. Tubers come in a fascinating array of shapes and colors, from red, yellow, brown, and white to even purple (Plantvillage, 2024). Cultivated mainly in small-scale subsistence farming in East Africa, sweet potatoes are gradually gaining recognition among other indigenous foods. Its tubers are usually white, red, or purple, and increasingly, yellow-fleshed types are garnering popularity due to their high sugar, vitamin A, and lower dry matter content (Plantvillage, 2024). Consumed either boiled or roasted, often accompanying milk, porridge, soups, or meat, they contribute significantly to diet diversity. Moreover, their young leaves, high in protein and essential vitamins like B1, B2, and folic acid, serve as a nutritious green vegetable. The vines also double as a fodder crop, providing a nutritious feed, especially during the dry season. This remarkable plant, thus, goes beyond being a mere staple, offering considerable nutritional and agronomic advantages (Plantvillage, 2024).

Propagation

Sweet potatoes are not typically grown from seed. Instead, they are propagated vegetatively via pieces of stems called "slips". Slips are available from seed companies and nurseries in the spring. These shoots are technically rootable cuttings that are grown from mature plants and shipped to farmers and gardeners around the country (Hailey, 2023). This plant is mostly propagated through vegetative propagation using vine cuttings or tubers. However, this process is costly, labour-intensive, and comparatively slow. Conventional propagation methods are not able to supply sufficient disease-free planting materials to farmers to sustain steady tuber production. Therefore, there is an urgent need to use various biotechnological approaches, such as cell, tissue, and organ culture, for the large-scale production of healthy and disease-free planting material for commercial purposes throughout the year. In the last five decades, a number of tissue culture protocols have been developed for the production of in vitro plants through meristem culture, direct adventitious organogenesis, callus culture and somatic embryogenesis. Moreover, little research has been done on synthetic seed technology for the in vitro conservation and propagation of sweet potato (Behera *et al*., 2022).

Cultivation

Sweet potatoes grow best where the summers are long and hot and there is plenty of rain. The plant does not tolerate frost. It grows best at an average temperature of 24°C. Depending on the cultivar and conditions, tuberous roots mature in 2 to 9 months. With care, early-maturing cultivars can be grown as an annual summer crop in temperate areas, such as the northern United States. They are mostly propagated by stem or root cuttings or by adventitious roots called "slips" that grow out from the tuberous roots during storage. True seeds are used for breeding only. Sweet potatoes became popular very early on in the islands of the Pacific, from Japan to Polynesia. One reason is that they were favored as an emergency crop that could be relied on if other crops failed, for instance because of typhoon flooding or tribal war. They are featured in many favorite dishes in Japan, Taiwan, and other island nations. The Solomon Islands in the South Pacific has the world's highest per capita consumption of sweet potatoes, 174 kg (380 lbs). Indonesia, Vietnam, India, and some other Asian countries are also large sweet potato growers. Uganda (the third-largest grower after Indonesia), Rwanda, and some other African countries also grow a large crop, which is an important part of their peoples' diets. North and South America, the original home of the sweet potato, together grow less than 3 percent of the world's supply. Europe has a very small sweet potato production, mostly in Portugal (Wikipedia, 2024).

Depending on the cultivar and conditions, tuberous roots mature in two to nine months. With care, early-maturing cultivars can be grown as an annual summer crop in temperate areas, such as the Eastern United States and China. Sweet potatoes rarely flower when the daylight is longer than 11 hours, as is normal outside of the tropics. They are mostly propagated by stem or root cuttings or by adventitious shoots called "slips" that grow out from the tuberous roots during storage. True seeds are used for breeding only (Wikipedia, 2024). Sweet potatoes are cultivated throughout tropical and warm temperate regions wherever there is sufficient water to support their growth. Sweet potatoes became common as a food crop in the islands of the Pacific Ocean, South India, Uganda and other African countries (Wikipedia, 2024).

Harvesting

In grain crops, where single harvesting is followed immediately after maturity; otherwise grains get shattered or spoiled if retained few more days in the field. Whereas in sweet potato single harvesting and double harvesting (progressive harvesting) are practiced as root yields are not affected by delaying few days after maturity. Staggered harvesting facilitates marketing and realizing reasonable price for the produce. However, varieties and environment play a significant role in deciding the time of harvest in sweet potato. In Papua New Guinea, non-marketable roots constituted a greater proportion of the total roots with progressive harvesting compared to single harvesting although the yield of marketable roots (100 g above) were 2-3.4 t ha^{-1} higher. A trial on double harvesting done between 90 and 150 days at intervals 15-60 days resulted in significantly higher root yield when harvested at 90 and 150 DAP as compared to single harvesting at 150 days under north Bihar conditions (Nedunchezhiyan *et al.,* 2012a). In North India, sweet potato takes about 5-6 months for maturity while it matures within 4 months in the South. Within limits, the yield ha^{-1} will increase if the crop remains in the ground longer but the root become less palatable and weevil damage and rots become more noticeable with age. The maturity of the roots can be determined by cutting the roots. The cut surface of the immature roots gives a dark greenish colour, while in mature roots the cut ends dry clearly. The field is irrigated 2-3 days prior to harvesting to facilitate easy lifting of the roots. After removing the vines the roots are dug out without causing injury. In the tropics, sweet potato harvesting is usually by manual labour (Nedunchezhiyan *et al.,* 2012a).

Yield

The storage root yield varies with the variety, season of planting, soil conditions and fertility. In general the storage root yield varies from 20-25 t ha^{-1} for promising varieties with improved crop management practices. In sandy loam soils sweet potato recorded tuber yield of 13.1 t ha^{-1} under rainfed conditions, whereas 26 t ha^{-1} tuber yield under irrigated conditions (Nedunchezhiyan *et al.,* 2012a). Its global production is approximately 131 million tons $year^{-1}$ on around 9 million hectares, having an average rated yield of 13.7 tons ha^{-1}. Around 97% of the sweet potatoes grown worldwide are produced in developing countries. The crop is widely cultivated in Africa, Asia, and Latin America, with 52% of the crop being grown in China on an acreage of about 4.7 million hectares. Today, thousands of sweet potato varieties are grown in all the tropical and subtropical climatic regions of the world (Sapakhova *et al*., 2023). In 2020, global production of sweet potatoes was 89 million tonnes, led by China with 55% of the world total. Secondary producers were Malawi, Tanzania, and Nigeria. In the Southeastern U.S., sweet potatoes are traditionally cured to improve storage, flavor, and nutrition, and to allow wounds on the periderm of the harvested root to heal. Proper curing requires drying the freshly dug roots on the ground for two to three hours, then storage at 29–32 °C with 90 to 95% relative humidity from five to fourteen days. Cured sweet potatoes can keep for thirteen months when stored at 13–15 °C with >90% relative humidity. Colder temperatures injure the roots (Wikipedia, 2024). Sweet potato is the seventh most important food crop, in terms of production, in the world. Sweet potato is grown mainly in developing countries with 80% of the world's production coming from Asia, about 15% in Africa, and only 5% from the rest of the world (Rossel, 2024).

In this review article on Origin, Domestication, Taxonomy, Botanical Description, Genetics and Cytogenetics, Genetic Diversity, Breeding of Sweet potato are discussed.

ORIGIN AND DITRIBUTION

Sweet potato is thought to be native to tropical South America where it has been used as a food source for more than 5000 years (Trinklein, 2009). Sweetpotato is called the batatas. This word eventually became patata in Spanish, patae in French and potato in English. Since the introduction of sweet potato into Europe is thought to have preceded that of Irish potato (another native of South America), the word "potato" was originally a reference to sweet potato and not Irish potato, as is the case today. Sweet potato probably first migrated from South America in a westerly direction given the fact it has been carbon-dated in the Cook Islands to 1000 A.D. and was grown in Polynesia before the Age of Discovery. Early Polynesians who traveled to South America and back are credited with its introduction to their homeland as well as to Hawaii and New Zealand. Columbus undoubted encountered sweet potato in his early voyages to the West Indies but it was not until his fourth voyage (to Yucatan and Honduras) that he recorded its discovery in his journals. He is credited with its introduction to the New World (Spain) in about 1500 and a number of different types were cultivated there by the mid-1600s. It was very slow to spread to more northern regions of Europe because of its affinity to warm temperatures (Trinklein, 2009).

The sweet potato genebank at the International Potato Center (CIP) maintains 5,526 cultivated *I. batatas* accessions from 57 countries. Knowledge of the genetic structure in this collection is essential for rational germplasm conservation and utilization. Sixty-nine sweet potato cultivars from 4 geographical regions (including 13 countries) of Latin America were randomly sampled and fingerprinted using AFLP markers. A total of 210 polymorphic and clearly scorable fragments were generated. A geographic pattern of diversity distribution was revealed by mean similarity, multidimensional scaling (MDS), and analysis of molecular variance (AMOVA). The highest genetic diversity was found in Central America, whereas the lowest was in Peru-Ecuador. The within-region variation was the major source of molecular variance. The between-regions variation, although it only explains 10.0% of the total diversity, is statistically significant. Cultivars from Peru-Ecuador, with the lowest level of within region diversity, made the most significant contribution to the between region differentiation. These results support the hypothesis that Central America is the primary center of diversity and most likely the center of origin of sweet potato. Peru-Ecuador should be considered as a secondary center of sweet potato diversity (Zhang *et al*., 2000).

Based on analysis of morphological characters of sweet potato and the wild *Ipomoea* species, the centre of origin of *I. batatas* was thought to be somewhere between the Yucatan Peninsula of Mexico and the mouth of the Orinoco River in Venezuela. Recently, the highest diversity in Central America revealed by the use of molecular markers provides evidence that Central America is the primary centre of diversity and most likely the centre of origin, considering the richness of the wild relatives of sweet potato. Sweet potato was introduced to Western Europe from West Indies after the first voyage of Columbus in 1492. In the 16th century, Portuguese explorers transferred sweet potato to Africa, India, South East Asia and the East Indies, while direct transfer of the plant was done by Spanish trading galleons from Mexico to the Philippines (Srisuwan *et al*., 2006). The earliest cultivation records of the sweet potato date to 750 BCE in Peru, although archeological evidence shows cultivation of the sweet potato might have begun around 2500-1850 BCE. By the time Christopher Columbus arrived in the 'New World' in the late 15th century, sweet potatoes were well established as food plants in South and Central America (Harbster, 2010). The sweet potato is of Central or tropical South American origin. It was suggested that Mexico as the centre of diversity of the Batatas section of *Ipomoea*. However, the earliest archaeological record of cultivated sweet potatoes is from the Peruvian coast (4500 **B P**) and the crop has not been recovered from any of the ancient Mexican sites such as Tehuacan. The fact that the earliest finds are from coastal Peru is a consequence of the area's climatic aridity, favouring the preservation of crop remains: the area cannot be the centre of domestication since no wild prototypes are found there (Norman *et al.,* 2012).

Sweet potato is one of the most important crops from the family of *Convolvulaceae*. It is widely reported that cultivated sweet potato was originated from *Ipomoea trifida*. However, diploid, tetraploid and hexaploid *I. trifida* were found in nature. The relationship, between them, and among them and sweet potato, is remaining unclear. These results provided new evidence that cultivated sweet potato originated from *I. trifida* 6×, and that *I. trifida* 6× evolved from *I. trifida* 4X and *I. trifida* 2×. Therefore, using *I. trifida* 6× as the model plant of sweet potato research should be more practical than using *I. trifida* 2× in the future. Meanwhile, sequence information and markers from the present study will be helpful for sweet potato and *I. trifida* studies in the future (Feng *et al.,* 2018). Transmission of the sweet potato around the planet was primarily the work of the Spanish and Portuguese, who got it from the South Americans and spread it to Europe. That doesn't work for Polynesia, though; it's too early by 500 years. Scholars generally assume that either seed of the potato were brought to Polynesia by birds such as the Golden Plover that regularly cross the Pacific; or by accidental raft drift by lost sailors from the South American coast. A recent computer simulation study indicates that raft drift is, in fact, a possibility (Hirst, 2019). The sweet potato is a root crop, probably first domesticated somewhere between the Orinoco river in Venezuela north to the Yucatan Peninsula of Mexico. The oldest sweet potato discovered to date was in the Tres Ventanas cave in the Chilca Canyon region of Peru, ca. 8000 BCE, but it is believed to have been a wild form. Recent genetic research suggests that *Ipomoea trifida*, native to Colombia, Venezuela, and Costa Rica, is the closest living relative of *I. batantas*, and maybe its progenitor. The oldest remains of domesticated sweet potato in the Americas were found in Peru, about 2500 BCE. In Polynesia, decidedly Precolumbian sweet potato remains have been found in the Cook Islands by CE 1000-1100, Hawai'i by CE 1290-1430, and Easter Island by CE 1525. Sweet potato pollen, phytoliths, and starch residues have been identified in agricultural plots alongside maize in South Auckland (Hirst, 2019). The sweet potato is considered to originate in the New World, although its precise origin is not well defined. Archaeological remains of the storage roots, or tubers, of sweet potato show it was long used as a food source by the inhabitants of Peru (EGA, 2020).

The origin and domestication of the cultivated sweet potato remain uncertain, although several hypotheses have been published providing support for various theories of its origin. It was suggested that *Ipomoea trifida* and *Ipomoea triloba* were the prime candidates to be the closest relatives of cultivated sweet potato and that *I. batatas* arose by unreduced gametes following hybridization of these wild species. Others have reported 2n pollen production of *I. trifida* and assessed the fertility of synthetic hexaploids leading to the hypothesis that sweet potato may have arisen from hybridization and unreduced gametes between *I. trifida* and a tetraploid *I. batatas*. It was suggested multiple origins evolving from two distinct autopolyploidization events from an ancestor cultivated sweet potato shares with *I.trifida*. Recently, a report suggested that *I. trifida* was the sole progenitor of sweet potato and that it had an autopolyploid origin. Other studies have proposed an allo-autohexaploid ($2n = 6x = 90$) origin with a B1B1B2B2B2B2 genome for sweetpotato which was produced by crossing a tetraploid and a diploid followed by whole genome duplication occurring ∼341,000 years ago (Anglin *et al.,* 2021). Sweet potatoes originated in Central and South America. But archaeologists have found prehistoric remnants of sweet potato in Polynesia from about A.D. 1000 to A.D. 1100, according to radiocarbon dating. They've hypothesized that those ancient samples came from the western coast of South America. Among the clues: One Polynesian word for sweet potato — "kuumala" — resembles "kumara," or "cumal," the words for the vegetable in Quechua, a language spoken by Andean natives. But until now, there was little genetic proof for this theory of how the tater traveled. Part of the reason why is that modern sweet potatoes are a genetic muddle — a hybrid of different cultivars that Europeans helped spread around the globe — so it's hard to decipher their origins from their DNA (Doucleff, 2023). **I. batatas** originates from the tropics of South America, where it has been cultivated for 5000 years (Sapakhova *et al*., 2023). Sweet potato is a hexaploid species ($2n = 6x = 90$) that originated in both Central and South America. Recent evidence suggests that sweet potato evolved from at least two autopolyploid events involving distinct populations of **I. trifida** or a now extinct species that was an ancestor to both **I. batatas** and **I. trifida**, which is similar to extant populations of wild tetraploid *Ipomoea*. The primary center of diversity for sweet potato includes Central and South America. Uganda in East Africa and the region including Papua New Guinea are both considered secondary centers of diversity (Barb and Mahama, 2023).

The sweet potato is a herbaceous, perennial vine, bearing alternate heart-shaped or palmately lobed leaves and medium-sized sympetalous (fused petals) flowers. The edible tuberous root is long and tapered, with a smooth skin, whose color ranges between red, purple, brown, and white. Its flesh ranges between white, yellow, orange, and purple. Sweet potatoes are native to the tropical Americas and were first cultivated there at least 5,000 years ago. They spread very early throughout the region, including the Caribbean and what is now the southeastern United States. They were brought to Europe by Spanish and Portuguese explorers and sweet potato cultivation quickly spread throughout much of the Old World. When Europeans first visited Polynesia, they found sweet potatoes being grown. How and when they first got there is a subject of much debate among anthropologists and historians with some saying that this is evidence of early contact with the peoples of South America, and others that the sweet potatoes arrived there from the other direction after 1492 (Wikipedia, 2024). The sweet potato originates in South America in what is present-day Ecuador. The domestication of sweet potato occurred in either Central or South America. In Central America, domesticated sweet potatoes were present at least 5,000 years ago, with the origin of *I. batatas* possibly between the Yucatán Peninsula of Mexico and the mouth of the Orinoco River in Venezuela. The cultigen was most likely spread by local people to the Caribbean and South America by 2500 BCE. *I. trifida*, a diploid, is the closest wild relative of the sweet potato, which originated with an initial cross between a tetraploid and another diploid parent, followed by a second complete genome duplication event. The oldest radiocarbon dating remains of the sweet potato known today were discovered in caves from the Chilca Canyon, in the south-central zone of Peru, and yield an age of 8080 ± 170 BC (Wikipedia, 2024).

Before the arrival of Europeans to the Americas, sweet potato was grown in Polynesia, generally spread by vine cuttings rather than by seeds. Sweet potato has been radiocarbon-dated in the Cook Islands to 1210–1400 CE. A common hypothesis is that a vine cutting was brought to central Polynesia by Polynesians who had traveled to South America and back, and spread from there across Polynesia to Easter Island, Hawaii and New Zealand. Genetic similarities have been found between Polynesian peoples and indigenous Americans including the Zenú, a people inhabiting the Pacific coast of present-day Colombia, indicating that Polynesians could have visited South America and taken sweet potatoes prior to European contact. Dutch linguists and specialists in Amerindian languages Willem Adelaar and Pieter Muysken have suggested that the word for sweet potato is shared by Polynesian languages and languages of South America: Proto-Polynesian **kumala* (compare Rapa Nui *kumara*, Hawaiian *ʻuala*, Māori *kūmara*) may be connected with Quechua and Aymara *k'umar ~ k'umara*. Adelaar and Muysken assert that the similarity in the word for sweet potato is proof of either incidental contact or sporadic contact between the Central Andes and Polynesia (Wikipedia, 2024). Some researchers, citing divergence time estimates, suggest that sweet potatoes might have been present in Polynesia thousands of years before humans arrived there. However, the present scholarly consensus favours the pre-Columbian contact model. The sweet potato arrived in Europe with the Columbian exchange. It is recorded, for example, in *Elinor Fettiplace's Receipt Book*, compiled in England in 1604. Sweet potatoes were first introduced to the Philippines during the Spanish colonial period (1521–1898) via the Manila galleons, along with other New World crops. It was introduced to the Fujian province of China in about 1594 from Luzon, in response to a major crop failure. The growing of sweet potatoes was encouraged by the Governor Chin Hsüeh-tseng (Jin Xuezeng). Sweet potatoes were also introduced to the Ryukyu Kingdom, present-day Okinawa, Japan, in the early 1600s by the Portuguese. Sweet potatoes became a staple in Japan because they were important in preventing famine when rice harvests were poor. Aoki Konyō helped popularize the cultivation of the sweet potato in Japan, and the Tokugawa bakufu sponsored, published, and disseminated a vernacular Japanese translation of his research monograph on sweet potatoes to encourage their growth more broadly. Sweet potatoes were planted in Shōgun Tokugawa Yoshimune's private garden. It was first introduced to Korea in 1764. Kang P'il-ri and Yi Kwang-ryŏ embarked on a project to grow sweet potatoes in Seoul in 1766, using the knowledge of Japanese cultivators they learned in Tongnae starting in 1764. The project succeeded for a year but ultimately failed in winter 1767 after Kang's unexpected death (Wikipedia, 2024).

How the sweet potato evolved has always been a mystery. Now, we have found this new species in Ecuador...a fundamental piece of the puzzle to understand the origin and evolution of this top-ten global food crop. This species, which most likely played a key role in the origin of the crop, is the latest in a series of discoveries by the Oxford team and collaborators at USDA and the International Potato Centre Peru, and one that represents an 'extraordinary discovery in untangling the evolution' of the plant, according to the researchers. 'How the sweet potato evolved has always been a mystery. Now, we have found this new species in Ecuador that is the closest wild relative of sweet potato known to date and is a fundamental piece of the puzzle to understand the origin and evolution of this top-ten global food crop' (Mystery, 2024).

TAXONOMY

Sweet potato belongs to the family Convolvulaceae, genus *Ipomoea* and species *Ipomoea batatas* (Wikipedia, 2024).

Family: Convolvulaceae- Commonly referred to as the morning glory family of flowering plants. This family includes members that are found in both temperate and tropical environments. Many members are erect and twining herbs but some are trees, shrubs or woody vines.

Genus: *Ipomoea*- This genus contains over 500 members making it one of the largest genera that fall under Convolvulaceae. Members are mostly found in warm climates and include herbaceous plants, shrubs and trees. Members of this genus feature flowers that are funnel shaped.

Species: *Ipomoea batatas*- This species is a widely cultivated food plant native to tropical America. *Ipomoea batatas* is a herbaceous perennial vine that has purplish flowers, large nutritious tuberous roots and heart-shaped lobed leaves (Bioweb, 2024).

The sweet potato is a plant that was probably originated in or near northwestern South America. The systematic classification of the sweet potato is as follow: Family, Tribe, Genus, Sub-genus, Section, Species,- Convolvulaceae, Ipomoeae, Ipomoea, <u>*Quamocllt batata*</u>., *Ipomoea batsta*. (L) Lam. However, In 1791 Lamarck classified this species within the genus *Ipomoea* on the basis of the stigma shape and the surface of the pollen grains. Therefore, the name was changed to *Ipomoea batatas* (L) Lam. Within the section *Batatas* there are 13 wild species that are considered to be related to the sweet potato. These are: *cordatotriloba* (= *I. trlchocarps*) *I. cynanchifolia I. grandifolia 1.lacunosa* I. x *leucantha I. littoralis I. ramos/ssima I. tabascana I. tenuissima I. tiliacea I. trifida I. triloba I. umbraticola* (Huaman, 1992).

The distribution and organization of 5S and 18S-5.8S-26S (18S) rDNA were studied in 10 varieties of hexaploid Ipomoea batatas, five accessions of tetraploid *Ipomeoa trifida*, and six related species (five diploids, *I. trifida, I. triloba, I. tiliacea, I. leucantha* and *I. setosa* and one tetraploid, *I. tabascana*), by using fluorescence *in situ* hybridization (FISH). The FISH data obtained indicated that polyploidization was followed by decrease in the number of 18S rDNA loci in higher ploidy level and provided evidence for major genomic rearrangements and/or diploidization in polyploid *I. batatas*. Among the five diploid species examined, *I. trifida* appeared to be the most closely related to *I. batatas*. By contrast, *I. leucantha* was closed to *I. tiliacea*, but both species were distant from sweet potato. *I. triloba* and *I. setosa* were distantly related to the rest of *Ipomoea batatas* complex. The close relationship between *I. trifida* and *I. batatas* was also demonstrated by the presence of one 18S and CMA marker in these two chromosome complements only. Based on chromosome morphology, tetraploid *I. trifida* appeared to be more closely related to sweet potato than *I. tabascana*. Taking all data obtained in this study, *I. trifida* might be the progenitor of *I. batatas*, and *I. tabascana*, interspecific hybrid between these two species (Srisuwan *et al*., 2006).

The cultivated varieties of *I. batatas* display an important morphological polymorphism. Among the species within the genus *Ipomoea* series *Batatas*, 13 are considered to be closely related to sweet potato, but the wild ancestor of this plant is not still identified. Several hypotheses have been put forward to explain the origin of sweet potato. Sweet potato was thought to originate from diploid *I. leucantha* Jacq., from which derived tetraploid *I. littoralis* Blume by polyploidization. The hybridization between these two species might have generated triploid *Ipomeoa trifida* (H.B.K.) Don., which was brought to hexaploid status by doubling of triploid chromosome set. Further selection and domestication of these wild plants might have given rise to hexaploid *I. batatas*. Another hypothesis for the origin of sweet potato suggested hybridization between *I. trifida* and *I. triloba*, resulting in the generation of the wild ancestor of *I. batatas. Ipomoea tiliacea* (Willd.) might have also been involved in the origin of sweet potato. In a third hypothesis, the autopolyploidy of *I. trifida* was discussed and particularly the occurrence of 2n gametes (diplogametes) might have been involved in the origin of the polyploidy series, and allowed sexual interconnection between different ploidy levels. In fact, the production of 2n pollen was reported in diploid *I. trifida* and tetraploid *I.Batatas* (Srisuwan *et al.,* 2006). Sweet potato is a member of the Convolvulaceae, or morning glory, family. The latter contains about 60 genera and over 1600 species, most of which are herbaceous vines (Trinklein, 2009). The sweet potato, a perennial which is cultivated as an annual, is a member of the Convolvulaceae. There are about 500 wild species of *Ipomoea*, but the sweet potato is not known in the wild state. The revision recognised 11 species in the section *Batatas*, which includes the sweet potato. Subsequently three species have been added and one removed. The closest wild relatives of the sweet potato appear to be *I. trifida* and *I. tabascana*. Economically important characteristics used in intra-specific classification include tuber shape and flesh colour. Recognised six basic shapes and three flesh-colour groups: white-yellow, pink-orange, and shades of purple (Norman *et al.,* 2012).

The sweet potato is one of the world's most widely consumed crops, yet its evolutionary history is poorly understood. Our research combined genome skimming and target DNA capture to sequence whole chloroplasts and 605 single-copy nuclear regions from 199 specimens representing the sweet potato and all of its crop wild relatives (CWRs). We present strongly supported nuclear and chloroplast phylogenies demonstrating that the sweet potato had an autopolyploid origin and that *Ipomoea trifida* is its closest relative, confirming that no other extant species were involved in its origin. Phylogenetic analysis of nuclear and chloroplast genomes shows conflicting topologies regarding the monophyly of the sweet potato. The process of chloroplast capture explains these conflicting patterns, showing that *I. trifida* had a dual role in the origin of the sweet potato, first as its progenitor and second as the species with which the sweet potato introgressed so one of its lineages could capture an *I. trifida* chloroplast. In addition, we provide evidence that the sweet potato was present in Polynesia in pre-human times. This, together with several other examples of long-distance dispersal in *Ipomoea*, negates the need to invoke ancient human-mediated transport as an explanation for its presence in Polynesia. These results have important implications for understanding the origin and evolution of a major global food crop and question the existence of pre-Columbian contacts between Polynesia and the American continent (Muñoz-Rodríguez *et al.,* 2018).

Cultivated sweet potatoes are classified as *Ipomoea batatas* in the family Convolvulaceae. The genus *Ipomoea* contains more than 600 species. Due to the large size of this genus, sweet potato and its near relatives were grouped in Series Batatas which consists of 14 taxa (Anglin *et al.,* 2021). Convolvulaceae is a family that includes approximately 2000 species and 58 genera distributed throughout the world, mainly in the tropics and subtropics. More than a third of the species are included in two main genera, Ipomoea and Convolvulus. The genus *Ipomoea* Linnaeus it represents 600 to 700 species distributed in the world, although more than half of them are concentrated in the Americas. Within the sweet potato series there are 13 wild species that are considered to be closely related to the sweet potato. Linnaeus (1737) described the sweet potato and assigned it its binomial nomenclature, designating it as *Convolvulus batatas* L. In 1791, Lamark considering the morphology of the stigma and pollen grains (genus *Ipomoea:* capitate stigmas and generally spiny pollen grains) changed the genus from Convolvulus to *Ipomoea* and definitively designated this species as *Ipomoea batatas* (L.) Lam (Rodríguez *et al.,* 2023). "Ipomoea" was derived from the Greek words *ipos*, meaning "bind weed," and *homoios,* meaning "resembling." When this is put together to form "Ipomoea" the direct translation is "resembling bindweed." This name makes sense because the sweet potato has a twining habit, much like the bindweed. The species name "*batatas*" was originally the Taino name for sweet potato. This name most likely spread by the Spanish who came in contact with sweet potatoes in Central America and brought them to the west indies. "Batata" is now the name for potato in Spanish (Bioweb, 2024). The Convolvulaceae family is broken up into two major clades. The first major clade including *Cresseae, Dichondreae, Jaquemontieae, Cardiochlamyeae*, and *Cuscuteae*, is known as the Dicranostyloideae clade and is based off of similar anatomy and morphology of these genera's seed dormancy. The second major clade including *Ipomoea, Merremieae, Convolvuleae*, and *Aniseieae* was named the Convolvuloideae clade. Again, based off of similar anatomy and morphology of the dormancy of these genera's seeds, this clade was formed. The group of species under *Ipomoea* were branched according to their exon sequences which were analyzed by the Department of Biological sciences at Clemson University, South Carolina. Exon analysis broke *Ipomoea* into three major clades, separating *I. littoralis, I. ramosissima*, and *I. umbraticola* into the first clade. *Ipomoea cyananchifolia, I. grandifolia, I. acunosa, I. tenuissima, I. tribola*, and *I. leaucantha* had identical exon sequences in all 414 bases. *Ipomoea tiliacea* had a substitution at the 111th nucleotide. *Ipomoea cordatotriloba* had two nucleotide substitutions, one of which was the same as *I. tiliacea,* and the other was in nucleotide 320. This explains why those two species created a second minor clade. The third major clade including *I. batatas* shows a 98.8% similarity in nucleotide sequences between *I. batatas* and *I. trifida* while *I. tabascana* shows a 97.8% similarity in nucleotide sequences with *I. batatas* (Bioweb, 2024).

BOTANICAL DESCRIPTION

The plant is a herbaceous perennial vine, bearing alternate triangle-shaped or palmately lobed leaves and medium-sized sympetalous flowers. The stems are usually crawling on the ground and form adventitious roots at the nodes. The leaves are screwed along the stems. The leaf stalk is 13 to 51 centimetres long. The leaf blades are very variable, 5 to 13 cm long, the shape is heart-, kidney- to egg-shaped, rounded or triangular and spear-shaped, the edge can be entire, toothed or often three to seven times lobed, cut or divided. Most of the leaf surfaces are bare, rarely hairy, and the tip is rounded to pointed. The leaves are mostly green in color, but the accumulation of anthocyanins, especially along the leaf veins, can make them purple. Depending on the variety, the total length of a stem can be between 0.5 and 4 metres. Some cultivars also form shoots up to 16 m in length. However, these do not form underground storage organs. The hermaphrodite, five-fold and short-stalked flowers are single or few in stalked, zymous inflorescences that arise from the leaf axils and stand upright. It produces flowers when the day is short. The small sepals are elongated and tapering to a point and spiky and (rarely only 7) 10 to 15 millimetres long, usually finely haired or ciliate. The inner three are a little longer. The 4 to 7 cm long, overgrown and funnel-shaped, folded crown, with a shorter hem, can be lavender to purple-lavender in color, the throat is usually darker in color, but white crowns can also appear.

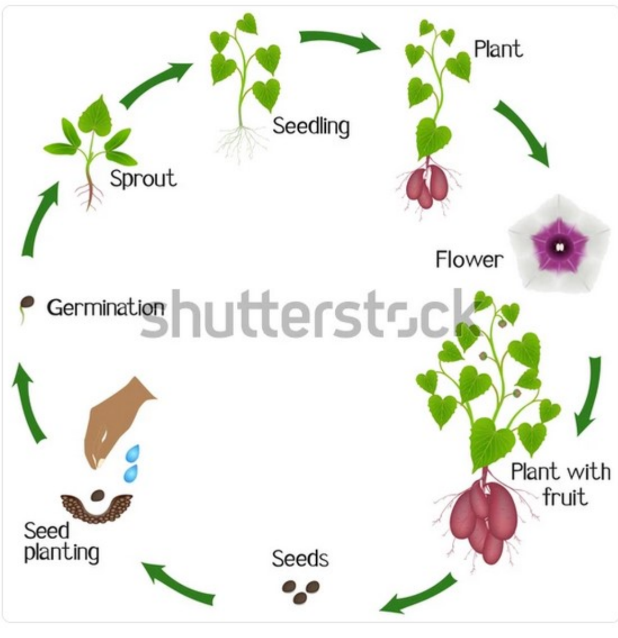

Fig. 1. Life cycle of sweet potato

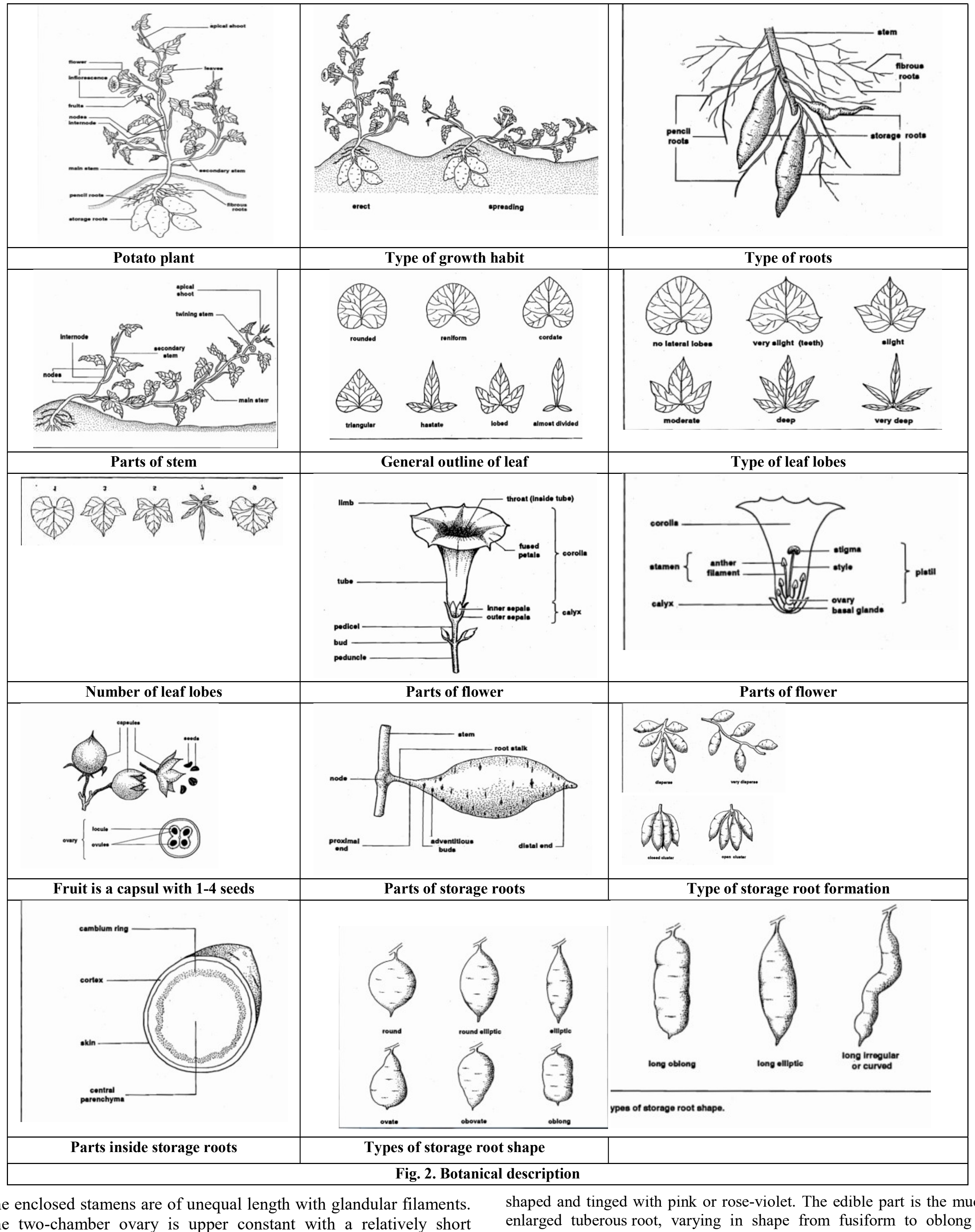

Fig. 2. Botanical description

The enclosed stamens are of unequal length with glandular filaments. The two-chamber ovary is upper constant with a relatively short stylus. Seeds are only produced from cross-pollination. The flowers open before sunrise and stay open for a few hours. They close again in the morning and begin to wither. The edible tuberous root is long and tapered, with a smooth skin whose color ranges between yellow, orange, red, brown, purple, and beige. Its flesh ranges from beige through white, red, pink, violet, yellow, orange, and purple. Sweet potato cultivars with white or pale yellow flesh are less sweet and moist than those with red, pink or orange flesh (Wikipedia, 2024). The starchy root is high in vitamin A. Sweet potato stems are usually long and trailing and bear lobed or unlobed leaves that vary in shape. The flowers, borne in clusters in the axils of the leaves, are funnel-shaped and tinged with pink or rose-violet. The edible part is the much-enlarged tuberous root, varying in shape from fusiform to oblong or pointed oval. Root colours range from white to orange and occasionally purple inside and from light buff to brown or rose and purplish red outside. The pulp consists largely of starch, and orange-fleshed varieties are high in carotene. Propagated vegetatively by sprouts arising from the roots, known as slips, or by cuttings of the vines, the plant is best adapted to light friable soils such as sandy loams. At least four to five months of warm weather are required for large yields (EEB, 2024). Sweet potato vines rarely bloom, but when they do, they're glorious. And, they look like purple or pink trumpeting morning glories. The plant is better known for its foliage which comes in various colors including purples, greens, and bronze. Life cycle and botanical description are given in Fig. 1, 2 and 3.

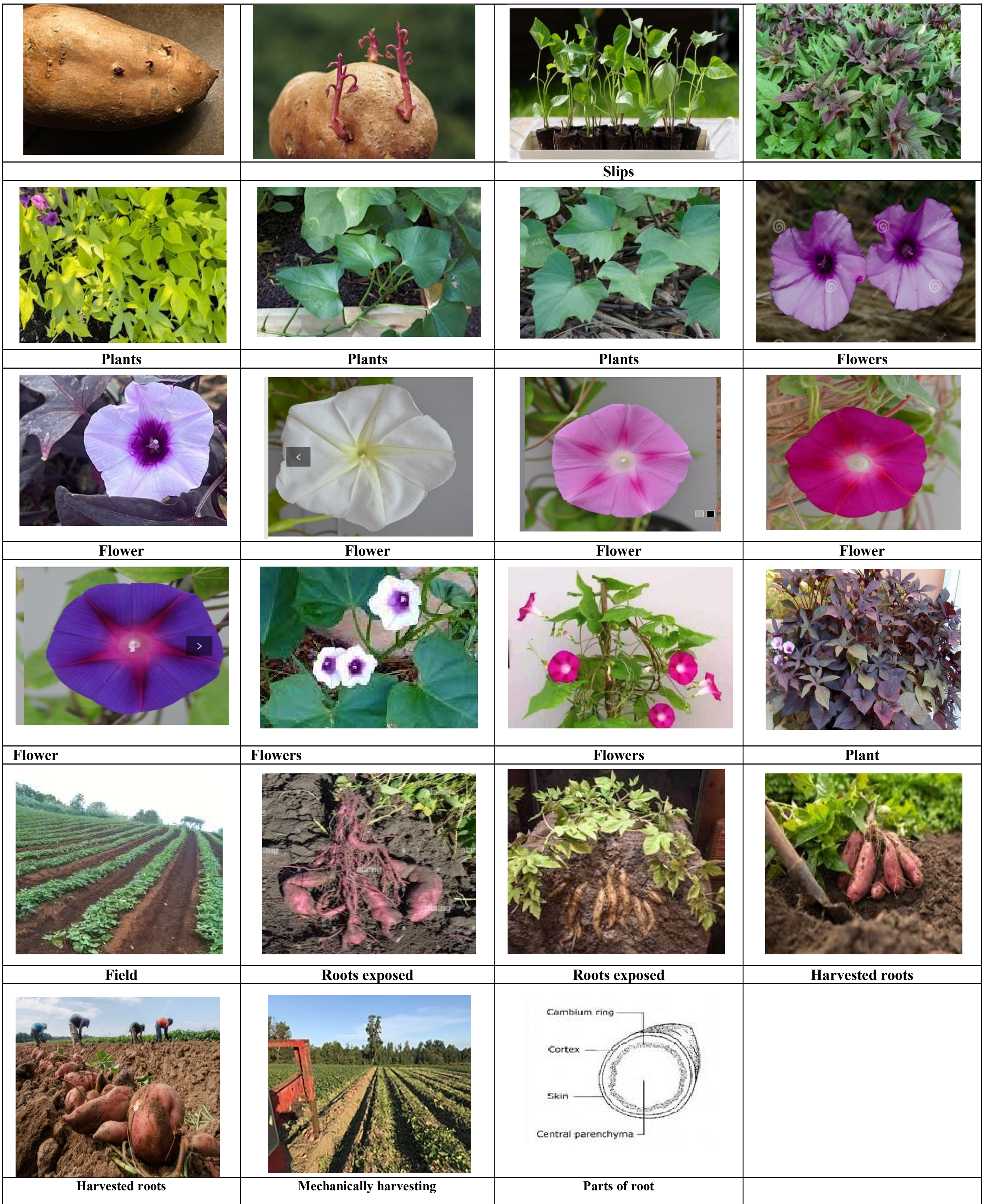

Fig. 3. Botanical description

Floral biology

Despite the fact that some aspects related to the flowering of the sweet potato have been studied previously, to date, in Cuba and tropical regions, only general descriptions have been documented without detailed information on the biology and floral phenology of the sweet potato, aspects of interest for genetic improvement. To carry out the research, four sweet potato genotypes obtained and released by the genetic improvement program of the Research Institute of Tropical Roots and Tuber Crops (INIVIT) were selected, one of them ("CEMSA 74-228") is of international reference. The average flower emission frequency per inflorescence was 1.5 days. The number of flowers per inflorescence fluctuated between 7.35 and 26.14. The time from pollination to seed maturation varied on average from 22.8 to 32.3 days. For the four genotypes, different moments of anthesis were found, ranging from 0444 h (± 8.3 min) to 0619 h (± 10.7 min). The pollen presented viability percentages above 90%

from 0600 to 1300 h. The results allowed a better knowledge of the floral biology of the sweet potato and the floral phenological phases and the approximate time of each one was determined, which will be useful for plant breeders (Rodríguez *et al*., 2023). The results allowed a better knowledge of the floral biology of the sweet potato and the floral phonological phases and the approximate time of each one ("CEMSA 74-228", "CEMSA 78-326", "INIVIT BS-16" and "INIVIT BM-90") was determined, which will be useful for plant breeders. The maximum growth reached of the floral peduncle varied between 5.3 and 10.2 cm. The frequency of emission of flowers per inflorescence was 1.5 days. The number of flowers per inflorescence fluctuated between 7.35 and 26.14. The time from pollination to seed maturation varied on average from 22.8 to 32.3 days. For the four genotypes, different moments of anthesis were found, ranging from 0444 h (± 8.3 min) to 0619 h (± 10.7 min). The total decontortion of the flower occurred between 1:53 and 2:38 h. The pollen presented viability percentages above 90% from 0600 to 1300 h, while the stigmatic receptivity was below 25% in the measurements made at 72, 48 and 24 h before anthesis. Between 0600 and 0800 h, the receptivity ranged from 79 to 93% (Fig. 4) (Rodríguez *et al.,* 2023).

Pollination

Sweet potato is an autopolyploid (2n=6x=90, x=15), a highly heterozygous clone hybrid with easy generation of true seeds (in Cuba) through directed crossing and open pollination (a successful pollination result in 1-3 true seeds), in the latter the main pollinating agent are bees. The plant has a sporophytic self-incompatibility system. Flower formation of sweet potato, is in general, related to latitude; it flowers frequently in the tropics while little or no flowering occurs in temperate regions. Even in the tropics, the intensity of flowering varies widely with seasons from poor to abundant, and some varieties produce little or no flowers at all. It is generally recognized that a short photoperiod and a slight humidity, promote sweet potato to flower. Most of the sweet potato genotypes flower naturally in the short days in the tropics in Cuba from November to April and it is not necessary to use grafts on *Ipomoea* spp. to induce flowering. Aspects related to sweet potato flowering have been previously studied due to the importance of this species for the world . However, to date, in Cuba and tropical regions, only general descriptions have been documented without detailed information on the biology and floral phenology of the sweet potato, aspects of interest for genetic improvement (Rodríguez *et al*., 2023).

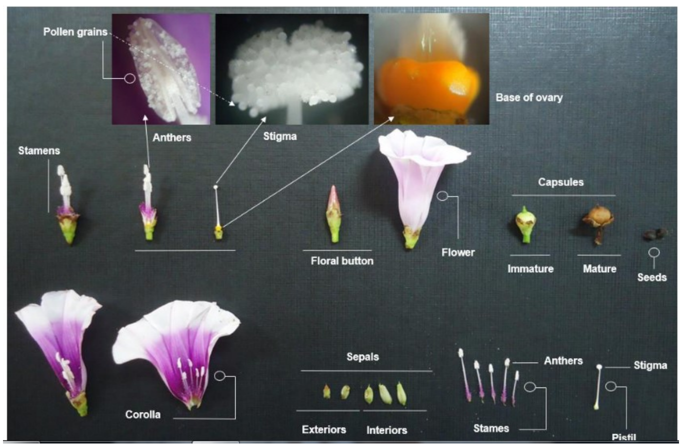

Fig. 4. Parts of the sweet potato flower, capsule and seed

GENETICS AND CYTOGENETICS

The number of chromosomes in the sweet potato plant is 2n = 6x = 90. This indicates that it is a hexaploid plant with a basic chromosome number x = 15. Among the wild species, *I. Jittoralis* and *I. tiliacea* are tetraploids. The other species are diploids with 2n = 2x =30. *I. trifida* includes plants that can be 2x, 3x, 4x and 6x. The ploidy level of *I. tabascana* and *I. umbraticola* is still unknown. The geographic distribution of the wild species of section *Batatas* is within the Americas. This is with exception of *I. littoralis* that is found in Australia and Asia (Huaman, 1992). The distribution and organization of 5S and 18S–5.8S–26S (18S) rDNA were studied in 10 varieties of hexaploid *Ipomoea batatas*, five accessions of tetraploid *Ipomeoa trifida*, and six related species (five diploids, *I. trifida, I. triloba, I. tiliacea, I. leucantha* and *I. setosa* and one tetraploid, *I. tabascana*), by using fluorescence *in situ* hybridization (FISH). The FISH data obtained indicated that polyploidization was followed by decrease in the number of 18S rDNA loci in higher ploidy level and provided evidence for major genomic rearrangements and/or diploidization in polyploid *I. batatas*. Among the five diploid species examined, *I. trifida* appeared to be the most closely related to *I. batatas*. By contrast, *I. leucantha* was closed to *I. tiliacea*, but both species were distant from sweet potato. *I. triloba* and *I. setosa* were distantly related to the rest of *Ipomoea batatas* complex. The close relationship between *I. trifida* and *I. batatas* was also demonstrated by the presence of one 18S and CMA marker in these two chromosome complements only. Based on chromosome morphology, tetraploid *I. trifida* appeared to be more closely related to sweet potato than *I. tabascana*. Taking all data obtained in this study, *I. trifida* might be the progenitor of *I. batatas*, and *I. tabascana*, interspecific hybrid between these two species (Srisuwan *et al*., 2006).

In the present study, we detected the genome diversity and relationship of sweet potato and different polyploidy types *I. trifida* using Restriction-site Associated DNA Sequencing (RAD-seq). A total of 38,605 RAD-tags containing 832,204 SNPs had been identified. These tags were annotated using five public databases, about 11,519 tags were aligned to functional genes in various pathways. Based on SNP genotype, phylogenetic relation analysis results confirmed that cultivated sweet potato has a closer relationship with *I. trifida* 6 × than with *I. trifida* 4X and *I. trifida* 2×. Besides, 5042 SSRs were detected in *I. trifida* 6×, and 3202 pairs of high-quality SSR primers were developed. A total of 68 primers were randomly selected and synthesized, of which 61 were successfully amplified (Feng *et al.,* 2018). Cultivated sweet potato is an allogamous species and is self-incompatible. Though, the majority of sweet potatoes are propagated and disseminated as clones or via slips rather than from seed produced from deliberate crossing. The sweet potato genome is characterized as a hexaploid (2n = 6x = 90). However, there are various reports of the existence of tetraploids (2n = 4x = 60) or feral *I. batatas.* The existence of tetraploids is rare as most all cultivated sweet potatoes are hexaploids. Because of the polyploidy nature of sweet potatoes, Mendelian genetics and segregation ratios are quite complex (Anglin *et al*., 2021).

GENETIC DIVERSITY

Their shape can be round, round elliptic, ovate, obovate, oblong, long oblong, long elliptic, and long irregular or curved. The root skin colour can be whitish, cream, yellow, orange, brown-orange, pink, red, red-purple and very dark purple. The intensity of the colour depends on the environmental conditions where the plant is grown. The flesh colour can be white, cream, yellow or orange. However, some cultivars show red-purple pigmentation in the flesh in very few scattered spots, pigmented rings or, in some cases, throughout the entire flesh (Huaman, 1992). We determined genetic diversity of 40 sweet potato accessions from ICAR-CTCRI and CIP by using microsatellite markers. They were analyzed for diversity using 10 simple sequence repeat (SSR) primers. The presence of bands was scored for each SSR and for each accession and the data were analysed by principal coordinate analysis. The polymorphic SSR loci revealed diverse relationship among the sweet potato cultivars, which was grouped into seven major clusters by unweighted pair group method analysis (UPGMA) method. Cluster analysis showed a Jaccard co-efficient ranging from 0.5 to 1.0 indicating high genetic diversity (Nair *et al*., 2017). Sweet potato (*Ipomoea batatas* L. Lam) is an important food crop widely cultivated in the world. In this study, nine chloroplast simple sequence repeat (cpSSR) markers were used to analyze the genetic diversity and relationships of 558 sweet potato accessions in the germplasm collection of the National Agrobiodiversity Center (NAC). Eight of the nine cpSSR showed polymorphisms, while Ibcp31 did not. The number of alleles per locus ranged from two to four. In general, the Shannon index for each cpSSR ranged from 0.280 to 1.123 and the diversity indices and unbiased diversity ranged from 0.148 to 0.626, and 0.210 to 0.627, respectively. Results of the median-joining network showed 33 chlorotypes in 558 sweet potato accessions. In factor analysis, 558 sweet potato accessions were divided into four clusters, with clusters I and II composed only of the sweet potato accessions from Korea, Japan, Taiwan, and the USA. The results of this study confirmed that the genetic diversity of the female parents of sweet potato accessions conserved at the NAC is low and therefore more sweet potato accessions need to be collected. These results will help to establish an efficient management plan for sweet potato genetic germplasms at the NAC (Lee *et al.,* 2019). In addition to genetic diversity, sweet potato varieties are diversified in terms of flesh and skin colors, size, shape, texture, and taste of the storage root. The color, width, thickness, and shape of leaves may also distinguish the various sweet potato varieties. The inside (flesh) and skin colors are mainly white, cream, yellow, orange, pink, red, and purple with their diversity attributed to their varying nutritional and phytochemical components. (Amoanimaa-Dede *et al.,* 2020). Sweet potato, a dicotyledonous and perennial plant, is the third tuber/root crop species behind potato and cassava in terms of production. Long terminal repeat (LTR) retrotransposons are highly abundant in sweet potato, contributing to genetic diversity. Retrotransposon-based insertion polymorphism (RBIP) is a high-throughput marker system to study the genetic diversity of plant species. To date, there have been no transposon marker-based genetic diversity analyses of sweet potato. Here, we reported a structure-based analysis of the sweet potato genome, a total of 21555 LTR retrotransposons, which belonged to the main LTR-retrotransposon subfamilies *Ty3-gypsy* and *Ty1-copia* were identified. After searching and selecting using Hidden Markov Models (HMMs), 1616 LTR retrotransposon sequences containing at least two models were screened. A total of 48 RBIP primers were synthesized based on the high copy numbers of conserved LTR sequences. Fifty-six amplicons with an average polymorphism of 91.07% were generated in 105 sweet potato germplasm resources based on RBIP markers. A Unweighted Pair Group Method with Arithmatic Mean (UPGMA) dendrogram, a model-based genetic structure and principal component analysis divided the sweet potato germplasms into 3 groups containing 8, 53, and 44 germplasms. All the three analyses produced significant groupwise consensus.

Table 1. Description of sweet potato genotypes studied

Genotypes	Tuber flesh colour
Bhu Krishna	Strongly pigmented with anthocyanins
Kamala Sundari	Pale yellow
Sree Rethna	Dark yellow
Sree Arun	Pale yellow
Bhu Ja	Intermediate orange
Kishan	Cream
Sree Kanaka	Dark orange
Sree Vardhini	Cream
Bhu Sona	Dark orange
Gouri	Dark orange
Varsha	Cream
S1609	Cream
S1712	Dark cream
S1603	Pale orange
S1652	Pale yellow
S27	White
S1710	Cream
Kanhangad	Dark yellow

However, almost all the germplasms contained only one primary locus. The analysis of molecular variance (AMOVA) among the groups indicated higher intergroup genetic variation (53%) than intrapopulation genetic variation. In addition, long-term self-retention may cause some germplasm resources to exhibit variable segregation. These results suggest that these sweet potato germplasms are not well evolutionarily diversified, although geographic speciation could have occurred at a limited level. This study highlights the utility of RBIP markers for determining the intraspecies variability of sweet potato and have the potential to be used as core primer pairs for variety identification, genetic diversity assessment and linkage map

Fig. 5. Representative leaves showing the classifications for the general leaf outline; Top row (left to right): rounded; reniform; cordate; cordate; middle row (left to right): triangular; triangular; hastate; hastate; bottom row (left to right): lobed; lobed; almost divided; almost divided

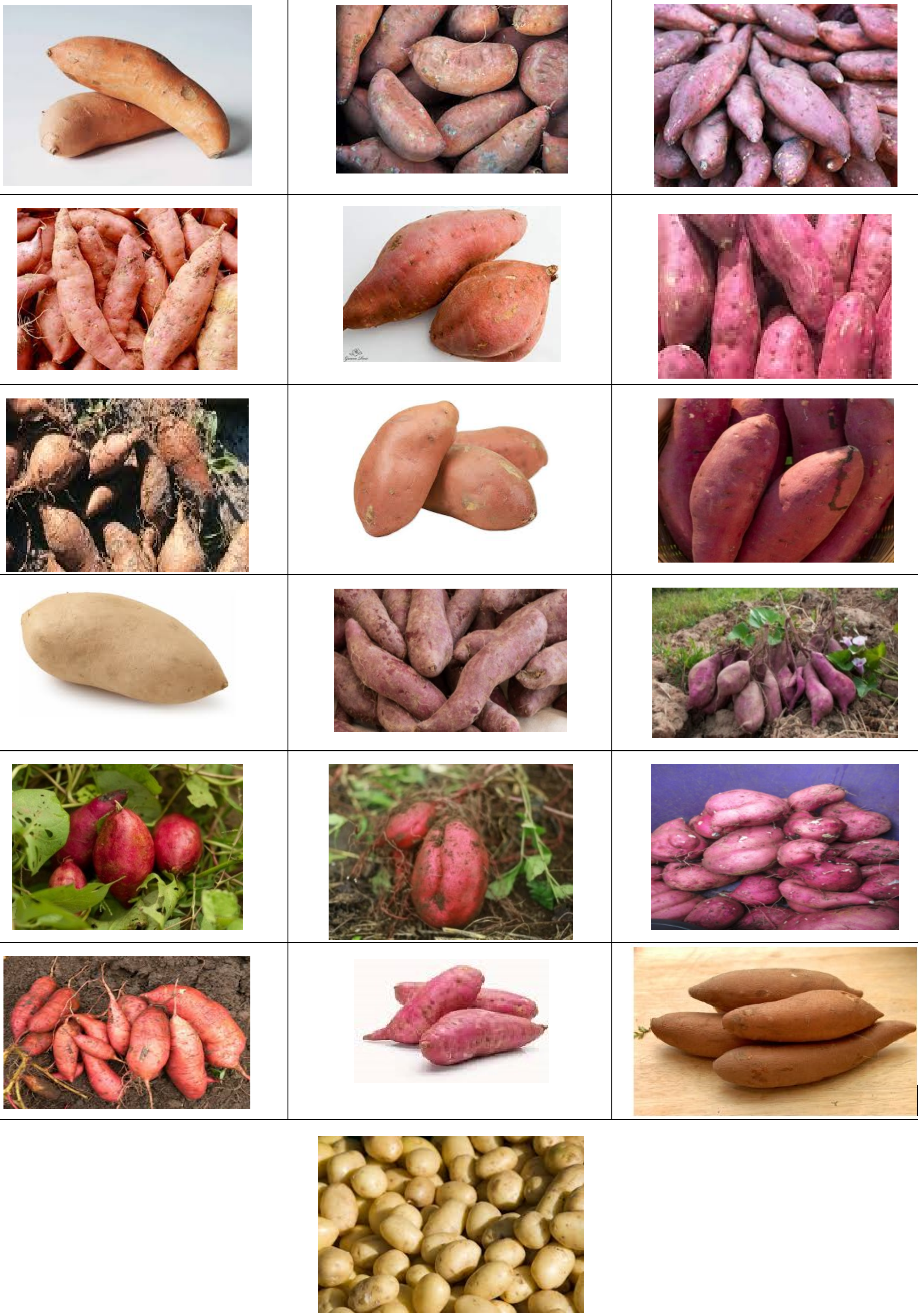

Fig. 6: Variability for root shape, color and size of sweet potato

construction (Yusha Meng *et al.,* 2021). Sweet potato flowers come in a variety of colors including pink, purple and white. They have a unique trumpet-like shape that is both striking and delicate at the same time. Sweet potato flowers have unique bell-shaped petals in colors ranging from light pink to deep purple, with a yellow or white center. These delicate blooms grow on vines that produce small green leaves. There are different types of sweet potatoes with varying flower colors such as Beauregard (pink/pale purple), Covington (white), and Garnet (light purple/pink). Eighteen sweet potato genotypes of various flesh colours namely purple, white, cream, yellow and orange were evaluated for important processing traits (Table 1). The plant materials studied included germplasm accessions, breeding lines and improved varieties (Visalakshi *et al.,* 2021). The present work considered collecting and characterizing the genetic diversity of sweet potato in Ecuador through morphological and molecular descriptors (SSRs). Germplasm collections were made to assemble a national sweet potato collection for Ecuador. Characterization of the genetic diversity of this species was done through 34 morphological descriptors (24 qualitative and 10 quantitative), plus 12 exclusive descriptors for flowering and 8 microsatellites (SSRs). Three hundred and sixty-eight sweet potato accessions were collected in 18 provinces of Ecuador. Morphological characterization showed seven morphological groups and the variables with the greatest discriminating power for the description of the germplasm ($p < .001$) were the color, shape and defects of the reservoir root, in addition to the shape of the profile and lobes of the leaves. Principal component analysis determined the association of the main quantitative morphological features to the components. Eight microsatellite markers detected 89 alleles, with an average of 11.12 allele/locus and average polymorphism (PIC) of 0.848. STRUCTURE software revealed the formation of 4 different genetic groups. Morphological and molecular data did not show the formation of any group defined according to the province of origin. Factors such as the sweet potato reproductive system (cross-pollination), random sweet potato mutations and farmer exchange, contributed to the greater genetic diversity present. High genetic diversity and low number of duplicates were identified. This collection could provide outstanding genotypes to be used in breeding programs.

Fig. 7. Variability for root shape, color and size of sweet potato

Fig. 8. Variability in flesh color of sweet potato

Local landraces still in the hands of local farmers suggest that in situ conservation projects must be put in place (Monteros-Altamirano *et al.,* 2021). A total of 32 sweet potato genotypes were evaluated to assess the genetic diversity based on quantitative traits and molecular markers, as well as stability for yield and related traits. Wider variability was observed for the traits like vine length (181.2–501.3 cm), number of leaves/plant (103.0–414.0 cm), internodal length (3.20–14.80 cm), petiole length (6.5–21.3 cm), leaf length (8.50–14.5 cm), leaf breadth (8.20–15.30 cm), leaf area (42.50–115.62 cm2), tuber length (7.77–18.07 cm), tuber diameter (2.67–6.90 cm), tuber weight (65.60–192.09 g), tuber yield (7.77–28.87 t ha−1), dry matter (27.34–36.41%), total sugar (4.50–5.70%) and starch (18.50–29.92%) content. Desirable traits such as tuber yield, dry matter and starch content have shown high heritability (>60%) with moderate to high genetic advance. Under molecular analysis, a total of 232 alleles were observed from all 32 microsatellite markers, which ranged from 4 to 14 with an average of 7.77 alleles per locus. In the population, the average observed heterozygosity (0.51) was higher than the expected heterozygosity (0.49). The contribution of genotype, genotype by environment interaction to the total variations was found to be significant. Based on the multi-trait stability index (tuber length, tuber diameter, tuber weight and tuber yield), genotypes X-24, MLSPC-3, MLSPC-5, ARSPC-1 and TSP-12-12 were found to be most stable. Among them, the high-yielding and stable genotypes TSP-12-10 (26.0 t ha−1) and MLSPC-3 (23.9 t ha−1) can be promoted for commercial production or used as parental material in future crop improvement programmes (Verma *et al.,* 2023). Vasriability for leaf shape and lobes (Fig. 5), root shape, size and color (Fig. 6 and 7), root flesh color (Fig.8) are given in Figures.

BREEDING

Germplasm: During the 18th century, sweet potatoes were brought from Japan to various parts of Korea as a famine-relief crop. At present, about 700 sweet potato germplasms have been collected worldwide at the National Agrobiodiversity Center (NAC) at the Rural Development Administration in Korea. However, analysis of genetic diversity in the preserved sweet potato accessions in NAC is lacking. Therefore, it is necessary to learn the genetic relationship of the sweet potato accessions to efficiently manage sweet potato germplasms. In this study, 558 sweet potato accessions conserved at the NAC were analyzed using nine cpSSRs to evaluate the genetic diversity and determine the appropriate panel of sweet potato germplasm for sweet potato improvement and conservation (Lee *et al*., 2019). Sweet potato collection housed by the International Center of Potato (CIP) is one of the largest assemblages of plant material representing the genetic resources of this important staple crop. The collection currently contains almost 6,000 accessions of *Ipomoea batatas* (cultivated sweetpotato) and over 1,000 accessions of sweet potato crop wild relatives (CWRs) (Anglin *et al.,* 2021). The principal purpose of an ex-situ genebanks is to preserve and safeguard the genetic diversity of important crops and their wild relatives for use today and for future generations. Clonal genebanks, as opposed to seed genebanks, are unique in that accessions are genetically static with fixed combinations of alleles that are preserved over time vs. seed accessions which are mostly populations with alleles that are in flux. In either case, each accession in a genebanks potentially contains new alleles or a combination of alleles that confer specific traits and adaptive potential. Access to this genetic diversity is a key component for breeders and related research activities to improve cultivated crops and ensure food security (Anglin *et al*., 2021). Frequently, elite lines continue to be improved while the exotic lines remain untapped, uncharacterized, and underutilized. In general, genebanks strive to preserve as much of the genetic diversity as possible found in their mandated crops and associated wild relatives. Thus, collection sizes are often quite large, but only rarely are they thoroughly characterized for traits of interest.

This limits the ability of the user to strategically select genotypes or phenotypes for their specific purpose. Consequently, only a relatively small proportion of holdings of the genebanks tend to be utilized in the short term, and most genebanks resources are utilized in maintaining accession viability and genetic integrity, and less so on understanding the specific genetic attributes and key traits of the accessions in the collections (Anglin *et al*., 2021). The International Potato Center (CIP) maintains one of the world's largest cultivated sweetpotato genebanks with over 5,500 accessions maintained in vitro. The overall objective is to conserve the diversity in the collection and make it available to the global community (Rossel, 2024).

Breeding Goals

Sweetpotato is grown for human consumption , processed starch, bioethanol, colorants/dyes, and for foliage for human and animal consumption. Examples of breeding goals include: resistance to sweetpotato virus disease (SPVD) and Alternaria stem blight, weevil resistance, improved yield, improved size, shape, and uniformity of roots, yield stability, high dry matter content, orange-flesh varieties with high nutritional value [*i.e.,* beta-carotene content for combating vitamin A deficiency, improved chemical composition (*i.e.,* starch, cellulose, sugars, protein content, carotenes, anthocyanins), improved micronutrient content (*e.g*., Zn and Fe), extended harvest for subsistence cropping, drought tolerance, dense foliage with high protein content, improved palatability, and digestibility, vine survival and vigor after planting (especially during periods of drought), improved storage, resistance to skinning, and lower acrylamide potential (Barb and Mahama, 2023).

Methods of Breeding

There are three methods of breeding 1st Collecting, evaluating, and selecting from the local germplasm. 2nd Importing cultivars that have been bred in other parts of the world and evaluating them under your conditions.3rd breeding cultivars in your own Programme (Belay, 2018). In Cuba, since 1967, a sweet potato Genetic Improvement Program (GIP) has been developed, which applies the principles of genetics to produce new cultivars, with superior characteristics, such as higher yield, resistance to biotic and abiotic factors, higher nutritional values, etc. Annually in the hybridization campaign, the blocks of crosses with the selected parents of different genetic constitution are designed to meet the objectives set. Hybridizations are carried out at the Research Institute of Tropical Roots and Tuber Crops (INIVIT). Currently, 40 000 hybrid seeds are produced annually and in total more than one million seeds have been obtained for uses in genetic improvement. The production of hybrid seed in sweet potatoes by directed crosses is expensive, very laborious and requires intense technical supervision. Given the importance of hybridization as a genetic improvement strategy and the lack of information regarding the floral biology of *I. batatas* in tropical regions, this research aimed to reveal the main aspects related to sweet potato floral biology and phenology (Rodríguez *et al*., 2023). There are 3 methods to obtain improved cultivars (agricultural varieties) of sweet potato (*Ipomoea batatas*) for distribution to farmers in your country: 1) Collecting, evaluating, and selecting from the local germplasm. 2) Importing cultivars that have been bred in other parts of the world and evaluating them under your conditions. 3) Breeding cultivars in your own programme (Wilson *et al.,* 2024).

Breeding Factors

The rate of progress that is achievable for a breeding program is dependent on the gene frequencies in the base population, the effectiveness of the breeding methods that are used, and the access the breeder has to field sites, greenhouses, lab equipment, and trained personnel needed to conduct a breeding program. A breeder should consider the following when deciding on which breeding method to use: 1) The germplasm that is available. 2) The inheritance of the target traits (if known). And 3) Biological constraints of the species (*i.e.,* low seed set per plant, self-incompatibility, *etc.*). Genetic improvement of sweet potato is complicated by a number of factors: 1) Self- and cross-incompatibility. 2) The highly heterozygous nature of individual clones. And 3) The large number of chromosomes (2n = 6x = 90). These factors contribute to a low correlation between parent performance and offspring performance. In general the success of a sweet potato breeding program relies mostly on the ability to grow and evaluate a large number of clones/hybrid progeny in a selective environment that closely resembles the target environment. Thus the development of rapid and reliable screening methods is critical (Barb and Mahama, 2023).

Hexaploid Nature of Sweet potato

Cultivars of sweet potato are phenotypically homogenous (because they are clonally reproduced) and genetically heterozygous (because they are self-incompatible outcrossers). Sweet potato is a hexaploid with 2 non-homologous genomes (B1B1B2B2B2B2) with tetradisomic inheritance, so the genetics of simple traits is more complex with up to six alleles per locus. Furthermore, because sweet potato is a hexaploid, heterozygous genotypes occur in much larger frequencies making heterosis more important for quantitatively inherited traits (*e.g.,* yield, yield stability, vigor after planting,). The hexaploid nature of sweetpotato and the fact that this species is self-incompatible makes it extremely difficult to fix recessively inherited traits like resistance to certain viruses and some quality traits *e.g.,* orange flesh) even if the frequency of these recessive alleles is greater than 70% (Barb and Mahama, 2023).

Table 2. Sweet potato varieties grown in different countries

Country	Variety	Reference
Bangladesh	BARISP-6 (Lalkothi), BARISP-7 (Kalmegh), BARISP-9	Golder et al. 2000; Bhuiyan et al. 2009
China	Xuzhou 18	Guoquan and George 2000
Ethiopia	Balella and Bareda	Teshome Abdissa et al. 2011
India	Pusa Safed, Co-1, VL Sakarkand-6, Sree Vardhini, Co-2, Co-3, Samrat, Sree Bhadra, Sree Arun, Sree Varun, Sankar, Gouri, Kalinga, Gautam, Sourin, Kishan, H-41, H-42, H-268, Rajendra Sakarakand-5, Sree Rethna, Sree Kanaka, Kamala Sundari, S-1221, WBSP-4, Tripti, Bidhana Jagannath BCSP-5, Bidhana Jagannath, BCSP-5, Birsa Sakarakand-1 and Indira Sakarakand-1	CTCRI 1999; CTCRI 2006
Japan	Quick Sweet, Kokei No. 14, Beniazuma, Norin No. 2, Koganesengan and Satsumahikari	Yamakawa 2000
Korea	Mokpo 32, Mokpo 34, Hongmi, Hwangmi, Sinjami, Shinmi, Wonmi, Poongmi, Borami and Enumi	Jeong et al. 1986; Jeong 2000
Malaysia	Jalomas, Minamiyutaka, Pisang Kapas, Madu Bawang, Gendut, Telong, Kangkung Cina, IKan Selavang, Kangkung, Bukit Naga, Taiwan and Pasar Borong-1, Serdang, Suberang Perai, Kundang, Bidor, Pantian, Rhu Tapai, Sungai Baging and Kuala Linggi	
New Zealand	Toka Toka Gold, Owairaka Red and Beauregard	Wright et al. 2003
Papua New Guinea (PNG)	Koitaki 2, K9, K42, UIB016, Wanmun Murua, Wanmun and Large	Bourke 2005
Taiwan	Taoyuan No. 1, Taoyun No. 2 and Tainung No. 71	Yi-Shin et al. 2000
Thailand	PIS 205, PIS 65-16, PIS 166-5, Maejo and Taiwan	Narin and Reungmaneepaitoon 2005
United States of America	Goldrush, Redgold, Centennail, Beauregard and Jewel	Schultheis and Jester 2000
Vietnam	H12, K51 and TV1	Ngoan 2006

Characteristics of Clonally Propagated Crops (Barb and Mahama, 2023).

Sweet potato is an open-pollinated clonally propagated crop. Characteristics common to clonally propagated crops include:

- A strong positive relationship between productivity/vigor and level of heterozygosity
- Selfing reduces vigor due to inbreeding depression
- Vigor/heterozygosity can be fixed and maintained for the life of the clone
- Polyploids/aneuploids can be maintained via clonal propagation
- Often difficult to create a large quantity of clones from one plant, whereas it is relatively easy to produce a large amount of seed from most sexually propagated crops
- Clonal propagules are typically bulky and difficult to store

A basic breeding procedure for a clonal crop like sweet potato includes the following steps (Barb and Mahama, 2023):

1. Define breeding objectives (*i.e.*, yield stability, adaptation, taste, and pest and disease resistance)
2. Assemble germplasm (*i.e.*, local varieties, wild species, cultivars developed in other parts of the world, *etc.*) and establish a breeding nursery
3. Develop segregating populations via hybridization (*i.e.,* biparental cross, polycross nursery, or diallel crosses) and/or induced mutagenesis
4. Evaluate and select superior clones
   - Plot size, the number of replications, and the number of locations where clones are evaluated is increased after each round of selection in an attempt to reduce the variability due to the environment
   - Select early for traits with high heritability, select later for traits with low heritability
5. Name and release a cultivar and multiply and distribute clones

There are four U.S. Grades for sweet potato (U.S. Extra No. 1, U.S. No.1, U.S. commercial and U.S. No. 2), and grades are based on degree of freedom from defects (dirt, roots, cuts, bruises, growth cracks, decay, insects, and diseases), but also size and weight categories (Belay, 2018).

Yield and Acreage over time: The lack of improved varieties of sweet potatoes is mostly the result of limited investment in sweet potato breeding programs in Africa, though this trend is changing as government and NGO's are now focusing more efforts towards the training and support of plant breeders working on secondary crops including sweet potato. Additional effort is also now being focused on linking farmers with breeders to ensure that varieties produced by breeding programs are meeting the needs of farmers and consumers of sweet potato (Barb and Mahama, 2023).

Varieties of Sweet Potatoes

There are two main varieties of sweet potatoes: dry flesh and moist flesh. Dry flesh sweet potatoes have tan-colored skin and lighter flesh that's higher in starch. Moist-flesh sweet potatoes have darker skin with a richer orange interior. Moist-flesh sweet potatoes taste sweeter and are more commonly available in the supermarket. Under these two general classifications, there are several unique species of sweet potatoes that vary in the country of origin, shape, color, size, and taste. Examples include Kumara sweet potatoes, Jersey sweet potatoes, and Cuban sweet potatoes (Cervoni, 2024). In sweet potato, varieties play a significant role in yield improvement. Many Research and Development organizations working on sweet potato have the major objective of developing location specific sweet potato varieties. The elite clones are developed by following different methods of breeding. The common methods are clonal selection, open pollinated selection, hybridization, mutation and biotechnology. Some of the high yielding varieties cultivated in different countries are given in Table 2 (Nedunchezhiyan *et al*., 2012a). The orange flesh sweet potato varieties/genotypes that are cultivated in India are Kamala, Sundari, Gouri, Sankar, Sree Kanaka, ST14. The carotene content in ST14 is 13.83 mg 100 g^{-1} fresh root. In Japan, Benihayato, Kyushu No. 114, in Mozambique, MGCL01, 440215, Resisto and in Thailand, PIS 226-24, PIS 227-6 aresome of the high yielding orange flesh varieties (Nedunchezhiyan *et al.,* 2012a). Purple-fleshed sweet potatoes have purple color in the skins and flesh of the storage root due to the accumulation of anthocyanins. Anthocyanins are natural soluble food pigments and contribute to the red, blue and purple colouration of leaves, flowers and other parts of the plants. Red and purple pigmentation in various parts of sweet potato such as stem, leaf and storage root is caused by the presence of acylated anthocyanins (Nedunchezhiyan *et al.,* 2012a). In Japan, Ayamurasaki, a high anthocyanin sweet potatovariety was developed by the Kyushu National Agricultural Experiment Station (KNAES). Regional Centre, Central Tuber Crops Research Institute (CTCRI), Bhubaneswar, India has developed a high anthocyanin line ST13 (CTCRI 2003). The variety PIS 189-257 from Thailand is rich in anthocyanin. In Indonesia, three high yielding purple fleshed clones (MSU 01017-16, MSU 01022-12 and MSU 01002-7) have been identified (Nedunchezhiyan *et al.,* 2012a).

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