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Chapter

Identification of Cassava Varieties in Ex-Situ Collections and Global Farmer's Fields: An Update from 1990 to 2020

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Abstract

The identification of cassava cultivars is important for understanding the crop's production system, enabling crop improvement practitioners to design and deliver tailored solutions with which farmers can secure high yields and sustainable production. Across the lowland tropics today, a large number improved varieties and landraces of cassava are under cultivation, making it inefficient for breeders and geneticists to set improvement goals for the crop. The identification and characterization of cassava genotypes is currently based on either morphological characters or molecular features. The major aim of cultivar identification is to catalog the crop's genetic diversity, but a consensus approach has still not been established. Of the two approaches to the identification of variety, morphological characters seem to account for most of the genetic variability reported in cassava. However, these characters must be treated with caution, as phenotypic changes can be due to environmental and climatic conditions as well as to the segregation of new highly heterozygous populations, thus, making the accurate identification of varieties difficult. The use of molecular markers has allowed researchers to establish accurate relationships between genotypes, and to measure and track their heterozygous status. Since the early 1990's, molecular geneticists working with cassava have been developing and deploying DNA-based tools for the identification and characterization of landraces or improved varieties. Hence, in the last five years, economists and social scientists have adopted DNA-based variety identification to measure the adoption rates of varieties, and to support the legal protection of breeder's rights. Despite the advances made in the deployment of molecular markers for cassava, multiple platform adoption, as well as their costs and variable throughput, has limited their use by practitioners of crop improvement of cassava. The post-genomic era has produced a large number of genome and transcriptome sequencing tools, and has increased our capacity to develop and deploy genome-based tools to account for the crop's genetic variability by accurately measuring and tracking allele diversity. These technologies allow the creation of haplotype catalogs that can be widely shared across the cassava crop improvement community. Low-density genome-wide SNP markers might be the solution for the wide adoption of molecular tools for the identification of cultivars or varieties of cassava. In this review we survey the efforts made in the past 30 years to establish the tools for cultivar

identification of cassava in farmer's fields and gene banks. We also emphasize the need for a global picture of the genetic diversity of this crop, at its center of origin in South America.

Keywords: cassava, genotype, varieties, SNPs, identification

1. Introduction

Cassava (*Manihot esculenta*) is a key food commodity in the tropics, being the second most important food staple in the least-developed countries, and the fourth highest source of calories in developing countries [1, 2]. Due to cassava's efficient use of soil nutrients and water resources, poor farmers can still expect reasonable harvests in areas where many other crops will fail to be productive. Thus cassava, as an agricultural commodity, has the potential to have significant global impact on nearly all of the United Nations Sustainable Development Goals (SDGs), with emphasis on SDG-1 (no poverty), SDG-2 (zero hunger), SDG-3 (good health and well-being), SDG-12 (responsible production and consumption), SDG-13 (climate action), and SDG-15 (life on land) [3].

Today, a large number of the varieties of cassava which are under cultivation have persisted from pre-Columbian times, having been perpetuated through vegetative propagation, particularly at its center of origin in South America [4, 5]. From South America, this crop spread to sub-Saharan Africa in the 16th century [6], and from South and Southeast Asia (SEA) in the late 18th and early 19th century to Asia [7]. Crop improvement, led by International Institute of Tropical Agriculture (IITA) in Africa and the International Centre for Tropical Agriculture (CIAT) in Latin America and the Caribbean (LAC), as well as in South Asia and SEA, has made improved varieties more common in farmer's fields [2, 8, 9]. For instance, CIAT and Kasetsart University in Thailand developed what is considered to be the most successful variety ever breed, KU50, which has a notably high fresh root yield and dry matter content [10, 11]. Since its official release in Thailand, this variety has spread throughout SEA. In Vietnam, KU50 was released in 1995 as KM94, and was later introduced in Cambodia as Malay [12–14]. It covers nearly one million hectares today. In cassava, it is quite common for the same variety to be re-named when it is introduced to a new area, leading to the existence of synonymous varieties. The opposite situation also occurs, where different varieties are identified under the same name (homonyms) [15–17].

There is currently little understanding of the number of cassava varieties grown throughout the lowland tropics, but, this number is likely to be in the order of thousands, based on the results obtained by Rabbi et al. [2] and Floro et al. [4]. This number can also be estimated from the total number of the crop accessions (genotypes) kept under conservation in different ex-situ gene banks. In 2010, CIAT commissioned a survey of the status of germplasm conservation of cassava across 50 cassava gene banks [18]. Out of the 50 gene banks surveyed, 34 provided information that allowed the estimation that as many as 14,791 distinct landraces were under conservation in gene banks [18]. The real number, however, is likely be significantly lower, once all varieties are characterized using DNA-based molecular markers [2, 4, 12].

In the past 30 years, a body of knowledge about the varietal identification and genetic diversity of cassava has been developed for genetic materials found in ex-situ collections, experimental field trials, and farmers' fields, using morphological descriptors [17, 19–48], morphological descriptors and molecular markers [16, 49–57], and molecular markers alone [2, 4, 12, 15, 25, 58–126]. The morphological

descriptors were first defined by CIAT in the late 70's and early 80's [47, 48], and were later revised by Fukuda et al. [21, 46]. Approximately 75 morphological descriptors, also known as traits, have been defined, and 199 alleles have been made available for distinguishing cassava varieties under ex-situ conservation or to catalog the local varietal inventory of farmers, In more than half of these studies, a measure of their genetic diversity was included [19, 23, 25, 29, 30, 33–37, 40, 41, 43]. Additional efforts to identify cassava varieties have been undertaken, combining morphological descriptors and molecular markers, under the assumption that combining knowledge of farmers with DNA-based genetic profiles should more accurately account for the large genetic differentiation observed among cassava varieties in gene banks, breeding programs, and in famers' fields [16, 49–57].

Across the scientific community investigating cassava, the most widely used methods for identification of varieties, and the estimation of its genetic diversity, have involved molecular markers [127]. Since the advent of DNA-based molecular marker technologies, cassava scientists have adopted nearly all of the most popular techniques to elucidate and describe the crop's varietal identities, diversity, domestication, and ancestry [2, 4, 64, 72–74, 78, 126]. These molecular approaches have focused on two primary objectives: (1) to access an adequate number of highly informative DNA-based molecular markers across the cultivated species; and (2) to assess the crop's global ex-situ germplasm, and that of populations produced at publicly funded breeding programs. Thus, the use of molecular markers could allow building a global varietal haplotype catalog, containing the molecular descriptions of the most common varieties of cassava grown during the last 50 years across sub-Saharan Africa, South and SEA, and LAC. This information will facilitate the development, registration, and release of varieties that will effectively replace old varieties with the latest modern cultivars.

Access to a global catalog of the crop's molecular haplotypes will enable the conducting of studies on the adoption of improved varieties [4]. DNA-based marker technology must be cost-effective, easy to use, and reproducible across laboratories. The reproducibility of molecular marker techniques is extremely important in cassava, due to the presence of fixed somatic mutations, which are potentially caused by clonal propagation, although evidence for this phenomenon is limited [36, 68, 95, 128, 129].

A robust set of highly informative DNA-based markers could be used for variety identification, quality control, and the measurement of genetic diversity, with a potential use in variety registration. Thus, cassava breeders will be able to trace infringements of Plant Breeder's Rights, particularly when the cassava variety is licensed for exclusive commercial use.

2. Morphological descriptors

The need to improve cassava varieties, to fight hunger, malnutrition, and poverty in the tropics, has led to the identification of the problem of discriminating between *M. esculenta* cultigens, particular between landraces and improved types. CIAT and IITA's publicly funded breeding programs have introduced new varieties and cultivars in tropical countries, increasing the number of crop varieties available to farmers in Africa (IITA), Asia, LAC, and SEA (CIAT) [130]. In the late 1970s, CIAT established and evaluated its cassava germplasm collection, developing and using 54 basic morphological descriptors [21], aimed at the efficient selection of parental lines for breeding. In the 2000's, Fukuda et al. [21, 46] revisited the morphological descriptor list by defining 75 descriptors, with the objective of standardizing the characterization data and improving the selection of new exotic

parental lines for breeding in Africa, The aim of this work was to reduce unavoidably subjective interpretations generated using the morphological method in light of the genetic variability of cassava.

Cassava has large phenotypic variance in the field, with a wide eco-geographic adaptation range, suggesting that there is a significant amount of genetic diversity available for breeding. Thus, the identification and differentiation of commercial and landrace cultivars is very important. It has been necessary until recently to rely on the morphological characteristics of the vegetative parts of cassava. Consequently, a range of vegetative descriptors has been used to distinguish cassava varieties from each other in Africa, Asia, LAC, SEA, and Oceania (**Table 1**). The resolution achieved by Fukuda's et al. morphological descriptors can account for cassava's genetic differentiation between accessions, facilitating the understanding of the crop's genetic resources. Among the 28 morphology-based cassava varietal identification and genetic differentiation studies used in this review, the ranges of qualitative (6–44) and quantitative (0–28) morphological descriptors are significantly different (**Table 1**). Approximately one-third of these studies jointly evaluated qualitative and quantitative morphological descriptors, producing a noticeable increase in the number of genetic targets sampled, and thus improving the assessment of genetic diversity in both natural and segregating populations, allowing for the selection of contrasting parents for breeding.

Although cassava displays strikingly high levels of heterozygosity, clonal propagation has permitted the spread of a small set of superior clones, increasing their frequency of occurrence across different regions. This set of clones is grown under large number of different names. A single genotype cultivated in a given geographical region might be found under different names, resulting in the unintentional presence of duplicated genotypes in any one collection. The results of variety identification based on morphological descriptors in cassava has not revealed the presence of these duplicated entries in the ex-situ collections or under cultivation (**Table 1**), although 20 to 25% genotypic redundancy is expected. This review covers a total of 4,285 cassava accessions from Africa, Asia, LAC, SEA, and the Pacific Islands, but the number of duplicate cassava accessions reported is extremely low (1.4%) (**Table 1**). This result might be explained by the high morphological variability reported in cassava due to changes in soil, climatic, and biotic factors, making it difficult to precisely describe the morphological characteristics of this crop. The inability to identify genetic duplicates in a germplasm collection has profound implication for cost-effective germplasm conservation, as well as for germplasm use by breeding programs. Thus, the accurate and reliable identification and elimination of duplicates within a germplasm collection will facilitate genetic resource management and use, while reducing maintenance costs.

These studies have revealed an important heterogeneity within cassava cultivars, particularly those held by farmers [31, 33, 37, 39, 43]. The use of morphological descriptors in the early characterization and identification of cassava varieties is useful to identify new genetic variability, but it can be a lengthy process, taking more than a year to obtain and analyze this type of data. The number of potentially uncharacterized varieties still used in traditional farming is estimated to be as high as 15,000 [18]. Thus, it is likely that the available number of morphological descriptors is inadequate to account for the crop's large genetic variability, as well as the number of cassava cultigens which are affected by environmental factors that influence their phenotypes. This situation highlights the need to develop a method to measure the crop's genetic variability, reducing or eliminating the need to use morphological descriptors. Molecular markers, due to their nature, could provide an immense advantage in the identification of varieties and the characterization of genetic variability, by providing more detailed information about its

Region	Location	Cassava (*M. esculenta*) Source	No.	Morphological Descriptors Scoring Schedule	No. of variables QLT	QNT	No. of Dupl.	Rev. Ref.
Africa	Côte d'Ivoire	Collection maintained at CNRA's research station at Bouaké	340	5–12 MAP	14	0	35	[42]
	Nigeria	Collection maintained at IITA, Ibadan, Nigeria	1766	NP	32	8	0	[39]
		Collection maintained at IITA, Ubiaja	1890	NP	28	8	0	
	Benin	Field collected in 55 villages surveyed in the southern region	125	NP	20	0	0	[37]
	Côte d'Ivoire	Field collected across 26 villages in the Centre-west, South-west and West region	159	5–12 MAP	14	0	16	[19]
	Chad	Field collected in Mandoul, Moyen Chari, Tandjilé, Logone Occidental and Oriental region	59	3, 6, 9 & 12 MAP	32	13	3	[35]
	Cameroon	Field collected across de Humid Forest & Guinea Savannah Agroecologies	89	3, 6, 9 & 12 MAP	35	14	0	[29]
	Côte d'Ivoire	Field collected in the forest zone of the Ivory Coast	44	NP	20	4	0	[30]
	Angola	Collection maintained at the Agronomic Investigation Institute	40	12 MAP	12	10	0	[25]
LAC	Brazil	Collection maintained at Embrapa Mandioca e Fruticultura, Cruz das Almas	14	8 MAP	10	4	0	[43]
	Brazil	Collection maintained at Mandioca do Cerrado (BGMC) - Embrapa	16	12 MAP	33	0	0	[41]
	Costa Rica	Collection maintained at Centro Agronómico Tropical de Investigación y Enseñanza (CATIE)	37	NP	44	28	0	[40]
	Brazil	Collection maintained at Embrapa Mandioca e Fruticultura, Cruz das Almas	200	NP	19	16	0	[26]
	Brazil	Collection maintained at Embrapa Mandioca e Fruticultura, Cruz das Almas	95	11–12 MAP	32	0	0	[38]
	Brazil	Collection maintained at Embrapa Mandioca e Fruticultura, Cruz das Almas	95	11–12 MAP	35	13	0	[32]
	Brazil	Regional Germplasm Bank of Eastern Amazon, situated in Belém, Pará, Brazil,	262	11–12 MAP	21	0	0	[28]
	Brazil	Collection maintained at Mato Grosso's State University (UNEMAT - Cáceres) and Embrapa Agrossilvipastoril)	158	6–8 & 12 MAP	29	9	0	[23]
	Brazil	Field collected in the Brazilian Middle North Regions, Viçosa-MG	10	8 MAP	24	0	0	[31]

| Region | Location | Cassava *(M. esculenta)* | | No. | Scoring Schedule | No. of variables | | No. of Dupl. | Rev. Ref. |
			Source			QLT	QNT		
Asia	India	Western Ghats region of Tamil Nadu, covering 32 villages in the southern region of Western Ghats with altitude ranging from 250 to 2552 feet above MSL		56	NP	6	2	0	[34]
SEA	Indonesia	Field collected in Java, Sumatera, Kalimantan, Sulawesi, Maluku, Nusa Tenggara Timur and Papua Islands		181	12 MAP	10	0	0	[33]
	Vietnam	Collection maintained at the Root Crop Research and Development Center (RCRDC), and Field Crops Research Institute, located in Chuong My, Hanoi		7	4–8 MAP	20	0	0	[20]
Pacific Islands (Oceania)	Vanuatu	Collection maintained at Vanuatu Agricultural Research and Training Centre (VARTC)		145	12MAP	12	0	4	[36]

The number of cassava (M. esculenta) varieties identified in Africa, LAC, Asia, SEA, and Oceania, as well as the number of qualitative (QLT) and quantitative (QNT) descriptors used for the morphological identification. NP = not provided, MAP = months after planting.

Table 1.
The literature pertaining to cassava (rev. ref.) on agro-morphological characterization reviewed in this paper.

polymorphisms, independent of the physiological status of the plant or the environmental conditions in which it grows.

3. Molecular markers deployed in cassava

Since the mid 80's, molecular markers have been used in cassava for a large number of genetic diversity and variety identification studies (**Table 2**). The scientific community working on cassava is therefore well acquainted with the development and use of these markers [64, 71–74, 78, 81, 126, 127, 131, 135–140]. The first attempt to use molecular markers for variety identification in crops was undertaken at CIAT by Hussain et al. [131], Ramirez et al. [139], and Ocampo et al. [122], using isozymes. In 1992, Ocampo et al. [122], using αβ-esterase isozymes, analyzed 86% of the global cassava collection of 4,034 *M. esculenta* accessions maintained at CIAT, and found 2,158 accessions (50%) with 2 to 39 clones sharing the same banding pattern. These results highlight the need to analyze morphological and molecular data together, to gradually eliminate duplicates from the germplasm collection.

In 1995, Ocampo et al. [121] implemented a DNA fingerprinting method for genetic analysis called restriction fragment length polymorphisms (RFLPs). RFLPs allowed Ocampo et al. [121] to estimate the number of duplicates in the CIAT collection; of the 5500 genotype approximately 1,000 could be duplicates indicating an approximate 18% redundancy in the global germplasm collection (**Table 2**). Therefore, the RFLP marker system is an attractive approach because they are inherited in a co-dominant mode, allowing homozygotes to be distinguished from heterozygotes, and are locus-specific and highly informative, targeting specific sites on the genome, due to restriction-site specificity [123]. However, the use of RFLPs can be challenging, as their use is laborious, costly, and can only resolve mutations at the enzyme cut site, limiting their use in phylogenetic reconstruction [123]. Nevertheless, these efforts demonstrate that the identification of genetic variety can be achieved using molecular genetic tools, and used for germplasm management, including quality control of experimental lines across breeding programs.

The polymerase chain reaction (PCR) technique, published in 1986 by Mullis et al. [141], allowed cassava scientists at CIAT to investigate genetic differences using minute amounts of DNA, coupled with random primer amplification to produce random amplified polymorphic DNA (RAPD) [70, 83, 86, 126, 142, 143]. RFLPs were therefore superseded by PCR-based markers [127]. Since then, other PCR-based molecular markers tools have been adapted and deployed, such as amplified fragment length polymorphisms (AFLPs) [72, 73], inter-simple sequence repeats (ISSRs) [56, 115, 117], single sequences repeats (SSRs) [71, 73, 74, 78], sequence-related amplified polymorphisms (SRAPs) [94], inter-sequence tagged repeats (ISTRs) [86], and diversity arrays technology (DArT) [67]. Over the past 30 years, SSRs have been the molecular marker approach most widely used in cassava, both for variety identification and to estimate the genetic diversity of the crop (**Table 2**). Chavarriaga-Aguirre et al. [73], used this approach to search for duplicates in the CIAT's core collection, but reported a lower frequency of duplicates than was reported by Ocampo and co-workers [121].

The release of the cassava reference genome by Prochnik et al. [144] allowed cassava geneticists in Africa and LAC to identify tens of thousands genome-wide sequence variations across multiple landraces and improved cultigens [2, 145, 146]. These genomic variations were unraveled by re-sequencing using restriction-site associated DNA-sequencing (RAD-seq) [145] or genotyping by sequencing (GBS) [147]. These two methods can detect small genetic differences between individuals, and therefore may be useful for studying organisms with reduced genetic

Region	Location	Source	No. of cassava samples	Morphological Descriptors	Isozymes	RFLPs	RAPDs	SSRs	ISSRs	SRAPs	ISTR	AFLPs	DaRTs	SNPs	No. of Duplicates	Rev. Ref.
Global	A	1	19		X										0	[131]
	A	1	4304		X										2158	[122]
	A	1	88			X									51	[121]
	A	1	7			X	X								0	[70]
	A	1	105	X								X			0	[72]
	A	1	552					X							0	[74]
	A	1	521	X		X		X				X			19	[73]
	A	1	38					X							0	[71]
	B	1&2	74											X	0	[89]

Region	Location	Source	No. of cassava samples	Morphological Descriptors	Isozymes	RFLPs	RAPDs	SSRs	ISSRs	SRAPs	ISTR	AFLPs	DaRTs	SNPs	No. of Duplicates	Rev. Ref.
Africa	C	3	365		X										181	[124]
	D	2	29									X			10	[66]
	D&E	4	283					X							0	[81]
	E	5	24				X				X				0	[86]
	F	6	28				X								1	[83]
	G	7	288	X				X							0	[53]
	D	2	63					X				X			0	[91]
	H	8	93	X								X			5	[50]
	B	1&2	53											X		[59]
	D	2	24					X							0	[101]
	I	9	43	X				X							10	[49]
	E	10	21					X							1	[58]
	I	11	320					X							0	[106]
	B	12	10					X							1	[104]
	J	13	12	X						X					0	[56]
	C	2&14	327		X										163	[15]
	I	15	981											X	629	[2]
	D	16	7376											X	2594	[63]
	K	17	96	X				X							22	[16]
	I	1, 2&11	89					X							0	[118]
	I	2&11	87	X				X						X	9	[119]
	G	18	547											X	461	[116]
	L	19	102	X										X	0	[112]

Region	Location	Source	No. of cassava samples	Morphological Descriptors	Isozymes	RFLPs	RAPDs	SSRs	ISSRs	SRAPs	ISTR	AFLPs	DaRTs	SNPs	No. of Duplicates	Rev. Ref.
Asia	M	20	218	X	X										62	[62]
	M	21	58	X				X							2	[52]
	M	20	110	X				X							0	[132]
	M	20	45					X							0	[93]
	N	21	18							X					0	[94]
	M	20	6						X						0	[117]
	M	20	14					X	X						0	[115]
EU	O	3	80			X									0	[123]
	O	3	20				X								2	[126]
LAC	P	22	32	X				X							1	[64]
	Q	23	31									X			0	[76]
	P	24	54				X	X				X			0	[133]
	P	1&25	118				X	X							0	[78]
	Q	26	29	X								X			0	[68]
	P	27	28		X										0	[80]
	P	28	117					X							0	[82]
	P	29	20		X										0	[85]
	R	30	66		X										0	[84]
	A	1	33										X		0	[67]
	P	31	137	X				X							42	[69]
	R	30	145					X							0	[88]
	P	32	42					X							2	[90]
	P	33	83					X							1	[98]

Region	Location	Source	No. of cassava samples	Morphological Descriptors	Isozymes	RFLPs	RAPDs	SSRs	ISSRs	SRAPs	ISTR	AFLPs	DaRTs	SNPs	No. of Duplicates	Rev. Ref.
LAC	P	34	14	X			X								0	[51]
	S	35	185					X							2	[95]
	P	25	93					X							4	[96]
	P	33&41	20					X							0	[99]
	P	36	16	X				X							0	[97]
	P	37	36					X							19	[61]
	P	38	419	X				X							0	[54]
	P	36	16	X			X								0	[55]
	P	25	1280											X	0	[103]
	A	39	173	X										X	20	[105]
	T	1&40	163					X							0	[108]
	P	41	60					X							1	[125]
	P	42	121					X							5	[109]
	A	43	436											X	316	[4]
	P	44	51					X							0	[110]
	P	25	2731											X	614	[134]
	P	45	303					X							18	[120]
	P	46	106					X							4	[113]
	P	47	144					X							0	[114]
	P	25	3354											X	1818	[65]

Region	Location	Source	No. of cassava samples	Morphological Descriptors	Isozymes	RFLPs	RAPDs	SSRs	ISSRs	SRAPs	ISTR	AFLPs	DaRTs	SNPs	No. of Duplicates	Rev. Ref.
SEA	U	48	10	X	X		X								0	[111]
	V	49	1570											X	1535	[12]
Total			29730	21	10	3	10	37	3	1	1	8	1	13	10783	

Plant materials used: [1] Collection maintained at CIAT's GRU, [2] Collection maintained at IITA's GRU, [3] Collection maintained at ORSTOM (IRD-France), [4] Field collection in Tanzania and Nigeria, [5] Field collected in Kibaha and Ikiriguru, [6] Collection maintained at National Agricultural Research Institute, Maputo, [7] Field collected in Hoima, Kumi, and Luwero districts, [8] Field collected in Baka, Mkondezi, Chitala, Chitedze, and Makoka Agricultural Research Stations, [9] Collection maintained at Plant Genetic Resource Research Institute at Bunso in the Eastern Region of Ghana and the University of Cape Coast, [10] Collection maintained at MARI, [11] Collection maintained at CSIR-Crops Research Institute (CRI), [12] Collection maintained at Kenya Agricultural Research Institute (KARI), [13] Collection maintained at University of Kinshasa, [14] Collection maintained at CNRA, [15] Field collected in Ghana Brong Ahafo, Ashanti, and Eastern, [16] Field collected in North Central followed by South–South, Southwest, and Southeast regions, [17] Field collected in Southern and Central Benin, [18] Field collected in Apac, Arua, Kibaale, and Masindi, [19] Collection maintained at Njala Agricultural Research Centre (NARC), [20] Collection maintained at ICAR-Central Tuber Crops Research Institute, Sreekariyam, Thiruvanathapuram, [21] Tapioca and Castor Research Station (T&CRS) GRU, [22] Field collected in Campinas, [23] Field collected in Makushi Village, [24] Field Collected in Sao Paolo state, [25] Embrapa Cassava and Fruit Crops, Cruz das Almas, BA, [26] Field collection in Rewa, a Makushi community, [27] Field collection in Pernanbuco, [28] Field collection in Amazonian region, [29] Field collected in Maringá, [30] Field collection in Talamanca and Coto Brus, [31] Southeastern part of the Brazilian Atlantic Forest, [32] Genetics Department of ESALQ/USP, [33] Instituto Agronómico at Campinas, Sao Paul, [34] Field collected in Maringá, Paraná, [35] Field collected across the island and gene bank, [36] Banco Regional de Germoplasma de Mandioca do Cerrado (BGMC), [37] Embrapa's germplasm collection Belém, Pará, [38] Escola Superior deAgricultura Luiz de Queiroz, Sao Paulo University, [39] Field collected by SINCHI, [40] Cuban Cassava Germplasm Collection, [41] Field collected in Campo Grande, Mato Grosso do Sul, [42] Field collected in Maringá, Cianorte, and Toledo, Paraná, [43] Field Collected in Cauca, [44] Field collected in Southern of Minas Gerais State, [45] Field collected in Paraná and Santa Catarina (South), Mato Grosso do Sul (Midwest), and Minas Gerais (Southeast), [46] Embrapa - Acre, Rio Branco, [47] Germplasm Bank (BGM) of Maringá State University (UEM) Paraná state, [48] West Bangka District, Bangka District, and South Bangka District, [49] Field collected across 32 villages and HLARC, RCRDC, and AGI's GRUs.
Countries where the studies took place: [A] Colombia, [B] Kenya, [C] Ivory Coast, [D] Nigeria, [E] Tanzania, [F] Mozambique, [G] Uganda, [H] Malawi, [I] Ghana, [J] Congo, [K] Benin, [L] Sierra Leone, [M] India, [N] China, [O] France, [P] Brazil, [Q] Guyana, [R] Costa Rica, [S] Puerto Rico, [T] Cuba, [U] Indonesia, [V] Vietnam.

Table 2.
Literature reviewed on the molecular characterization of cassava (rev. ref.).

variation, such as those found in clonal lineages, such as cassava, or highly inbred organisms, such as maize. However, one has to ask whether the large number of SNPs resolved with or without prior knowledge of the genome are more reliable than SSRs or SNP arrays built from expressed sequence tag databases with a high frequency of heterozygous loci in the population. Two SNP arrays have been built for cassava: the Illumina GoldenGate 1,190SNPs-assay by Ferguson et al. [59], and the Fluidigm® Dynamic 96 SNP Array™ SNPY-Chip by Becerra Lopez-Lavalle and co-workers at CIAT [4, 12, 105].

4. Current status of PCR-based DNA analysis for variety identification

PCR-based DNA molecular markers have been used to assess the genetic diversity of cassava, and to establish the relationships among genotypes (**Table 2**). In 1994, Marmey et al. [126] showed the value of RADPs for analyzing the crop's genetic diversity, as well as for detecting duplicated accessions (10%) among collections. In 1996, Angel et al. [70] showed that RADPs give comparable results to RFLPs, offering a cost- and time-effective alternative to restriction and hybridization DNA analysis. Another powerful PCR-based molecular marker tool used in cassava [72] is the AFLP method used by Vos et al. [148], in which selected restriction fragments from the digestion of total DNA are reduced in complexity by PCR and resolved with 1 to 2 bp difference. Roa et al. [72] concluded that AFLPs were an effective and efficient molecular methodology with which to estimate genetic similarities in the genetic variability of cassava, and among other Manihot species.

Of the 77 studies listed in **Table 2**, 13% used RAPDs, and 12% used AFLPs, including studies incorporating morphological descriptors [50, 51, 55, 64, 68, 72, 73, 111]. Both molecular marker methods have been shown to be powerful and able to provide genetic data that reflects the observed phenotypic differences, geographic origins, and pedigree background of the plants. The AFLP fingerprinting technique detected a larger number of duplicates in the African and LAC cassava landraces than RAPDs, suggesting that AFLPs are a suitable for estimating genetic similarity and dissimilarity [72]. The identification of duplicates across these studies ranged from 4 to 35%. AFLP data indicated that cassava varieties can become widespread and adopted by farmers under different names, leading germplasm curators to consider them to be different varieties.

SSRs, which were used in 47% of the studies reviewed here (**Table 2**), and their use has been favored over that of RADPs or AFLPs in cassava. SSR markers are abundant and evenly distributed across the cassava genome, are co-dominant, highly polymorphic, and are not influenced by the environment [149]. Compared with AFLPs, SSRs are less technically challenging to implement. These marker system data can easily be shared across different laboratories, particularly if fingerprinting data is generated with fluorescently labeled SSR markers and resolved in capillary DNA-sequencing instruments. Overall, the authors consulted for this review agreed that SSR profiles generated for improved and landrace genomes were extremely useful in the conservation of diversity in Africa, Asia, LAC, and SEA, as well as for guiding the best crop improvement strategy. Studies involving the development of molecular tools to accelerate the introgression of observed phenotypic differences on disease resistance, such as cassava mosaic disease (CMD) have been extremely successful in identifying the SSRs that will best guide this effort. CMD resistance has been efficiently introgressed into LAC's breeding lines, and successfully transferred to Africa [150–152].

Over the last decade, we have witnessed an important shift in the cassava research community in Africa and LAC, led by IITA and CIAT, toward

sequence-based nucleotide variation mining. In sub-Sahara Africa, Ferguson et al. [59] characterized and validated 1,190 SNPs using the V4.1 of the cassava genome [144] and Illumina's GoldenGate assay. They demonstrated that SNP markers could successfully measure the genetic variability of cassava, while accurately detecting duplicates in the IITA's gene bank collection. The SNP data of Ferguson et al. [59] allowed, the comparison of the genetic diversity between cassava varieties from the Americas and Africa, and showed that cassava from the Americas displayed greater genetic diversity than their counterparts in Africa. These researchers showed that the levels of genetic diversity in west, southern, eastern, and central Africa were similar. These two observations suggested a massive adoption by IITA of improved varieties developed for African farmers.

In 2015, Rabbi et al. [2] undertook a large varietal identification survey on 917 accessions using 56,489 SNP loci generated by next-generation sequencing [147], compared against 64 released cassava varieties and popular landraces in Ghana. Rabbi et al. [2] accomplished variety identification and ancestry estimation through two complementary cluster methods: distance-based hierarchical clustering, and model-based maximum likelihood admixture analysis. They found that 30% of the identified accessions from farmers' fields matched specific released varieties. A hierarchical clustering analysis revealed that the number of major varieties was 11, and 69% of the accessions belonged to one of the 11 groups, while the remaining accessions had two or more ancestries. Rabbi et al. [2] demonstrated that reduced subsets of SNP markers could reproduce the results obtained from the full set of markers, concluding that GBS can be performed at higher DNA multiplexing. However, these results, as well as those by Ferguson et al. [59], indicated that a large numbers of SNPs may not be needed to achieve accurate identification of cassava varieties, whether in farmers' fields or in formal germplasm collections.

Concurrently, CIAT and the Beijing Genome Institute (BGI) [153] committed to developing genomic resources in the post-genomic era, with the aim of increasing scientists' understanding of the evolution and distribution of cassava from its origin in the Americas to Africa and Asia. Next-generation sequence information from both wild and domesticated species offered cassava researchers the opportunity to investigate individual genes which have played a role in the domestication of cassava. Whole genome sequences allow researchers to exploit genomic variations associated with resistance to pests such as whiteflies or mites, and diseases such as frog skin disease and cassava brown streak disease, as well as to improve the nutritional value of the crops, such as by increasing the pro-vitamin A content. In 2013, CIAT's geneticists and bioinformaticians explored the genetic variation present in 150 LAC accessions, and identified a panel of 180 highly informative single nucleotide variants (SNVs, MAF > 0.25), with high discriminative power and a uniform genome distribution of 5 to 10 SNP per chromosome. These SNVs were transferred to a SNPtype™ allele-specific PCR assay and validated on the same set of samples (Fluidigm® Dynamic Array™, USA) (Becerra Lopez-Lavalle, personal communication).

Of the 180 SNVs identified by CIAT, a 96 SNPs Fluidigm® Dynamic Array™ (referred to as an "SNPY-CHIP") was first assembled and used by Peña-Venegas et al. [105], who aimed to validate the identity of 173 Amazonian cassava landraces classified as unique by indigenous growers. The cassava SNPY-CHIP allowed the classification of 44 genotypes into 21 duplicate-genotype clusters, confirming the uniqueness of 150 (87%) of the 173 materials identified as unique by indigenous people of the Colombian Amazon. The SNPY-CHIP array also allowed the exploration of the diversity and population structure of these materials. When the 150 unique genotypes characterized in this study were compared with genotypes from the CIAT core collection, the cassava genotypes from the Tikuna community of San Martín de Amacayacu (AMA) appeared to be closely related to Peruvian manioc

genotypes (PER). CIAT scientist demonstrated that these SNP markers have a very low genotyping error rate, and are easy to store and share in genotype databases. The information generated from the 99 accessions evaluated along with the 150 from the Peña-Venegas et al. [105] study allow us to assess the value of each SNP with a high MAF, indicating a genotyping success. The 99 cassava genotypes represents a good sampling of the global cassava germplasm collection. Of the 99 genotypes, 71 were from the Americas: five from Argentina, two from Bolivia, four from Brazil, 26 from Colombia, three from Costa Rica, three from Cuba, three from Ecuador, five from Guatemala, five from Mexico, two from Panama, two from Paraguay, five from Peru, one from Puerto Rico, and five from Venezuela; nine from Asia: two from China, three from Thailand, two from Indonesia, and two from Malaysia; three hybrids from ICA-CIAT (Colombia), three genotypes from Africa (TMS60444, C18 and TME3) and 13 samples of unknown origin (AM206-5, AM560-2, FLA 21, FLA61, FLA 19, GLA8, GM905-52, GM905-57, GM905-60, SM301-3, SG107-35, GUT64, and JAC3). These 99 genotypes exhibit good phenotypic differentiation and are likely to be of ancient origin in the Americas. Of the 272 genotypes analyzed, 249 (91%) were unique genotypes, showing the effectiveness of these SNPs for varietal identification and the identification of duplicates (9%). The SNP results unequivocally identified all accessions, including those nominated as morphological duplicates.

The accurate identification of cassava varieties in the Colombian Amazon using DNA-based SNPY-CHIP provided the opportunity to undertake large variety adoption studies using SNP-based DNA fingerprinting. This approach established the basis for the methodology of a multidisciplinary approach and for synergy of efforts between agricultural scientists and economists [4]. Floro et al. [4] estimated the level and determinants of adoption of improved varieties in the Cauca department of Colombia, using the SNPY-CHIP. They collected cassava samples from each variety identified by cassava growers, and interviewed 217 households in Cauca, Colombia. Four hundred and thirty six cassava samples were collected, and DNA fingerprinting was undertaken using the SNPY-CHIP. The genetic analysis allowed the identification of duplicated genetic material, as well as the improved hybrids developed by CIAT, thus reducing the 117 named varieties by farmers to 60 true genetic types found in CIAT's germplasm collection or its global cassava breeding program (**Figure 1**). A set of 60 unique genotypes was identified showing this set of genotypes are missing at CIAT's germplasm collection (**Figure 1**). DNA fingerprinting was therefore shown to be important in the procurement of new germplasm to introduce into breeding programs or furnish publicly funded gene banks with the most diverse and complete set of accessions. The cassava genetics research team at CIAT reorganized the 436 stem samples collected, and planted them back in the Cauca region in the Morales Municipality, to assess their morphological features. The morphology displayed by each of the 120 varietal plots confirmed the results obtained by SNP fingerprinting (**Figure 2**).

An ambitious variety adoption study using DNA fingerprinting (SNPY-CHIP) and socioeconomic approaches was undertake by CIAT scientists in Vietnam [154]. The cassava germplasm found in Vietnam has very limited morphological description and molecular information, limiting its use for breeding. However, farming communities in Vietnam have maintained traditional knowledge about this genetic diversity through the vernacular names given to varieties. Depending on the context, however, informal naming of varieties can lead to either overestimates or underestimates of crop diversity. Ocampo et al. [12] studied the varietal composition found in Vietnamese cassava production regions using SNP markers. They procured 97 different varieties based on farmer identification, from a total of 1,570 cassava genotypes collected across six agro-ecological zones. Vietnamese farmers distinguished the different varieties mainly by the morphology of the vegetative parts, such as Bamboo Leaf, Long Leaf, Purple Bud, Red Bud, and Red
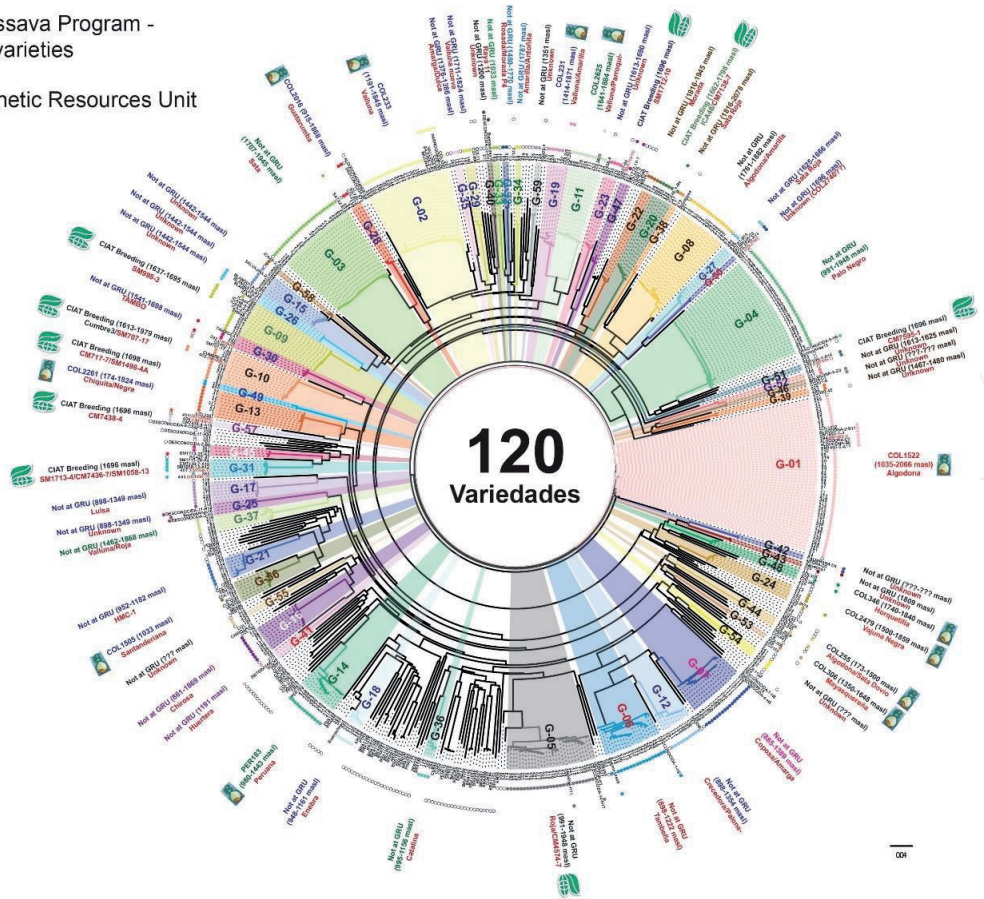
Figure 1.
Cluster analysis of 436 accessions constructed with the neighbor joining (NJ) method using shared alleles to define genetic distances.
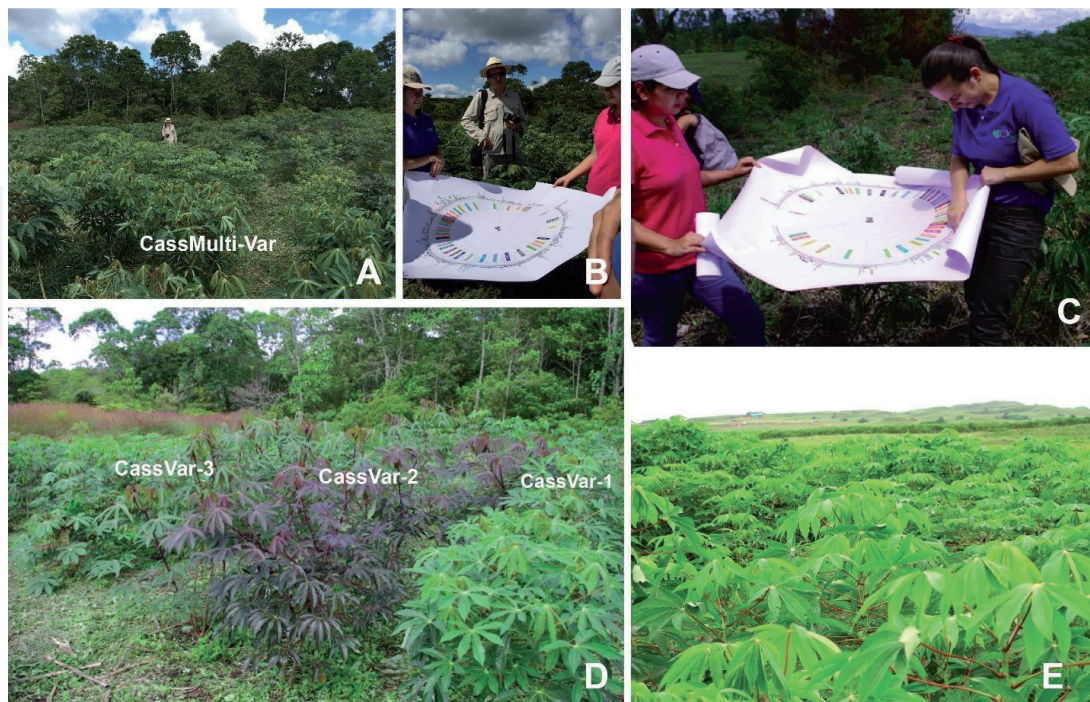

Figure 2.
(A) The process of field-based varieties collection in Cauca, Colombia, (B&C) molecular-based selection, (D) cassava variety [CassVar] clustering for morphological validation based on molecular information and (E) agronomic performance evalaution of variety clusters.

Branch. CIAT's SNPY-CHIP allowed for the characterization of 85 distinct genetic groups out of the 1570 genotypes collected, and indicated a 12.4% overestimation of varietal differences based on vernacular names given by local farmers. When compared against CIAT's global germplasm reference set, the allele diversity contained in 85 genetically distinct varieties represents a rich and diverse collection. Hence, a set of ten major varieties grown across Vietnam, named KM94, KM419, BRA1305, KM101, KM140, PER262, KM60, KM57, and two unidentified varieties with a high accounted for 82% of the frequency distribution, of which KM94 (KU50) and KM419 represented 48% of the genotypes investigated.

5. Conclusions: challenges and future perspective for the varietal and cultivar identification of cassava

This review has highlighted the potential of SNP-based variety identification in cassava, as a means to assess the rate of variety adoption, acquisition of novel genetic resources, and quality control of breeding products. Further progress toward a full characterization of varieties across all cassava growing regions, using SNP-based approaches, can be anticipated. Among the 21 morphological and 77 molecular-based variety identification studies used in this review (**Tables 1** and **2**), those based on morphological descriptors are lengthy, time consuming, labor intensive, and space demanding. As the number of varieties to be evaluated increases, the number of morphological descriptors available for the identification of new genotypes is limited.

The basic principles of molecular marker technologies focus on the detection of polymorphisms, from protein or ribonucleic acid information. For cassava isozymes, RFLPs, RAPDs, SSRs, ISSRs, SRAPs, ISTR, AFLPs, DaRTs, and SNPs have been successfully used for detecting genetic variation in the crop (**Table 2**). Of these markers, SSRs are by far the most popular molecular method used by cassava scientists order to describe the differentiate among varieties and to measure the crop's genetic diversity. Nearly 17% of the 4,950 materials that underwent varietal identification were fingerprinted using SSR markers. However, SSR-based fingerprinting data has limited use outside the discrete experimental units evaluated in this review, thus limiting the opportunity to consolidate and globally use SSR genotyping information into a general database, which could enable a global variety identification system.

Unlike SSRs, SNP alleles have been recommended for the construction of shared DNA fingerprinting databases [155]. CIAT's newly designed SNPY-CHIP has been used to genetically characterized approximately 2,100 cassava genotypes, collected from both farmers' fields and in ex-situ collections (**Table 2**). This set of 96 single SNPs are well-distributed throughout the cassava genome. These SNP markers have proven to be stable and repeatable, and have a high power of discrimination. The SNPY-CHIP alleles initially deployed in the Fluidigm® Dynamic Array™ technology (San Francisco, CA, USA) should be transferable across platforms, allowing for direct global data analysis, with SNP information coming from next-generation sequencing performed by other laboratories or research groups. CIAT, through CGIAR, has a collaborative agreement with Intertek-AgriTech (https://www.intertek.com/agriculture/agritech/) to access genotyping services, thus ensuring high quality, cost-effective data production. The emphasis on high quality breeding products stresses the need for quality control at all levels of the variety development pipeline, ensuring traceability and preservation of identity. This is the first step toward building a robust identification platform for the global conservation and use of cassava, as well as standardizing the administration and management of plant varieties. Considering the effectiveness the 96 SNPY-CHIP

markers, in 2021, we transferred them to the Intertek genotyping platform with the support from the Excellence in Breeding (EiB, https://excellenceinbreeding.org/toolbox/collection/236), and 93 markers passed the validation stage with 345 diverse accessions from the genebank and breeding progenitors. These markers are publicly available in the EiB low-density genotyping platform for quality control and variety identification for the cassava community. A databased with more than 2,100 accessions genotyped using these 96 SNP markers has been developed and maintained in the cassava program at CIAT, which will enhance the variety identification and genetic diversity analysis for the global cassava community.

As growing emphasis is placed on quality, at all levels, and on traceability and the preservation of the identity of varieties, accurate identification of the varieties of cassava grown by farmers will improve its management and production, and facilitate tracking and replacing specific varieties. Breeders can replace varieties susceptible to pests and diseases with more tolerant or resistant varieties. Knowledge of the distribution of susceptible varieties will help policy makers to target breeding for the development of resistant of tolerant varieties for full varietal replacement and seed system development.

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Conflict of interest

The authors declare no conflict of interest.

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References

[1] Kennedy G, Raneri JE, Stoian D, Attwood S, Burgos G, Ceballos H, et al. Roots, tubers and bananas: Contributions to food security. In: Ferranti P, Berry EM, Anderson JR, editors. Encyclopedia of Food Security and Sustainability. Oxford: Elsevier, 2019. 231-56 p.

[2] Rabbi IY, Kulakow PA, Manu-Aduening JA, Dankyi AA, Asibuo JY, Parkes EY, et al. Tracking crop varieties using genotyping-by-sequencing markers: A case study using cassava (*Manihot esculenta* Crantz). BMC Genetics. 2015,16:115. DOI: 10.1186/s12863-015-0273-1.

[3] United Nations. Sustainable development goals. https://sdgs.un.org/goals, 2015. Accessed 2020.

[4] Floro VO, Labarta RA, Becerra López-Lavalle LA, Martinez JM, Ovalle TM. Household determinants of the adoption of improved cassava varieties using DNA fingerprinting to identify varieties in farmer fields: A case study in Colombia. Journal of Agricultural Economics. 2018,69:518-36. DOI: 10.1111/1477-9552.12247.

[5] Isendahl C. The domestication and early spread of manioc (*Manihot esculenta* Crantz): A brief synthesis. Latin American Antiquity. 2011,22:452-68. DOI: 10.7183/1045-6635.22.4.452.

[6] Jones WO. Manioc in Africa. Manioc in Africa. California, USA: Stanford University Press, 1959.

[7] Hillocks RJ, Thresh JM, Bellotti AC. Cassava: Biology, Production and Utilization. Wallingford: CABI Publishing, 2002.

[8] Le Thi DP, Labarta RA, de Haan S, Maredia M, Becerra López Lavelle LA, Nhu L, et al. Characterization of Cassava Production Systems in Vietnam.

Cali, Colombia: International Center for Tropical Agriculture. p. 54, 2019.

[9] Becerra López-Lavalle LA, Ovalle TM, Marín DV, Patricia GJ, Moreno MP, Moreno M, et al. Catálogo de variedades de yuca, Cauca-Colombia. In: International Center for Tropical A, editor. Palmira, Colombia: International Center for Tropical Agriculture, 2020. 82 p.

[10] CGIAR. Cassava to support a multibillion-dollar industry. https://www.cgiar.org/innovations/cassava-to-support-a-multibillion-dollar-industry/, 2021.

[11] Labarta R, Wossen T, Phuong Le D. The adoption of improved cassava varieties in South and Southeast Asia. The 9th ASAE International Conference. Bangkok, Thailand. Asian Society of Agricultural Economists (ASAE), 2017. p. 1445-54.

[12] Ocampo J, Ovalle T, Labarta R, Le DP, de Haan S, Vu NA, et al. DNA fingerprinting reveals varietal composition of Vietnamese cassava germplasm (*Manihot esculenta* Crantz) from farmers' field and gene bank collections. Plant Molecular Biology. 2021. DOI: 10.1007/s11103-021-01124-0.

[13] Kim H, Mai NTT, Mai NB, Howeler R. Cassava conservation and sustainable development in Vietnam. A new future for cassava in Asia: Its use as food, feed and fuel to benefit the poor. Proceedings of the 9th regional workshop, held in Quangxi, China, 2014. p. 35-56.

[14] Malik AI, Kongsil P, Nguyễn VA, Ou W, Sholihin SP, Srean P, et al. Cassava breeding and agronomy in Asia: 50 years of history and future directions. Breeding Science. 2020,70:145-66. DOI: 10.1270/jsbbs.18180.

[15] Edmond KK, Guy BK, Modeste KK, Michel KA, Gisèle KA-y, Pierre ZG. Enzymatic polymorphism of genetic diversity in cassava (*Manihot esculenta* Crantz) accessions in Côte d'Ivoire. Greener Journal of Biochemistry and Biotechnology. 2015,2:9-17. DOI: 10.15580/GJBB.2015.1.090814351.

[16] Agre AP, Bhattacharjee R, Rabbi IY, Alaba OA, Unachukwu NN, Ayenan MAT, et al. Classification of elite cassava varieties (*Manihot esculenta* Crantz) cultivated in Benin Republic using farmers' knowledge, morphological traits and simple sequence repeat (SSR) markers. Genetic Resources and Crop Evolution. 2018,65:513-25. DOI: 10.1007/s10722-017-0550-0.

[17] Agre AP, Dansi A, Rabbi IY, Battachargee R, Dansi M, Gedil M, et al. Agromorphological characterization of elite cassava (*Manihot esculenta* Crantz) cultivars collected in Benin. International Journal of Current Research in Biosciences and Plant Biology. 2015,2:1-14.

[18] Hershey C. A Global Conservation Strategy for Cassava (*Manihot esculenta*) and Wild *Manihot* species, 2010.

[19] Boni N, Pamelas OM, Michel KA, Dibi KEB, Zohouri GP, Essis BS, Dansi AA. Morphological Characterization of Cassava (*Manihot esculenta* Crantz) Accessions Collected in the Centre-west, South-west and West of Côte d'Ivoire. Greener Journal of Agricultural Sciences. 2014,4:220-31.

[20] Ha CD, Ngoc Quynh LT, Hien NT, Ly Thu PT, Ham LH, Dung LT. Morphological characterization and classification of cassava (*Manihot esculenta* Crantz) in Vietnam. TAP Chi Sinh Hoc. 2016,38:8. DOI: 10.15625/0866-7160/v38n3.8570.

[21] Fukuda W, Guevara C, Kawuki R, Ferguson ME. Selected Morphological and Agronomic Descriptors for the Characterization of Cassava. Ibadan, Nigeria: IITA, 2010.

[22] Pujol B, Mühlen G, Garwood N, Horoszowski Y, Douzery EJP, McKey D. Evolution under domestication: Contrasting functional morphology of seedlings in domesticated cassava and its closest wild relatives. New Phytologist. 2005,166:305-18. DOI: 10.1111/j.1469-8137.2004.01295.x.

[23] Zago BW, Barelli MAA, Hoogerheide ESS, Corrêa CL, Delforno GIS, da Silva CJ. Morphological diversity of cassava accessions of the south-central mesoregion of the State of Mato Grosso, Brazil. Genetics and Molecular Research. 2017,16:1-10. DOI: 10.4238/gmr16039725.

[24] Boampong E, Gyan D, Dorgbetor W. Morphological characterization of local and exotic cassava germplasm. Journal of the Ghana Science Association. 2016,17:45-52.

[25] Afonso SDJ, Alfredo TJDC, Canário JA, de Oliveira ANA, Abrantes AT. Genetic diversity of cassava varieties (*Manihot esculenta* Crantz) in the agro-morphological conditions of Malanje, Angola. IOSR Journal of Agriculture and Veterinary Science. 2020,13:36-44. DOI: 10.9790/2380-1304023644.

[26] João Afonso SD, Silva Ledo CAd, Cunha Moreira RF, e Silva SdO, Jesus Leal VDd, Silva Conceição ALd. Selection of descriptors in a morphological characteristics considered in cassava accessions by means of multivariate techniques. IOSR Journal of Agriculture and Veterinary Science. 2014,7:13-20.

[27] Koefender J, Golle D, Manfio C, Horn R, Schoffel A, De Oliveira J, et al. Caracterización morfológica Y agronómica de accesos en yuca en la

region noroeste Del Rio grande do SUL, brasil. Holos. 2018,34:2-15. DOI: 10.15628/holos.2018.7747.

[28] Silva RS, Moura EF, Farias-Neto JT, Ledo CA, Sampaio JE. Selection of morphoagronomic descriptors for the characterization of accessions of cassava of the Eastern Brazilian Amazon. Genetics and Molecular Research. 2017,16:gmr16029595. DOI: 10.4238/gmr16029595.

[29] Temegne NC, Mouafor BI, Ngome AF. Agro-morphological characterization of cassava (*Manihot esculenta* Crantz) collected in the humid forest and guinea savannah agro-ecological zones of Cameroon. Greener Journal of Agricultural Sciences. 2016,6:209-25.

[30] Djaha KE, Abo K, Bonny BS, Kone T, Amouakon WJL, Kone D, Kone M. Agromorphological characterization of 44 accessions of cassava (*Manihot esculenta* crantz) grown in Côte d'Ivoire. International Journal of Biological and Chemical Sciences. 2017,11:174-84.

[31] Ronaldo SG, Cleverson FdA, Jose RdSC, Ronaldo MJ, Fabio TD, Francisco CdSS, Derly JHdS. Genetic diversity in sweet cassava from the Brazilian Middle North Region and selection of genotypes based on morpho-agronomical descriptors. African Journal of Agricultural Research. 2016,11:3710-9. DOI: 10.5897/AJAR2016.11267.

[32] Oliveira EJ, Oliveira Filho OS, Santos VS. Classification of cassava genotypes based on qualitative and quantitative data. Genetics and Molecular Research. 2015,14:906-24.

[33] Laila F, Zanetta CU, Waluyo B, Amien S, Karuniawan A. Early identification of genetic diversity and distance from Indonesia cassava potential as food, industrial and biofuel based on morphological characters.

Energy Procedia. 2015,65:100-6. DOI: 10.1016/j.egypro.2015.01.039.

[34] Kanagarasu S, Ganeshram S, Prem Joshua J, John Joel A. Exploration, collection and characterization of cassava landraces (*Manihot esculenta* Crantz.) grown in western ghats region. Electronic Journal of Plant Breeding. 2014,5:310-6.

[35] Nadjiam D, Sarr PS, Naïtormbaïdé M, Mbaïguinam JMM, Guisse A. Agro-morphological characterization of cassava (*Manihot esculenta* Crantz) cultivars from Chad. Agricultural Sciences. 2016,7:479-92. DOI: 10.4236/as.2016.77049.

[36] Lebot V, Malapa R, Sardos J. Farmers' selection of quality traits in cassava (*Manihot esculenta* Crantz) landraces from Vanuatu. Genetic Resources and Crop Evolution. 2015,62:1055-68. DOI: 10.1007/s10722-014-0209-z.

[37] Agre AP, Bhattacharjee R, Dansi A, Becerra Lopez-Lavalle LA, Dansi M, Sanni A. Assessment of cassava (*Manihot esculenta* Crantz) diversity, loss of landraces and farmers preference criteria in [southern Benin using farmers' participatory approach. Genetic Resources and Crop Evolution. 2017,64:307-20. DOI: 10.1007/s10722-015-0352-1.

[38] Oliveira EJd, Oliveira Filho OSd, Santos VdS. Selection of the most informative morphoagronomic descriptors for cassava germplasm. Pesquisa Agropecuária Brasileira. 2014,49:891-900. DOI: 10.1590/S0100-204X2014001100008.

[39] Bhattacharjee R, Dumet D, Ilona P, Folarin S, Franco J. Establishment of a cassava (*Manihot esculenta* Crantz) core collection based on agro-morphological descriptors. Plant Genetic Resources. 2012,10:119-27. DOI: 10.1017/S1479262112000093.

[40] Torres Vargas LA. Caracterización morfológica de 37 accesiones de yuca (*Manihot esculenta* Crantz) del banco de germoplasma del Centro Agronómico Tropical de Investigación y Enseñanza (CATIE). Turrialba: Costa Rica, Centro Agronómico Tropical de Investigación y Enseñanza, 2010.

[41] Vieira EA, Fialho JdF, Silva MS. Morphologic Characterization of Colored Cassava Accessions. Boletim de pesquisa e desenvolvimento Volume 241:15 p. Embrapa Cerrados, 2009.

[42] N'Zue B, Sangare A, Letourmy P, Zohouri G, Vernier P. Morphological characterization of the national cassava *Manihot esculenta* Crantz collection in Côte d'Ivoire. African Journal of Root and Tuber Crops. 2009,7:32.

[43] de Queiroz Tavares Filho LF, da Silva Ledo CA, da Cunha Alves AA, Santos AS, Gonçalves LSA. Diversidade genética entre cultivares de mandioca e espécies silvestres de *Manihot* mediante caracterização morfológica. Revista Raízes e Amidos Tropicais. 2009,5:697-701.

[44] Nassar NMA. Cassava, *Manihot esculenta* Crantz, genetic resources: Their collection, evaluation, and manipulation. In: Sparks DL, editor. Advances in Agronomy. Academic Press, 1999. 179-230 p.

[45] Hershey C, Henry G, Best R, Iglesias C. Cassava in Latin America and the Caribbean: Resources for Global Development. Regional Review Report. Rome, Italy: IFAD, 1997.

[46] Fukuda WMG, Guevara CL. Descritores morfológicos e agronômicos para a caracterização de mandioca (*Manihot esculenta* Crantz). Embrapa Mandioca e fruticultura-documentos (INFOTECA-E). Cruz das Almas, Bahia, Brasil: Embrapa. p. 38, 1998.

[47] Dominguez CE. Morphology of the casava plant: Study guide. vol 04EC-Q2.03. Ciat. 1983.

[48] Gulick P, Hershey C, Esquinas-Alcazar JT. Genetic Resources of Cassava and Wild Relatives. Rome: International Board for Plant Genetic Resources (IBPGR). p. 56, 1983.

[49] Asare P, Galyuon I, Sarfo J, Tetteh J. Morphological and molecular based diversity studies of some cassava (*Manihot esculenta* crantz) germplasm in Ghana. African Journal of Biotechnology. 2013,10:13900-8.

[50] Benesi I. Ethnobotany, morphology and genotyping of cassava germplasm from Malawi'IRM. Benesi,"MT. Labuschagne," L. Herselman And N. Mahungu'Chitedze Research Station, PO Box 158, Lilongwe, Malawi "Department of Plant Sciences, University of the Free State, PO Box 339, Bloemfontein 9300, South Africa. Journal of Biological Sciences. 2010,10:616-23.

[51] Rimoldi F, Vidigal Filho PS, Kvitschal MV, Gonçalves-Vidigal MC, Prioli AJ, Prioli SMAP, Costa TRd. Genetic divergence in sweet cassava cultivars using morphological agronomic traits and RAPD molecular markers. Brazilian Archives of Biology and Technology. 2010,53:1477-86.

[52] Raghu D, Senthil N, Saraswathi T, Raveendran M, Gnanam R, Venkatachalam R, et al. Morphological and simple sequence repeats (SSR) based finger printing of South Indian cassava germplasm. International Journal of Integrative Biology. 2007,1:141-8.

[53] Balyejusa Kizito EB, Chiwona-Karltun L, Egwang T, Fregene M, Westerbergh A. Genetic diversity and variety composition of cassava on small-scale farms in Uganda: An interdisciplinary study using genetic markers and farmer interviews. Genetica. 2007,130:301-18. DOI: 10.1007/s10709-006-9107-4.

[54] Mezette TF, Blumer CG, Veasey EA. Morphological and molecular diversity

among cassava genotypes. Pesquisa Agropecuária Brasileira. 2013,48:510-8.

[55] Vieira EA, de Freitas Fialho J, Faleiro FG, Bellon G, da Fonseca KG, Silva MS, et al. Phenotypic and molecular characterization of industrial purpose cassava accessions with potential for adaptation to the conditions of cerrado of Central Brazil. Semina: Ciências Agrárias. 2013,34:567-82.

[56] Mamba-Mbayi G, Nkongolo K, Narendrula R, Djim PT, Kalonji-Mbuyi A. Molecular relatedness and morpho-agronomic characteristics of congolese accessions of cassava (*Manihot esculenta* Crantz) for breeding purposes. British Biotechnology Journal. 2014,4:551-65.

[57] Dissanayake UHK, Senevirathna RWKM, Ranaweera LT, Wijesundara WWMUK, Jayarathne HSM, Weebadde CK, Sooriyapathirana SDSS. Characterization of cassava (*Manihot esculenta* crantz) cultivars in Sri Lanka using morphological, molecular and organoleptic parameters. Tropical Agricultural Research. 2019,30:51-70. DOI: 10.4038/tar.v30i4.8328.

[58] Elibariki G, Njahira M, Wanjala B, Hosea K, Ndunguru J. Genetic diversity and identification of duplicates in selected Tanzanian farmer-preferred cassava landraces using simple sequence repeat (SSR) markers. Inernational Journal of Research in Plant Science. 2013,3:81-7.

[59] Ferguson ME, Hearne SJ, Close TJ, Wanamaker S, Moskal WA, Town CD, et al. Identification, validation and high-throughput genotyping of transcribed gene SNPs in cassava. TAG. Theoretical and Applied Genetics. Theoretische und Angewandte Genetik. 2012,124:685-95. DOI: 10.1007/s00122-011-1739-9.

[60] de Albuquerque HYG, de Oliveira EJ, Brito AC, de Andrade LRB, do Carmo CD, Morgante CV, et al.

Identiffcation of duplicates in cassava germplasm banks based on single. Scientia Agricola. 2019,76:328-36. DOI: 10.1590/1678-992X-2017-0389.

[61] Moura EF, Farias Neto JTd, Sampaio JE, Silva DTd, Ramalho GF. Identification of duplicates of cassava accessions sampled on the North Region of Brazil using microsatellite markers. Acta Amazonica. 2013,43:461-7. DOI: 10.1590/S0044-59672013000400008.

[62] Sumarani GO, Pillai SV, Harisankar P, Sundaresan S. Isozyme analysis of indigenous cassava germplasm for identification of duplicates. Genetic Resources and Crop Evolution. 2004,51:205-9. DOI: 10.1023/B:GRES.0000020862.61748.26.

[63] Wossen T, Girma G, Abdoulaye T, Rabbi I, Olanrewaju A, Bentley J, et al. The Cassava Monitoring Survey in Nigeria. Ibadan, Nigeria: International Institute of Tropical Agriculture (IITA). p. 66, 2017.

[64] Colombo C, Second G, Valle TL, Charrier A. Genetic diversity characterization of cassava cultivars (*Manihot esculenta* Crantz).: I) RAPD markers. Genetics and Molecular Biology. 1998,21:105-13. DOI: 10.1590/S1415-47571998000100018.

[65] Ogbonna AC, Braatz de Andrade LR, Mueller LA, de Oliveira EJ, Bauchet GJ. Comprehensive genotyping of a Brazilian cassava (*Manihot esculenta* Crantz) germplasm bank: Insights into diversification and domestication. TAG. Theoretical and Applied Genetics. Theoretische und Angewandte Genetik. 2021,134:1343-62. DOI: 10.1007/s00122-021-03775-5.

[66] Fregene M, Bernal A, Duque M, Dixon A, Tohme J. AFLP analysis of African cassava (*Manihot esculenta*, Crantz) germplasm resistant to the cassava mosaic disease (CMD). Theoretical and Applied Genetics.

2000,100:678-85. DOI: 10.1007/
s001220051339.

[67] Xia L, Peng K, Yang S, Wenzl P, Vicente MCd, Fregene M, et al. DArT for high-throughput genotyping of cassava (*Manihot esculenta*) and its wild relatives. Theoretical and Applied Genetics. 2005,110:1092-8. DOI: 10.1007/s00122-005-1937-4.

[68] Elias M, McKey D, Panaud O, Anstett MC, Robert T. Traditional management of cassava morphological and genetic diversity by the Makushi Amerindians (Guyana, South America): Perspectives for on-farm conservation of crop genetic resources. Euphytica. 2001,120:143-57. DOI: 10.1023/A:1017501017031.

[69] Peroni N, Kageyama PY, Begossi A. Molecular differentiation, diversity, and folk classification of "sweet" and "bitter" cassava (*Manihot esculenta*) in Caiçara and Caboclo management systems (Brazil). Genetic Resources and Crop Evolution. 2007,54:1333-49. DOI: 10.1007/s10722-006-9116-2.

[70] Angel F, Barney VE, Tohme J, Roca WM. Stability of cassava plants at the DNA level after retrieval from 10 years of in vitro storage. Euphytica. 1996,90:307-13. DOI: 10.1007/BF00027481.

[71] Roa AC, Chavarriaga-Aguirre P, Duque MC, Maya MM, Bonierbale MW, Iglesias C, Tohme J. Cross-species amplification of cassava (*Manihot esculenta*) (Euphorbiaceae) microsatellites: Allelic polymorphism and degree of relationship. American Journal of Botany. 2000,87:1647-55.

[72] Roa AC, Maya MM, Duque MC, Tohme J, Allem AC, Bonierbale MW. AFLP analysis of relationships among cassava and other *Manihot* species. Theoretical and Applied Genetics. 1997,95(5-6):741-50. DOI: 10.1007/s001220050620.

[73] Chavarriaga-Aguirre P, Maya MM, Tohme J, Duque MC, Iglesias C, Bonierbale MW, et al. Using microsatellites, isozymes and AFLPs to evaluate genetic diversity and redundancy in the cassava core collection and to assess the usefulness of DNA-based markers to maintain germplasm collections. Molecular Breeding. 1999,5:263-73.

[74] Chavarriaga-Aguirre PP, Maya MM, Bonierbale MW, Kresovich S, Fregene MA, Tohme J, Kochert G. Microsatellites in Cassava (*Manihot esculenta* Crantz): Discovery, inheritance and variability. Theoretical and Applied Genetics. 1998,97:493-501. DOI: 10.1007/s001220050922.

[75] Olsen KM, Schaal BA. Evidence on the origin of cassava: Phylogeography of *Manihot esculenta*. Proceedings of the National Academy of Sciences of the United States of America. 1999,96:5586-91. DOI: 10.1073/pnas.96.10.5586.

[76] Elias M, Panaud O, Robert T. Assessment of genetic variability in a traditional cassava (*Manihot esculenta* Crantz) farming system, using AFLP markers. Heredity. 2000,85:219-30.

[77] Olsen KM, Schaal BA. Microsatellite variation in cassava (*Manihot esculenta*, Euphorbiaceae) and its wild relatives: Further evidence for a southern Amazonian origin of domestication. American Journal of Botany. 2001,88:131-42.

[78] Carvalho LJCB, Schaal BA. Assessing genetic diversity in the cassava (*Manihot esculenta* Crantz) germplasm collection in Brazil using PCR-based markers. Euphytica. 2001,120:133-42.

[79] Second G, Iglesias C. The state of the use of cassava genetic diversity and a proposal to enhance it. In: Cooper HD, Spillane C, Hodgkin T, editors. Broadening the Genetic Base of Crop

Production. London, UK: CABI Publishing Joinlty with FAO and IPGRI, 2001. 201-21 p.

[80] Montarroyos AVV, de Lima MAG, dos Santos EO, de França JGE. Isozyme analysis of an active cassava germplasm bank collection. Euphytica. 2003,130:101-6. DOI: 10.1023/A:1022363122834.

[81] Fregene MA, Suarez M, Mkumbira J, Kulembeka H, Ndedya E, Kulaya A, et al. Simple sequence repeat marker diversity in cassava landraces: Genetic diversity and differentiation in an asexually propagated crop. TAG. Theoretical and Applied Genetics. Theoretische und Angewandte Genetik. 2003,107:1083-93. DOI: 10.1007/s00122-003-1348-3.

[82] Elias M, Mühlen GS, McKey D, Roa AC, Tohme J. Genetic diversity of traditional South American Landraces of Cassava (*Manihot esculenta* Crantz): An analysis using microsatellites. Economic Botany. 2004,58:242-56. DOI: 10.1663/0013-0001(2004)058[0242:GDOTSA]2.0.CO;2.

[83] Zacarias AM, Botha A-M, Labuschagne MT, Benesi IRM. Characterization and genetic distance analysis of cassava (*Manihot esculenta* Crantz) germplasm from Mozambique using RAPD fingerprinting. Euphytica. 2004,138:49-53. DOI: 10.1023/B:E UPH.0000047057.05642.74.

[84] Zaldivar ME, Rocha OJ, Aguilar G, Castro L, Castro E, Barrantes R. Genetic variation of cassava (*Manihot esculenta* Crantz) cultivated by Chibchan Amerindians of Costa Rica. Economic Botany. 2004,58:204-13. DOI: 10.1663/0013-0001 (2004)058[0204:GVOCME]2.0.CO;2.

[85] Resende AG, Vidigal Filho PS, Machado MdFPS. Esterase polymorphism marking cultivars of *Manihot esculenta*, Crantz. Brazilian Archives of Biology and Technology. 2004,47:347-53.

[86] Herzberg F, Mahungu N, Mignouna J, Kullaya A. Assessment of genetic diversity of local varieties of cassava in Tanzania using molecular markers. African Crop Science Journal. 2004,12:171-87.

[87] Chacón J, Madriñán S, Debouck D, Rodriguez F, Tohme J. Phylogenetic patterns in the genus *Manihot* (Euphorbiaceae) inferred from analyses of nuclear and chloroplast DNA regions. Molecular Phylogenetics and Evolution. 2008,49:260-7. DOI: 10.1016/j.ympev.2008.07.015.

[88] Rocha OJ, Zaldivar ME, Castro L, Castro E, Barrantes R. Microsatellite variation of cassava (*Manihot esculenta* Crantz) in home gardens of Chibchan Amerindians from Costa Rica. Conservation Genetics. 2008,9:107-18. DOI: 10.1007/s10592-007-9312-4.

[89] Kawuki RS, Ferguson M, Labuschagne M, Herselman L, Kim D-J. Identification, characterisation and application of single nucleotide polymorphisms for diversity assessment in cassava (*Manihot esculenta* Crantz). Molecular Breeding. 2009,23:669-84. DOI: 10.1007/s11032-009-9264-0.

[90] Siqueira MVBM, Queiroz-Silva JR, Bressan EA, Borges A, Pereira KJC, Pinto JG, Veasey EA. Genetic characterization of cassava (*Manihot esculenta*) landraces in Brazil assessed with simple sequence repeats. Genetics and Molecular Biology. 2009,32:104-10.

[91] Raji AAJ, Fawole I, Gedil M, Dixon AGO. Genetic differentiation analysis of African cassava (*Manihot esculenta*) landraces and elite germplasm using amplified fragment length polymorphism and simple sequence repeat markers. Annals of Applied Biology. 2009,155:187-99. DOI: 10.1111/j.1744-7348.2009.00329.x.

[92] Carvalho L, de Souza C, de Mattos Cascardo J, Agostini MV, Vieira EA, Anderson J, et al. Natural genetic variation in cassava (*Manihot esculenta* Crantz) landraces: A tool for gene discovery. In: Shu QY, editor. Induced Plant Mutations in the Genomics Era. Rome, Italy: Joint FAO/IAEA Prorgramme Nuclear Techniques in Food and Agriculture, 2009.

[93] Lekha SS, Pillai SV, Kumar JS. Molecular genotyping of Indian Cassava Cultivars using SSR markers. Advances in Environmental Biology. 2010,4:224-33.

[94] Qi L, Wang W-Q, Zhang Z-W, Ye J-Q, Li K-M. DNA fingerprints of 18 cassava varieties based on sequence-related amplified polymorphism markers. Acta agronomica sinica. 2010,36:1642-8. DOI: 10.1016/S1875-278060076-6.

[95] Montero-Rojas M, Correa AM, Siritunga D. Molecular differentiation and diversity of cassava (*Manihot esculenta*) taken from 162 locations across Puerto Rico and assessed with microsatellite markers. AoB Plants. 2011,2011. DOI: 10.1093/aobpla/plr010.

[96] Ribeiro MdNO, Carvalho SPd, Santos JBd, Antonio RPGenetic variability among cassava accessions based on SSR markers. Crop Breeding and Applied Biotechnology. 2011,11:263-9.

[97] Vieira EA, Fialho JdF, Faleiro FG, Bellon G, Fonseca KGd, Carvalho LJCB, et al. Characterization of sweet cassava accessions based on molecular, quantitative and qualitative data. Crop Breeding and Applied Biotechnology. 2011,11:232-40.

[98] Siqueira MVBM, Pinheiro TT, Borges A, Valle TL, Zatarim M, Veasey EA. Microsatellite polymorphisms in cassava landraces from the cerrado biome, Mato Grosso do sul, Brazil. Biochemical Genetics.

2010,48(9-10):879-95. DOI: 10.1007/s10528-010-9369-5.

[99] Siqueira MVBM, Borges A, Valle TL, Veasey EA. A comparative genetic diversity assessment of industrial and household Brazilian cassava varieties using SSR markers. Bragantia. 2011,70:745-52.

[100] Turyagyenda L, Kizito E, Ferguson M, Baguma Y, Harvey J, Gibson P, et al. Genetic diversity among farmer-preferred cassava landraces in Uganda. African Crop Science Journal. 2012,20.

[101] Kabeya MJ, Kabeya UC, Bekele BD, Ingelbrecht IL. Genetic Analysis of selected cassava (*Manihot esculenta*) genetic pool in Africa assessed with simple sequence repeats. World Journal of Agricultural Sciences. 2012,8:637-41. DOI: 10.5829/idosi.wjas.2012.8.6.1695.

[102] Kizito EB, Turyagyenda L, Ferguson M, Baguma Y, Harvey J, Gibson P, et al. Genetic diversity among farmer-preferred cassava landraces in Uganda. African Crop Science Journal. 2012,20(s1):15-30.

[103] de Oliveira EJ, Ferreira CF, da Silva Santos V, de Jesus ON, Oliveira GAF, da Silva MS. Potential of SNP markers for the characterization of Brazilian cassava germplasm. Theoretical and Applied Genetics. 2014:1-18.

[104] Chepkoech E, Kinyua M, Kiplagat O, Arunga EE, Kimno S. Genetic diversity of cassava mutants, hybrids and landraces using simple sequence repeat markers. American Journal of Experimental Agriculture. 2014,5:XX-XX.

[105] Peña-Venegas C, Stomph T, Verschoor G, Lopez-Lavalle LA, Struik P. Differences in manioc diversity among five ethnic groups of the Colombian Amazon. Diversity. 2014,6:792-826.

[106] Acquah E, Quain M, Twumasi P, Parkes E. Genetic relationships revealed by simple sequence repeat (SSR) markers among Ghanaian cassava cultivars released by different research groups. Ghana Journal of Agricultural Science. 2014,48:99-109.

[107] Vidal ÁM, Vieira LJ, Ferreira CF, Souza FV, Souza AS, Ledo CA. Genetic fidelity and variability of micropropagated cassava plants (*Manihot esculenta* Crantz) evaluated using ISSR markers. Genetics and Molecular Research. 2015,14:7759-70.

[108] Beovides Y, Fregene M, Gutiérrez JP, Milián MD, Coto O, Buitrago C, et al. Molecular diversity of Cuban cassava (*Manihot esculenta* Crantz) cultivars assessed by simple sequences repeats (SSR). Base. 2015,19:364-77.

[109] Ortiz AHT, Rocha VPC, Moiana LD, Gonçalves-Vidigal MC, Galván MZ, Vidigal Filho PS. Population structure and genetic diversity in sweet cassava cultivars from Paraná, Brazil. Plant Mol Biol Rep.. Plant Molecular Biology Reporter. 2016,34:1153-66. DOI: 10.1007/s11105-016-0995-x.

[110] Tiago MG, Pedro SVF, Maria CGV, Rebecca CUF, Vanesca PCR, Alex HTO et al. Genetic diversity and population structure of traditional sweet cassava accessions from Southern of Minas Gerais State, Brazil, using microsatellite markers. African Journal of Biotechnology. 2017,16:346-58. DOI: 10.5897/AJB2016.15768.

[111] Lestari T, Apriyadi R. Genetic potential of cassava biodiversity in Bangka Island, Indonesia. Cell Biology and Development. 2017,1:41-5. DOI: 10.13057/cellbioldev/v010201.

[112] Karim KY, Ifie B, Dzidzienyo D, Danquah EY, Blay ET, Whyte JBA, et al. Genetic characterization of cassava (*Manihot esculenta* Crantz) genotypes using agro-morphological and single nucleotide polymorphism markers. Physiology and Molecular Biology of Plants. 2020,26:317-30. DOI: 10.1007/s12298-019-00740-x.

[113] Costa N, Azevedo HdS, da Silva L, Cunha E, Siviero A. Campos Td. Molecular characterisation and core collection evaluation of *Manihot esculenta* Crantz. Bioscience Journal. 2020,36:22-35. DOI: doi. http://dx.doi.org/BJ-v36n0a2020-48247.

[114] Rocha VPC, Gonçalves-Vidigal MC, Ortiz AHT, Valentini G, Ferreira RCU, Gonçalves TM, et al. Population structure and genetic diversity in sweet cassava accessions in Paraná and Santa Catarina, Brazil. Plant Mol Biol Rep.. Plant Molecular Biology Reporter. 2020,38:25-38. DOI: 10.1007/s11105-019-01175-0.

[115] Asha K, Maria VA, Koundinya A, Krishnan P. Molecular profiling of selected cassava (*Manihot esculenta* Crantz) germplasm using ISSR and SSR markers. Journal of Root Crops. 2020,45:24-32.

[116] Iragaba P, Kawuki RS, Bauchet G, Ramu P, Tufan HA, Earle ED, et al. Genomic characterization of Ugandan smallholder farmer-preferred cassava varieties. Crop Science. 2020,60:1450-61. DOI: 10.1002/csc2.20152.

[117] Asha K, Philip RR, Mohan N. Molecular profiling of landraces of cassava (*Manihot esculenta* Crantz) using ISSR markers. International Journal of Research in Engineering. Science and Management. 2020,3:343-9.

[118] Adjebeng-Danquah J, Manu-Aduening J, Asante IK, Agyare RY, Gracen V, Offei SK. Genetic diversity and population structure analysis of Ghanaian and exotic cassava accessions using simple sequence repeat (SSR) markers. Heliyon. 2020,6:e03154. DOI: 10.1016/j.heliyon.2019.e03154.

[119] Adu BG, Yeboah A, Akromah R, Bobobee E, Amoah S, Kena AW, Amoah RA. Whole genome SNPs and phenotypic characterization of cassava (*Manihot esculenta* Crantz) germplasm in the semi-deciduous forest ecology of Ghana. Ecological Genetics and Genomics. 2020,17. DOI: 10.1016/j.egg.2020.100068. 100068.

[120] Ortiz AHT, Vidigal Filho PS, Rocha VPC, Ferreira RCU, Gonçalves TM, Gonçalves-Vidigal MC. Population structure and genetic diversity of sweet cassava accessions from the midwestern, southeastern and southern regions of Brazil. Brazilian Archives of Biology and Technology. 2019,62:(e19180556). DOI: 10.1590/1678-4324-2019180556.

[121] Ocampo CH, Angel F, Jiménez A, Jaramillo OG, Hershey CH, Granados FE, et al. DNA fingerprinting to confirm possible genetic duplicates in cassava germplasm. In: Brekelbaum T, editor. The Cassava Biotechnology Network. Proceedings of the Second Internatio' nal Scientific Meeting. Bogor, Indonesia. International Center for Tropical Agriculture (CIAT), 1995. 145-51 p.

[122] Ocampo C, Hershey CH, Iglesias C, Iwanaga M. Esterase isozyme fingerprinting of the cassava germplasm collection held at CIAT. In: Roca W, Thro AM, editors. First International Scientific Meeting Cassava Biotechnology Network. Cartagena de Indias. Colombia: CIAT, 1992. 81-9 p.

[123] Beeching JR, Marmey P, Gavalda M-C, Noirot M, Haysom HR, Hughes MA. An assessment of genetic diversity within a collection of cassava (*Manihot esculenta* Crantz) germplasm using molecular markers. Annals of Botany. 1993,72:515-20. DOI: 10.1006/anbo.1993.1139.

[124] Lefèvre F, Charrier A. Isozyme diversity within African *Manihot* germplasm. Euphytica. 1993,66(1-2):73-80. DOI: 10.1007/BF00023510.

[125] Ulbricht Ferreira RC, Vidigal Filho PS, Gonçalves-Vidigal MC, Moiana LD, Kvitschal MV. Genetic and population structure of sweet cassava (*Manihot esculenta* Crantz) germplasm collected from Campo Grande, Mato Grosso do Sul, Brazil. Australian Journal of Crop Science. 2015,9:458-67.

[126] Marmey P, Beeching JR, Hamon S, Charrier A. Evaluation of cassava (*Manihot esculenta* Crantz) germplasm collections using RAPD markers. Euphytica. 1994,74-74:203-9. DOI: 10.1007/BF00040402.

[127] Becerra Lopez-Lavalle LA. Molecular approaches in cassava breeding. In: Hershey C, editor. Achieving Sustainable Cultivation of Cassava Volume 2 Cultivation techniques. Cambridge, UK: Burleigh Dodds Science Publishing Limited, 2017.

[128] Sardos J, McKey D, Duval MF, Malapa R, Noyer JL, Lebot V. Evolution of cassava (*Manihot esculenta* Crantz) after recent introduction into a South Pacific Island system: The contribution of sex to the diversification of a clonally propagated crop. Genome. 2008,51:912-21. DOI: 10.1139/G08-080.

[129] Bredeson JV, Lyons JB, Prochnik SE, Wu GA, Ha CM, Edsinger-Gonzales E, et al. Sequencing wild and cultivated cassava and related species reveals extensive interspecific hybridization and genetic diversity. Nature Biotechnology. 2016,34:562-70. DOI: 10.1038/nbt.3535.

[130] Nestel B, Cock J. Cassava, the Development of an International Research Network, 1976.

[131] Hussain A, Bushuk W, Ramirez H, Roca W. Identification of cassava (*Manihot esculenta* Crantz) cultivars by electrophoretic patterns of esterase

isozymes. Seed Science and Technology. 1987,15:19-22.

[132] Lekha SS, Kumar S, Pillai SV. Assessing genetic diversity of Indian cassava: A comparison of old and new collections using microsatellite markers. Asian and Australasian Journal of Plant Science and Biotechnology. 2010,4:43-52.

[133] Mühlen GS, Martins PS, Ando A. Variabilidade genética de etnovariedades de mandioca, avaliada por marcadores de DNA. Scientia Agricola. 2000,57:319-28.

[134] de Albuquerque HYG, Oliveira EJd, Brito AC. Andrade LRBd, Carmo CDd, Morgante CV, et al. Identification of duplicates in cassava germplasm banks based on single-nucleotide polymorphisms (SNPs). Scientia Agricola. 2019,76:328-36. DOI: 10.1590/1678-992X-2017-0389.

[135] Cabral BLR, Souza JAd, Ando A, Veasey EA, Cardoso EMR. Isoenzymatic variability of cassava accessions from different regions in Brazil. Scientia Agricola. 2002,59:521-7. DOI: 10.1590/S0103-90162002000300017.

[136] Second G, Allem AC, Mendes R, Carvalho L, Emperaire L, Ingram C, et al. Molecular marker (AFLP)-based Manihot and cassava numerical taxonomy and genetic structure analysis in progress: Implications for their dynamic conservation and genetic mapping. African Journal of Root and Tuber Crops. 1997,2(1-2):140-7.

[137] Ferguson ME, Shah T, Kulakow P, Ceballos H. A global overview of cassava genetic diversity. PLOS ONE. 2019,14:e0224763. DOI: 10.1371/journal.pone.0224763.

[138] Hershey C, Mendes RA, Alvarez MN, Bai KBV, Bueno A, Lian TS, et al. CASSAVA BREEDING: A multidisciplinary review. In: Hershey C, editor. CASSAVA BREEDING:A Multidisciplinary Review. Philippines: International Center for Tropical Agriculture (CIAT), 1985.

[139] Ramirez H, Hussain A, Roca W, Bushuk W. Isozyme electrophoregrams of sixteen enzymes in five tissues of cassava (*Manihot esculenta* Crantz) varieties. Euphytica. 1987,36:39-48. DOI: 10.1007/BF00730645.

[140] Wong HL, Yeoh HH, Lim SH. Customisation of AFLP analysis for cassava varietal identification. Phytochemistry. 1999,50:919-24.

[141] Mullis K, Faloona F, Scharf S, Saiki R, Horn G, Erlich H. Specific enzymatic amplification of DNA in vitro: The polymerase chain reaction. Cold Spring Harbor Symposia on Quantitative Biology. 1986,51:263-73. DOI: 10.1101/sqb.1986.051.01.032.

[142] Welsh J, McClelland M. Fingerprinting genomes using PCR with arbitrary primers. Nucleic Acids Research. 1990,18:7213-8. DOI: 10.1093/nar/18.24.7213.

[143] Program C. Cassava Program 1987-1991. Cali, Colombia: International Center for Tropical Agriculture (CIAT), 1992.

[144] Prochnik S, Marri PR, Desany B, Rabinowicz PD, Kodira C, Mohiuddin M, et al. The cassava genome: Current progress, future directions. Tropical Plant Biology. 2012,5:88-94. DOI: 10.1007/s12042-011-9088-z.

[145] Becerra Lopez-Lavalle LA, Perea CS, Duitama J, Ruiz M, Parsa S, Ovalle T, et al. Cassava digital gene bank. In: Cali, editor Program C. Colombia: International Center of Tropical Agriculture (CIAT), 2015.

[146] Becerra Lopez-Lavalle LA, Rodriguez Zapata FV, Ovalle T, Ruiz M,

Gkanogiannis A, Tohme J. Capturing next-generation genome wide molecular markers in cassava helps to untangle the Crop's genetic improvement history. Plant and animal genome Conference Volume XXVI. San Diego, California, USA: PAG, 2018, January 13-17, 2018. p. 1.

[147] Hamblin MT, Rabbi IY. The effects of restriction-enzyme choice on properties of genotyping-by-sequencing libraries: A study in cassava (*Manihot esculenta*). Crop Science. 2014,54:2603-8. DOI: 10.2135/cropsci2014.02.0160.

[148] Vos P, Hogers R, Bleeker M, Reijans M, van de Lee T, Hornes M et al. AFLP: A new technique for DNA fingerprinting. Nucleic Acids Research. 1995,23:4407-14. DOI: 10.1093/nar/23.21.4407.

[149] Mba Rec., Mba REC, Stephenson P, Edwards K, Melzer S, Nkumbira J, Gullberg U et al. Simple sequence repeat (SSR) markers survey of the cassava (*Manihot esculenta* Crantz) genome: Towards an SSR-based molecular genetic map of cassava. Theoretical and Applied Genetics. 2001,102:21-31.

[150] Fregene M, Okogbenin E, Egesi C, Ogbe FO, Eke-Okoro N. UMUCASS 33. In: CIAT, ed. ICfTA, editor. Nigeria: Nigerian Seed Portal Initiative, 2010. CR41-10 p.

[151] Fregene M, Okogbenin E, Egesi C, Olasanmi B, Akinbo O, Kulakow P, et al. UMUCASS 41. In: CIAT, ed. ICfTA, editor. Nigeria: Nigerian Seed Portal Initiative, 2012. CR36-5 p.

[152] Ferguson M, Rabbi I, Kim D-J, Gedil M, Lopez-Lavalle LAB, Okogbenin E. Molecular markers and their application to cassava breeding: Past, present and future. Tropical Plant Biology. 2012,5:95-109. DOI: 10.1007/s12042-011-9087-0.

[153] BGI, CIAT. BGI and CIAT announce collaboration for large-scale genome sequencing of cassava. In: Russell N, Peng J, Yang B, editors. Shenzhen: EurekAlert, 2011.

[154] Ocampo J, Ovalle TM, Labarta R, Le DP, De Haan S, Nguyen AV, et al. DNA fingerprinting reveals varietal composition of Vietnamese cassava germplasm (*Manihot esculenta* Crantz) from farmers' field and gene bank collections. Plant Molecular Biology. In press.

[155] Button P. The international Union for the Protection of New Varieties of Plants (UPOV) recommendations on variety denominations. In: Acta Horticulturae International Symposium on the Taxonomy of Cultivated Plants 799 Groendijk-Wilders N, editor. 2008:191-200.