

Review

Not peer-reviewed version

Advancing Cassava Improvement Through Multi-Omics Technologies

Varsha Acharya , [Kalidas Pati](#) ^{*} , [Biswajit Jena](#) , [R. Arutselvan](#) , Hanume Gowda , [Aria Dolatabadian](#) ^{*}

Posted Date: 22 September 2025

doi: 10.20944/preprints202509.1782.v1

Keywords: cassava; omics; multi-omics; genomics; proteomics; transcriptomics



Preprints.org is a free multidisciplinary platform providing preprint service that is dedicated to making early versions of research outputs permanently available and citable. Preprints posted at Preprints.org appear in Web of Science, Crossref, Google Scholar, Scilit, Europe PMC.

Copyright: This open access article is published under a Creative Commons CC BY 4.0 license, which permit the free download, distribution, and reuse, provided that the author and preprint are cited in any reuse.

Disclaimer/Publisher's Note: The statements, opinions, and data contained in all publications are solely those of the individual author(s) and contributor(s) and not of MDPI and/or the editor(s). MDPI and/or the editor(s) disclaim responsibility for any injury to people or property resulting from any ideas, methods, instructions, or products referred to in the content.

Review

Advancing Cassava Improvement Through Multi-Omics Technologies

Varsha Acharya ¹, Kalidas Pati ^{1,*}, Biswajit Jena ¹, R. Arutselvan ¹, Hanume Gowda ¹ and Aria Dolatabadian ^{2,*}

¹ Regional Centre, ICAR-Central Tuber Crops Research Institute, Bhubaneswar, Odisha – 751019, India

² School of Biological Sciences, The University of Western Australia, Perth, WA, Australia

* Correspondence: kalidas9555@gmail.com (K.P.); aria.dolatabadian@uwa.edu.au (A.D.)

Abstract

Cassava (*Manihot esculenta* Crantz) is a key staple food and the world's fourth-largest source of calories. Among other biotechnological and bioinformatics methods, genomic-assisted breeding, molecular tools, and genome editing technologies have enhanced the potential of commercially significant crops through the application of functional genomics, proteomics, transcriptomics, and metabolomics. However, the creation, enhancement, and eventual adoption of the enhanced cultivars have proven difficult, necessitating all-encompassing methods to their resolution. This review aims to highlight advancements in genetic research and various omics studies in cassava. This article discusses the potential risks and global acceptance of improved cultivars. It reviews research findings on cassava production, quality, and adaptability, while also highlighting recent advancements in cassava research worldwide. This review also explores the potential future use of omics methods to enhance desired outcomes. It provides a summary of cassava molecular resources, with a focus on the most relevant and up-to-date multi-omics technologies, including genomics, transcriptomics, metabolomics, and proteomics. Additionally, it examines how multi-omics tools can be applied to uncover correlations between biological processes and metabolic pathways across various omics layers. Overall, this article highlights the most significant advancements achieved in cassava research to date.

Keywords: cassava; omics; multi-omics; genomics; proteomics; transcriptomics

1. Introduction

Cassava was first developed and cultivated in the Neotropics [1]. It is one of the major crops, as a large region of western and central Africa is covered by cassava cultivation known as the “cassava belt” [2]. Cassava was introduced to Asia in the seventeenth century, where it is cultivated for both human consumption and animal feed, often for the European export market [3]. According to the systematic classification, Cassava belongs to the Euphorbiaceae family, comprising approximately 90 species. The superfamily of cassava is Fabid (also known as Eurosids) [3,4]. It is one of the most important dietary sources of energy after rice (*Oryza sativa* L.), maize (*Zea mays* L.), and sugarcane (*Saccharum* spp.) for most of the tropical countries in the world [5]. Millions of people are using cassava as their staple food in their diet. It has become an essential calorie-producing crop among tropical crops [6]. As per Scott's estimation, the yearly output of cassava in 1993 was over 172.4 million tonnes, with a value of almost US \$ 9.31 billion. The output improved at a rate of 2.35% per year between 1961 and 1963 and 1995 and 1997. The rise in cassava output was predicted by 1.1% per year between 1994 and 2005. In reality, over the past decade, productivity has increased globally by approximately 18.4% [5]. *Manihot esculenta* Crantz, often known as cassava, consists of 100 species distributed throughout the New World tropics, originating from the Southern Amazon basin [7]. With rising climatic unpredictability, cassava has become a crucial crop in global agriculture [8].

It has been demonstrated to be a climate-resilient nature crop or a commercial crop for subsistence farmers with limited resources due to its ability to grow in marginal soils in any environment [9]. It is cultivated throughout the tropical regions of Asia, Africa, and the Americas [10]. Research on cassava has been successfully carried out by national research institutions located worldwide, including those in Colombia, Cuba, Brazil, Indonesia, Nigeria, India, Vietnam, China, and Thailand [11]. It is a vital source of starch due to its enormous storage roots. For more than a billion people, especially in tropical areas and all over the world, it is also recognised as a staple food crop [12]. The use of information technology to analyse biological data, helping to decode plant genomes, is known as bioinformatics [13,14]. Previously, biological research work was conducted in biological laboratories, plant clinics, and fields; however, it is now being increasingly replaced by In-silico work for examining data, refining hypotheses, and planning experiments [15,16]. Modern technology has improved the study of plant biology. The study of plant biology has advanced significantly in recent years [17]. Recently, bioinformatics has played a crucial role in the growth of agro-based industries, the utilisation of agricultural by-products, the agricultural sector, and the improved management of the environment [18]. Along with the increase in sequencing projects, bioinformatics makes significant advances in biology by providing scientists with access to genomic data. There is a strong likelihood that this field will make another giant leap in the next decade, with computational methods of systems and broad properties providing the foundation for crop improvement innovation and experimentation [19].

To understand the benefits of crops, numerous researchers have worked on the topic. Currently, various technically advanced bioinformatics tools and biological databases have been developed for analysing crop data. These tools are also accessible to others for conducting research work in similar fields [13]. Various omics analyses have been conducted to gain a clear understanding of crop utilities. There are various omics analysis methods available for building, managing, and integrating databases, which aid in transitional research work in multi-omics data analysis, a process that has become an integral part of systems biology [20]. This review article intends to provide an exhaustive summary of all the advanced research work made in the Cassava crop using the multi-omics techniques, i.e., genomics, proteomics, transcriptomics and metagenomics. We believe that in the digital era of big omics data, the role of bioinformatics in promoting cassava biological research will be greater than ever before. The prospects of using omics approaches in improving the desired cassava are also discussed in this review paper. Finally, the paper identified future research priorities for effectively integrating and commercialising cassava around the world.

2. Cassava's Genetic Diversity

Genetic diversity was defined as the key pillar of biodiversity and diversity in species, between species, and in ecosystems by the Rio de Janeiro (Earth Summit) [21]. The first step towards genetic advancement is obtaining and analysing a variety of genetic resources [9]. Cassava's vast genetic variety is thought to have evolved through apomixis, or natural and artificial hybridisation between wild *Manihot* spp. and farmed cassava. [22]. A number of evolutionary forces that are responsible for plant variation are migration, polyploidization, mutation and hybridisation [23]. Many international and national institutes hold extensive collections of cassava germplasm. More than 6000 cassava accessions, of which 30% are of Brazilian provenance, have been collected by the International Centre for Tropical Agriculture (CIAT) in Colombia, with the majority of the accessions (97%) coming from Latin America [24]. The International Institute for Tropical Agriculture (IITA) in Nigeria comprises over 2,000 genotypes, the majority of which are of West African origin [25]. Specific evolutionary forces, such as mutation, selection, genetic drift, and migration, act continuously, resulting in continuous changes in allelic frequency within a population and thus affecting genetic diversity [26]. The knowledge of genetic diversity of species is the foundation for breeding programs and building strategies for germplasm collection, management, conservation and enhancement for food security and sustainable agricultural development. Genetic diversity studies in cassava have been conducted using both molecular and morphological methods in several countries, including Brazil [27], Benin

Republic [28], Chad [29], Nigeria [30], and Tanzania [31]. The diversity analysis can be conducted using various methods, such as cytological, biochemical, morphological, and molecular characterisation. Initiation of genomic tools resulted in making the molecular markers the primary choice for the assessment of genetic diversity. Due to their high reproducibility, hyper-variability, better genomic coverage, and zero environmental fluctuation, molecular markers are the technique of choice for assessing genetic diversity [32].

3. Genetic Diversity Analysis via Molecular Marker

Gregor Mendel used phenotype-based genetic markers in his research since the nineteenth century, so the concept of genetic or molecular markers is not new. Due to the limitations of phenotype-based genetic markers, DNA-based markers, or molecular markers, were generated [33]. A molecular marker denoted as a genomic locus, detected by probe or specific starters (primer), that unequivocally distinguishes the chromosomal trait it represents as well as the flanking regions at the 3' and 5' extremities [34]. In cassava, SSRs have been the most often utilised molecular markers, particularly for studies of genetic variation [35]. The commonly used genetic or DNA-based marker techniques are Amplified Fragment Length Polymorphism (AFLP), Random Amplified Polymorphic DNA (RAPD), Simple Sequence Repeats (SSR) and Restriction Fragment Length Polymorphism (RFLP). A few thousand SSR markers for cassava have been created by multiple organisations using enriched genomic DNA libraries and expressed sequence tags (ESTs) [36–39]. These markers are used for evolutionary, taxonomic, ecological, genetic, and phylogenetic studies in plant sciences. The limitations and advantages of the above commonly used molecular markers are documented [40,41]. The Restriction length polymorphisms (RFLPs) and random amplified polymorphisms (RAPDs) were first used in cassava to analyse the genetic diversity within the genus *Manihot* [42]. In 1993, to study the assessment of genetic diversity within the collections of African cultivars of cassava maintained in vitro at ORSTOM, Montpellier, Beeching and coauthors demonstrated the use of RFLP to detect and measure the genetic diversity of the collection of cassava crop [1]. Marmey et al. conducted a preliminary study of three cassava species using twenty primers, demonstrating the use of RAPD markers in examining their genetic diversity [42]. This study reveals the genetic diversity among African *Manihot esculenta* accessions, which may be utilised in a program of genetic improvement of cultivars. A study has proven that the RAPD technique is the most powerful and effective tool for analysing the genetic diversity of *Manihot esculenta* [42]. Wong and group designed primers for RAPD analysis of cassava, testing random primers with 60-80% G+C content on genomic DNA of leaves of eight varieties of cassava [43]. The genetic diversity of 31 Brazilian cassava clones originating in different Brazilian areas with diverse cultivation purposes was examined using RAPD markers [44]. The AFLP technique is utilised to evaluate the five wild *Manihot* subspecies as close relatives or ancestors of cassava, and one distant species was analysed. Based on the results, the origin and ancestry of cassava were revised [45]. Colombo and co performed an experiment using AFLP and RAPD molecular markers to examine the genetic relatedness between two naturally occurring species, *M. peruviana* and *M. flabellifolia* and cultivated cassava [23]. An experiment was conducted to assess the genetic variability and diversity of 31 *Manihot esculenta* varieties traditionally cultivated by Makushi Amerindians in Guyana using AFLP markers [46]. In an experiment, the genetic diversity of Ghana's cassava accessions was assessed using the RAPD approach at the district-group and individual accession levels. Around fifty cassava accessions were used for the study [47]. In 2003, Fregene and co-authors worked on the cassava landraces to find out the genetic diversity and differentiation in an asexually propagated cassava crop. It concluded with two findings, i.e., directly associated with the cassava findings. Firstly, the distinctive and extensive variety of the cassava land races discovered in southeast Tanzania provides an excellent genetic source for localised cassava development. The occurrence of such diversity due to the presence of certain genes at high frequencies for adaptation to an area, while the high genetic diversity implies high additive genetic variance, upon which plant breeding development depends. Secondly, the high level of variation among land races from Nigeria and Guatemala may characterise a heterotic pool and deliver an

opportunity for the systematic exploitation of hybrid vigour in cassava [35]. Cassava breeding and genomics would advance considerably if a high density of SNPs were found in the plant. SSRs, which are typically multi-allelic (many alleles at a locus), are more informative than SNPs, which are typically biallelic (two alleles at a site) [48]. A total of 2,954 putative EST-derived SNPs were used to identify and validate 1,190 SNP markers in cassava [49]. These SNPs were discovered on scaffolds in the cassava genome sequence (v.4.1). Genetic variations between closely related and wild species can be detected using molecular markers (Table 1). To evaluate the genetic diversity of cassava germplasm, various DNA marker systems have been created and are being used [50].

Table 1. Genetic markers list.

Marker System	No. of Acc. Evaluated	Species	References
RFLP	80	<i>M. esculenta</i> , <i>M. glaziovii</i> , <i>M. Caerulescens</i> , <i>M. esculenta ssp. esculenta</i> , <i>M. esculenta ssp. flabellifolia</i>	[1]
AFLP	105	<i>M. aesculifolia</i> , <i>M. carthaginensis</i> , <i>M. tristis</i> , <i>M. brachyloba</i>	[45]
RAPD	31	Cultivated cassava <i>M. esculenta</i> , <i>M. flabellifolia</i> , <i>M. peruviana</i> , <i>M. glaziovii</i> ,	[51]
RAPD/AFLP	53	<i>M. glaziovii</i> , <i>M. reptans</i> , <i>M. chlorostica</i> , <i>M. aesculifolia</i> , <i>M. michaelis</i>	[23]
AFLP	76	Cultivated cassava <i>M. esculenta ssp. flabellifolia</i>	[46]
SSR	212	<i>M. esculenta ssp. flabellifolia</i> , <i>M. pruinosa</i>	[7]
RAPD	24	<i>M. esculenta ssp. esculenta</i>	[52]
Isozyme	46	Cultivated cassava	[53]
SSR	117	Cultivated cassava	[54]
SSR	185	Cultivated cassava	[55]
SSR	55	Provitamin-A cassava	[56]
SSR	54	Cultivated cassava	[57]
SSR	1401	<i>M. esculenta</i>	[58]
SSR	163	<i>M. esculenta</i>	[59]
ISSR	17	Landraces	[60]
SSR	596	<i>M. esculenta ssp. esculenta</i> , <i>M. esculenta ssp. flabellifolia</i>	[61]
SNP	1580	Cultivated and wild cassava	[62]
SNP	3000	Cultivated cassava	[49]
SSR	120	<i>M. esculenta</i>	[63]
SSR	157	Cultivated cassava	[64]
SNP	183	Provitamin-A cassava	[65]
SNP	105	Cultivated cassava	[66]
SSR	89	Cultivated cassava	[67]
SNP	102	Cultivated cassava	[68]

4. Omics or Multi-Omics Technology Used in Cassava

Omic technologies are essential for understanding the molecular processes behind the various plant functions [69]. These omics-based techniques have proven helpful in investigating the genetic and molecular basis of crop development, particularly in response to changes in DNA, transcript levels, proteins, metabolites, and mineral nutrients, against a backdrop of physiological and environmental stress responses [70]. Genomes, metagenomics, transcriptomics, proteomics, metabolomics, phenomics, and ionomics are just a few of the omics techniques that have made each

corresponding molecular biological component integrated with plant systems visible [71–74]. The term “multi-omics” refers to any method of analysing a specific issue using the concepts of various -omics sciences [75]. In several crops, relationships between various biological elements and metabolic pathways have already been successfully identified using multi-omics knowledge [76]. The development of omics resources has progressed in various plant species to address specific biological traits of each species. Researchers are facing a new challenge: combining the facts from omics-based research to identify significance, gain biological insights, and enhance translational research [20]. These omics techniques have been used with certain significant crops including rice (*Oryza sativa* L.), barley (*Hordeum vulgare* L.), wheat (*Triticum aestivum* L.), tomato (*Solanum lycopersicum*), millet (*Setaria italica* L.), soybean (*Glycine max*), maize (*Zea mays* L.) and cotton (*Gossypium hirsutum* L.) [76].

5. Genome and Genomics Study on Cassava

The development of high-throughput sequencing methods allows scientists to exploit the structure of genetic material at the molecular level, a process known as “genomics” [77]. The term ‘Genomics’ describes the study of genes and genomes while focusing on the function, structure, mapping, evolution, metagenomics, epigenomics and genome editing aspects [70]. Genome and gene sequences are now crucial pieces of knowledge for a variety of biological studies. Only a model of well-researched species could be found with high-quality reference sequences a decade ago. Now, because of the recent developments in next-generation sequencing (NGS), it is possible to create reference genome sequences for many species, including plants. Advanced study of bioinformatics in genome assembly is another significant factor supporting the widespread adoption of de novo whole-genome sequencing in numerous species [78]. One of the first “orphan” crop genomes to be sequenced was cassava over the past ten years. As new advances in genome sequencing and bioinformatics have been made, the quality of the cassava genome sequence has progressively increased [79]. The Global Cassava Partnership was formed in 2003 to begin the project of sequencing the cassava genome (GCP-21) [80]. Simon and co-authors in 2012 described the future goals of genome sequencing efforts in cassava. Cassava’s (*Manihot esculenta*, Euphorbiaceae) chloroplast genome has been completely sequenced with a genome of 161,453 bp (Genbank accession number EU117376) in length, including the pair of inverted repeats (IR) of 26,954 bp [81]. In 2009, a draft cassava genome was released and made publicly available via the V10 Phytozome platform [80]. After obtaining the genomic sequence, it was believed that there would be a rapid realisation of the benefits of cassava consumption, its nutrient content, as well as its biofuel feedstock [80]. The genome of cassava was created using the whole-genome shotgun approach, assembled into scaffolds totalling 12,977, with a total of 532.5 Mb of sequence [80,82]. Cassava is one of the naturally diploid (2n = 36) tuber crop species, with a genome size of 770Mbp [83]. Wang and colleagues reported the genome assembly of two cassava varieties, i.e., W14 and KU50. The cassava variety was reported to be *M.esculenta* ssp. *Flabellifolia* is known to be wild cassava or wild ancestor [84]. However, subsequent analysis using Wang et al.’s sequence reads revealed that the plant sequenced as W14 does not belong to *M. esculenta* but is more closely related to *M. glaziovii* [85]. The cassava variety SC205 was analysed further; this variety is widely used in China as a parent cassava breeding variety for whole genome sequencing. The genome size of the variety is 770.3Mb. The raw sequencing data from this study have been uploaded to the Sequence Read Archive under an NCBI BioProject accession (PRJNA578024). The cassava SC205 genome sequences have been preserved as an NCBI BioSample accession number (WIGR00000000). The RNA-seq data have been saved as NCBI BioSample accessions (SRR10480846–SRR10480905) [86]. The list of total genome assemblies available in NCBI (<https://www.ncbi.nlm.nih.gov/>) is mentioned in the Table.2 below.

Table 2. Genome assembly and annotation report of cassava.

Serial no.	Assembly	GenBank	WGS accession	Date
1	<i>M.esculenta_v8</i>	GCA_001659605.2	LTYI02	Sep, 2021

Ref: GCF_001659605.2				
2	MK_v2b	GCA_000737115.1	JPQF01	Sep, 2014
3	ASM395788v1	GCA_003957885.1	RSFS01	Jan, 2018
4	ASM395799v1	GCA_003957995.1	RSFT01	Jan, 2018
5	ASM1361896v1	GCA_013618965.1	WIGR01	Sep. 2020
6	hifiasm152_l3.hic.hap2.p _ctg	GCA_020916425.1	JAIPMC01	Dec, 2021
7	hifiasm152_l3.hic.hap1.p _ctg	GCA_020916445.1	JAIPMD01	Dec, 2021
8	MW_v2d	GCA_000737105.1	JPQE01	Sep, 2014

6. Cassava Enhancement by Genome Editing Techniques

Recently, plant genome editing technologies have shown great potential. The CRISPR/Cas9-based genome editing system is now proving to be a powerful tool in plant science research due to its advantages of simplicity and efficiency. This technology is now an effective tool for basic research and the development of crop plant traits [87]. Developments in genome editing technology have demonstrated promise in crops, making the creation of new varieties easier [88]. The technologies that can perform knockout, chromosomal recombination, and site-directed insertion/substitution at specific gene and chromosomal sites are known as genome editing technologies [89]. Genome editing technologies encompass three primary SSN systems, i.e., the clustered regularly interspaced short palindromic repeats/CRISPR-associated protein 9 (CRISPR/Cas9) system, the transcription activator-like effector nucleases (TALENs), and the zinc finger nucleases (ZFNs). The ZFNs were the first SSNs to be used to edit plant genomes [90–96]. More recently, CRISPR has emerged as a significant method for gene-specific genome editing [97]. The usefulness of CRISPR technology in cassava has received less attention than in other crops like rice [98]. The CRISPR/Cas9 technique has recently been used in several genome editing studies to increase the output of cassava, a drought-resistant crop, by adding disease resistance, quick blooming, herbicide tolerance, and decreased cyanide levels in the leaves and roots [99–101]. To generate the CRISPR/Cas9 technology capacity in the tropical staple cassava (*Manihot esculenta*), in two cultivars, the *Phytoene desaturase* (MePDS) gene was targeted with constructs containing gRNAs targeting two sequences within MePDS exon 13. PDS genes present in cassava were targeted using CRISPR/Cas9 technology. As previously observed, PDS encodes key enzymes involved in the carotenoid biosynthesis pathway, and a defect in the PDS gene causes dwarfism and albinism in *Arabidopsis* [102]. To avoid failure of the experiment of CRISPR/Cas9-targeted genome editing in cassava, they chose an alternative to the PDS gene. They used two gRNAs that targeted exon 13 in cassava cultivars 60444 and TME 204 to disrupt MePDS function. Minor (1 bp) nucleotide substitutions and/or deletions upstream of the 5' and/or downstream of the 3' targeted MePDS region were observed. According to the data presented, CRISPR/Cas9-mediated genome editing of cassava is highly efficient and relatively simple, resulting in multi-allelic mutations in both cultivars studied [100]. Cassava leaves and roots contain toxic amounts of the cyanogenic glycoside linamarin, and their consumption causes conversion of cyanogens to cyanide, resulting in poisoning of the body [103]. Thus, acyanogenic cassava cultivars are required to make cassava safe and edible [104]. Thus, the CRISPR/Cas9 system is used for genome editing in cassava, targeting mutagenesis of the MeCYP79D1 gene in exon 3 via *Agrobacterium*-mediated transformation. However, the cassava cyanide and linamarin were not completely eradicated by the MeCYP79D1 knockout. However, the analysis revealed that CRISPR/Cas9-mediated mutagenesis is a viable alternative approach for developing cassava plants with reduced cyanide content [105]. Another experiment using the CRISPR/Cas9 system for genome editing in cassava to mediate the starch biosynthetic genes and

generate novel varieties with high starch content crops. CRISPR/Cas9-mediated mutagenesis of the starch branching enzyme 2 results in the production of high-amylose cassava (SBE2) [106].

7. Transcriptomic Analysis in Cassava

Transcriptomics is concerned with the transcriptome, which refers to the entire set of RNA transcripts produced by an organism's genome in a cell or tissue. Depending on the experiment, the term may also be used to refer to all RNAs or just mRNA [107]. Dong and co-author, via transcriptomic analysis, created a 60-mer oligonucleotide microarray spanning 20,840 cassava transcripts, which was used to profile the gene expression in the apical shoots of cassava plants that had been exposed to low temperatures. A total of 508 differentially expressed genes (DEGs) were found. The research may contribute to a better understanding of how cassava genes are regulated under cold stress and suggest new strategies for genetically enhancing cold tolerance [108]. The transcriptomic analysis was performed on three cassava genotypes, i.e., MPER417-003, MECU72, and MTAI16, demonstrating a newly created cassava oligo-microarray, which is utilised for the analysis of cassava transcriptome in different cassava genotypes under drought stress. The analysis revealed that three genotypes exhibited a similar pattern of gene expression in both untreated and drought-stress-treated settings, as determined by a hierarchical clustering analysis of the 168 genes upregulated by drought stress and the 69 genes downregulated by it [109]. To understand the functions and regulatory mechanisms of melatonin in the delay of (Postharvest Physiological Deterioration) PPD of cassava, a comparative, physiological and transcriptomic analysis was carried out. They provided the possible molecular evidence through the transcriptomic analysis that was carried out between water and melatonin-treated tuberous roots during the process of PPD. Among the DEGs, 30 out of 34 genes encoding enzymes allied with ROS scavenging, including POD, SOD, APX, CAT, PrxR, were transcriptionally induced by melatonin at the early storage stage (6 h) during PPD [110]. Further, about 10,347 differentially expressed genes were identified via transcript analysis to investigate the distribution of the differential expression pattern during PPD (Postharvest Physiological Deterioration). The majority of genes showed upregulation throughout the PPD process. Collectively, our studies provide a fresh understanding of the network of transcriptional control throughout PPD development and suggest potential gene resources for delaying cassava PPD [111]. Another experiment was conducted on cassava to investigate the molecular mechanisms underlying tolerance to postharvest physiological deterioration (PPD). By the RNA-Seq method, the transcriptome changes in the tuberous roots were analysed for both the SC8 and RYG1 genes. These genes and pathways were essential to maintain the longer shelf life in cassava. In this transcriptomic experiment, it was shown that photosynthesis-related gene expression was higher in RYG1 than in SC8. This helps delay the deterioration of cassava roots during PPD [112]. A total of eight hub genes related to photosynthesis were also identified in this experiment [112]. Due to its unique feature of developing a massive underground storage root, cassava is considered one of the major food crops in most regions. Wilson and co-authors performed RNA-sequencing and developed an open-access, web-based interface for future examination of the data, providing molecular identities for 11 cassava organ/tissue types. In total, 31 expressed genes were identified and represented [113]. Ding and co-authors worked on integrating proteomic and transcriptomic analysis in the cassava crop, providing new insights into the post-transcriptional regulation of cassava drought stress. They analysed a total of 1242 and 715 differentially expressed genes (DEGs), together with 237 and 307 differentially expressed proteins (DEPs). These were identified in cassava roots and leaves via RNA-seq and iTRAQ techniques [114]. Furthermore, an analysis was carried out to determine the photoperiodic flowering pathway in cassava, including its associated transcription factor and downstream genes. An RNA-seq study was performed on cassava plants that had been cultivated in a field. From the analysis, two unique developmental changes take place in cassava that have been cultivated in a field and have been identified by the transcriptome analysis. The photoperiodic pathway regulators GI and CO, forigen and antiforigen FT and CEN/TFL1, transcription factor components of FAC (FD), and the FAC target genes AP1/FUL and SOC1 were among the genes investigated [115]. The transcriptomic

analysis of cassava tuberous root at two developmental stages (S1, S2) was carried out using 10x Genomics technology. An uncommon cell type, known as a Casparian strip, was observed using up-regulated genes and pseudotime analysis [116].

8. Metabolomics Analysis of Cassava

Metabolomics has been a constantly evolving field due to advancements in materials, equipment, and methodologies since the conceptual foundation of metabolite analysis as one of the “omics” approaches [117]. Metabolomics is a constantly evolving technology for the biochemical study of complex mixtures. It aims to enable objective, quantitative analysis of many metabolites in a biological material extract [118]. The recently developed, widely targeted metabolomic approach, based on liquid chromatography-mass spectrometry, allows for high-throughput metabolite detection and has been applied to several species [119]. In general, basic, secondary, and specialised metabolites can be distinguished in plants [120]. To increase the nutritional value of crops, it is crucial to investigate metabolic diversity and understand the genetic control of nutritional metabolites [121]. A bridge between genotypes and phenotypes, the metabolome is an effective method for determining the metabolic profiles of an interesting crop under specified conditions. Techniques for metabolome-assisted breeding have been developed and utilised to enhance the nutritive value of crops [122]. A metabolite test was carried out in 2019 by Laise Rosado-Souza et al., utilising a variety of methods. In this experiment, identical pools of frozen cassava are divided into two aliquots, one of which is examined in the fresh state, and the other after being freeze-dried. The protocols described in this article enable relative and/or absolute quantification of metabolites derived from various pathways, ranging from the central, highly abundant, and essential metabolites found in both plant and non-plant species, such as sugars and organic acids, to more specialised metabolites found in cassava, such as linamarin [123,124]. Cassava root metabolites contain a variety of nutrients that are essential for human health. Exploiting the variety of nutritional ingredients found in cassavas is critical for increasing their nutritional value. Metabolome is an effective method for determining the metabolic profiles of crops under specific conditions, and it is regarded as a link between genotypes and phenotypes. Metabolome-assisted breeding techniques have been developed and used to improve crop nutrition [122]. Cassava roots are a significant source of dietary and industrial carbohydrates, but they suffer significantly from PPD. In 2014, Uarrota and co-authors carried out metabolomic analysis on cassava roots during PPD. The analysis showed an increase in the metabolites like flavonoids, anthocyanins, carotenoids, reactive scavenging species, enzymes and phenolics until 3-5 days of postharvest [125]. To expand the knowledge on the composition of metabolites in the roots of three cassava cultivars, i.e., light-yellow-flesh, yellow-flesh and white-flesh, metabolomic analysis was performed. They also acquire knowledge on the genetic improvement of cassava’s high nutritional value. In total, 508 metabolites were identified in cassava roots, including 300 primary metabolites and 185 secondary metabolites [126]. Furthermore, an integrated metabolomic and transcriptomic analysis was also carried out using two different varieties, i.e., yellow and white Cassava tuberous roots, to reveal the mechanisms involved in colour formation at seven different stages. The experiment revealed coordinated regulation of 16 metabolites and 11 co-expression genes involved in anthocyanin biosynthesis, indicating that anthocyanin biosynthesis plays a vital role in yellow pigmentation in cassava tuberous roots. Two transcriptional factors were also identified, such as MeMYB5 and MeMYB42, which are associated with anthocyanin biosynthesis genes [127].

9. Proteomics Analysis of Cassava

In the late 1990s, the term “proteomics” was first coined [128]. Proteomics is a vital source of data about biological systems because it generates information about the interactions, functions, concentrations, and catalytic activities of proteins, which are the major structural and functional determinants of cells in living organisms [129]. It has a central role in systems biology as it complements the analysis of the metabolome and the transcriptome [130]. The identification of

proteins from various tissues and organs of rice and *Arabidopsis* was first reported in studies [131,132]. A large-scale proteomics study was carried out on the cassava storage root, and it was observed that over 2600 unique proteins were analysed. About 300 proteins showed significant abundance regulation during PPD, i.e., postharvest physiological deterioration [133]. Xuchu Wang and colleagues conducted a comparative proteomics experiment on cassava root at nine different developmental stages. About 154 proteins were identified that expressed differentially during root tuberization and starch accumulation [134]. An experiment was conducted to investigate the chloroplast proteome, which is responsible for drought stress in cassava leaves. Many drought-responsive proteins were discovered to be involved in ion transport, the antioxidant system, secondary metabolism, signal transduction, and gene regulation [135]. A research work was conducted to find out the effects of short-term exposure to extreme hot and cold temperatures on proteomics, photosynthesis and biochemical changes in plants grown in pots. The experiment was carried out on two cassava cultivars, namely Kasetsart 50 and Rayong 9. Proteomics analysis uncovered some intriguing differentially expressed proteins (DEPs), such as annexin, a multifunctional protein involved in the early stages of heat stress signalling [136].

10. Future Perspectives

Significant progress has been made in studying multi-omics in cassava over the last few decades. Many studies are currently focusing on the identification and characterisation of the cassava crop. That said, very few studies to date have focused on exploring the proteomics and metabolomics aspects of the crop. On the other hand, several studies have been carried out in depth, focusing on the development of various traits of cassava, as well as the transcriptomic analysis of the crop. This analysis has helped identify several regulatory genes, which will prove beneficial for future studies. The genome editing technologies are also playing a vital role in cassava crop improvement and better analysis of the crop variety development. The NGS technologies are continually advancing, with improvements to both the quantity and quality of reads. Although capturing the cassava genome remains difficult, it is expected that we will gradually find better solutions, as has been the case in previous studies. Large-scale publicly available genome and transcript sequence resources, as well as international genome sequencing streams, are expected to promote cassava genome sequence dissection in tandem with the development of bioinformatics approaches.

Author Contributions: Conceptualisation, K.P. and A.D.; writing—original draft preparation, V.A., B.J. and K.P.; writing—review and editing, K.P., A.D., R.A. and H.G.; supervision, K.P. and A.D. All authors have read and agreed to the published version of the manuscript.

Funding: This research received no external funding.

Data Availability Statement: No new data were created or analysed in this study. Data sharing is not applicable to this article.

Acknowledgments: The authors are thankful to the Director, ICAR-CTCRI, Trivandrum, Kerala, India, for their kind support in carrying out the research work. Research was supported by the Indian Council of Agricultural Research, Department of Agricultural Research and Education, Government of India.

Conflicts of Interest: The authors declare no conflicts of interest.

References

1. Beeching, J.R.; Marmey, P.; Gavalda, M.-C.; Noirot, M.; Haysom, H.R.; Hughes, M.A.; Charrier, A. An Assessment of Genetic Diversity within a Collection of Cassava (*Manihot Esculenta* Crantz) Germplasm Using Molecular Markers. *Ann. Bot.* **1993**, *72*, 515–520.
2. Hershey, C.H. Cassava Germplasm Resources. *Cassava Breed. A Multidiscip. Rev.* **1987**, 1–24.
3. Nations, F. and A.O. of the U. *Dimensions of Need: An Atlas of Food and Agriculture*; FAO, 1995;

4. Fregene, M.; Angel, F.; Gómez, R.; Rodríguez, F.; Chavarriaga, P.; Roca, W.; Tohme, J.; Bonierbale, M. A Molecular Genetic Map of Cassava (*Manihot Esculenta* Crantz). *Theor. Appl. Genet.* **1997**, *95*, 431–441.
5. Scott, G.J.; Rosegrant, M.W.; Ringler, C. *Roots and Tubers for the 21st Century: Trends, Projections, and Policy Options*; Intl Food Policy Res Inst, 2000; Vol. 31; ISBN 0896296350.
6. Kawano, K. The Role of Improved Cassava Cultivars in Generating Income for Better Farm Management. In Proceedings of the Proc. 6th Regional Workshop, held in Ho Chi Minh City, Vietnam; 2000; pp. 5–15.
7. Olsen, K.M. SNPs, SSRs and Inferences on Cassava's Origin. *Plant Mol. Biol.* **2004**, *56*, 517–526, doi:10.1007/s11103-004-5043-9.
8. Gowda, K.H.; Chauhan, V.B.S.; Bhagwat, A.; Pati, K.; Nedunchezhiyan, M.; Hegde, V. Plant Genetic Resources in Cassava: Collection, Characterization, Evaluation, Conservation, and Utilization. In *Vegetable Crops*; Springer, 2025; pp. 1431–1459.
9. Ceballos, H.; Iglesias, C.A.; Pérez, J.C.; Dixon, A.G.O. Cassava Breeding: Opportunities and Challenges. *Plant Mol. Biol.* **2004**, *56*, 503–516.
10. FAO Cassava for Food and Energy Security. *FAO Newsroom* 2008.
11. Ceballos, H.; Okogbenin, E.; Pérez, J.C.; López-Valle, L.A.B.; Debouck, D. Cassava BT - Root and Tuber Crops. In; Bradshaw, J.E., Ed.; Springer New York: New York, NY, 2010; pp. 53–96 ISBN 978-0-387-92765-7.
12. Lebot, V. *Tropical Root and Tuber Crops*; Cabi, 2019; ISBN 178924336X.
13. Marsh, J.I.; Hu, H.; Gill, M.; Batley, J.; Edwards, D. Crop Breeding for a Changing Climate: Integrating Phenomics and Genomics with Bioinformatics. *Theor. Appl. Genet.* **2021**, *134*, 1677–1690.
14. Aslam, Z.; Khattak, J.Z.K.; Ahmed, M.; Asif, M. A Role of Bioinformatics in Agriculture BT - Quantification of Climate Variability, Adaptation and Mitigation for Agricultural Sustainability. In; Ahmed, M., Stockle, C.O., Eds.; Springer International Publishing: Cham, 2017; pp. 413–434 ISBN 978-3-319-32059-5.
15. Xue, J.; Zhao, S.; Liang, Y.; Hou, C.; Wang, J. Bioinformatics and Its Applications in Agriculture. In Proceedings of the International Conference on Computer and Computing Technologies in Agriculture; Springer, 2007; pp. 977–982.
16. Kumar, S. *The Role of Bioinformatics in Agriculture*; CRC Press, 2014; ISBN 1771880031.
17. Schuster, S.C. Next-Generation Sequencing Transforms Today's Biology. *Nat. Methods* **2008**, *5*, 16–18, doi:10.1038/nmeth1156.
18. Singh, V.K.; Singh, A.K.; Chand, R.; Kushwaha, C. Role of Bioinformatics in Agriculture and Sustainable Development. *Int. J. Bioinforma. Res.* **2011**, *3*, 221–226, doi:dx.doi.org/10.9735/0975-3087.3.2.221-226.
19. Kushwaha, U.; Indra Deo, P.; Jaiswal, J.P.; Prasad, B. Role of Bioinformatics in Crop Improvement. *Glob. J. Sci. Front. Res.* **2017**, *17*, 13–23.
20. Zainal-Abidin, R.-A.; Ruhaizat-Ooi, I.-H.; Harun, S. A Review of Omics Technologies and Bioinformatics to Accelerate Improvement of Papaya Traits. *Agromony* **2021**, *11*.
21. Evenson, R.E.; Gollin, D. Assessing the Impact of the Green Revolution, 1960 to 2000. *Science (80-.)*. **2003**, *300*, 758–762, doi:10.1126/science.1078710.
22. Nassar, N.M.A. Cassava: Some Ecological and Physiological Aspects Related to Plant Breeding. *Gene Conserv.* **2004**, 229–245.
23. Colombo, C.; Second, G.; Charrier, A. Genetic Relatedness between Cassava (*Manihot Esculenta* Crantz) and *M. Flabellifolia* and *M. Peruviana* Based on Both RAPD and AFLP Markers. *Genet. Mol. Biol.* **2000**, *23*, 417–423.
24. CIAT *Ciat in Perspective 2001-2002*; 2002;
25. Manyong, V.M.; Dixon, A.G.O.; Makinde, K.O.; Bokanga, M.; Whyte, J. The Contribution of IITA-Improved Cassava to Food Security in Sub-Saharan Africa: An Impact Study. *Int. Inst. Trop. Agric. Ibadan, Niger.* **2000**.
26. Yilmaz, A.; Boydak, E. The Effects of Cobalt-60 Applications on Yield and Yield Components of Cotton (*Gossypium Barbadosense* L.). *Pakistan J. Biol. Sci.* **2006**, *9*, 2761–2769.
27. Moura, E.F.; Farias Neto, J.T. de; Sampaio, J.E.; Silva, D.T. da; Ramalho, G.F. Identification of Duplicates of Cassava Accessions Sampled on the North Region of Brazil Using Microsatellite Markers. *Acta Amaz.* **2013**, *43*, 461–468.

28. Agre, A.P.; Badara, G.; Adjatin, A.; Dansi, A.; Bathacharjee, R.; Rabbi, I.Y.; Dansi, M.; Gedil, M. Folk Taxonomy and Traditional Management of Cassava (*Manihot Esculenta* Crantz) Diversity in Southern and Central Benin. *Int. J. Innov. Sci. Res.* **2016**, *20*, 500–515.
29. Nadjiam, D.; Sarr, P.S.; Naitormbaïdé, M.; Mbaïguinam, J.M.M.; Guisse, A. Agro-Morphological Characterization of Cassava (*Manihot Esculenta* Crantz) Cultivars from Chad. *Agric. Sci.* **2016**, *7*, 479–492, doi:10.4236/as.2016.77049.
30. Rabbi, I.Y.; Kayondo, S.I.; Bauchet, G.; Yusuf, M.; Aghogho, C.I.; Ogunpaimo, K.; Uwugiaren, R.; Smith, I.A.; Peteti, P.; Agbona, A.; et al. Genome-Wide Association Analysis Reveals New Insights into the Genetic Architecture of Defensive, Agro-Morphological and Quality-Related Traits in Cassava. *Plant Mol. Biol.* **2022**, *109*, 195–213, doi:10.1007/s11103-020-01038-3.
31. Ray, S.; Maunsell, J.H.R. Different Origins of Gamma Rhythm and High-Gamma Activity in Macaque Visual Cortex. *PLOS Biol.* **2011**, *9*, e1000610.
32. Bhandari, H.R.; Bhanu, A.N.; Srivastava, K.; Singh, M.N.; Shreya; Hemantaranjan, A. Assessment of Genetic Diversity in Crop Plants - An Overview. *Adv. Plants Agric. Res.* **2017**, *7*, 279–286, doi:10.15406/apar.2017.07.00255.
33. Ayad, W.G.; Hodgkin, T.; Jaradat, A.; Rao, V.R. Molecular Genetic Techniques for Plant Genetic Resources: Report of an IPGRI Workshop, 9-11 October 1995, Rome, Italy. **1997**.
34. Barcaccia, G.; Albertini, E.; Rosellini, D.; Tavoletti, S.; Veronesi, F. Inheritance and Mapping of 2n-Egg Production in Diploid Alfalfa. *Genome* **2000**, *43*, 528–537, doi:10.1139/g00-017.
35. Fregene, M.A.; Suarez, M.; Mkumbira, J.; Kulembeka, H.; Ndedya, E.; Kulaya, A.; Mitchel, S.; Gullberg, U.; Rosling, H.; Dixon, A.G.O.; et al. Simple Sequence Repeat Marker Diversity in Cassava Landraces: Genetic Diversity and Differentiation in an Asexually Propagated Crop. *Theor. Appl. Genet.* **2003**, *107*, 1083–1093, doi:10.1007/s00122-003-1348-3.
36. Chavarriaga-Aguirre, P.P.; Maya, M.M.; Bonierbale, M.W.; Kresovich, S.; Fregene, M.A.; Tohme, J.; Kochert, G. Microsatellites in Cassava (*Manihot Esculenta* Crantz): Discovery, Inheritance and Variability. *Theor. Appl. Genet.* **1998**, *97*, 493–501, doi:10.1007/s001220050922.
37. Mba, R.E.C.; Stephenson, P.; Edwards, K.; Melzer, S.; Nkumbira, J.; Gullberg, U.; Apel, K.; Gale, M.; Tohme, J.; Fregene, M. Simple Sequence Repeat (SSR) Markers Survey of the Cassava (*Manihot Esculenta* Crantz) Genome: Towards an SSR-Based Molecular Genetic Map of Cassava. *Theor. Appl. Genet.* **2001**, *102*, 21–31.
38. Sraphet, S.; Boonchanawiwat, A.; Thanyasiriwat, T.; Boonseng, O.; Tabata, S.; Sasamoto, S.; Shirasawa, K.; Isobe, S.; Lightfoot, D.A.; Tangphatsornruang, S.; et al. SSR and EST-SSR-Based Genetic Linkage Map of Cassava (*Manihot Esculenta* Crantz). *Theor. Appl. Genet.* **2011**, *122*, 1161–1170, doi:10.1007/s00122-010-1520-5.
39. Tangphatsornruang, S.; Sraphet, S.; Singh, R.; Okogbenin, E.; Fregene, M.; Triwitayakorn, K. Development of Polymorphic Markers from Expressed Sequence Tags of *Manihot Esculenta* Crantz. *Mol. Ecol. Resour.* **2008**, *8*, 682–685, doi:10.1111/j.1471-8286.2007.02047.x.
40. Agarwal, M.; Shrivastava, N.; Padh, H. Advances in Molecular Marker Techniques and Their Applications in Plant Sciences. *Plant Cell Rep.* **2008**, *27*, 617–631, doi:10.1007/s00299-008-0507-z.
41. Primmer, C.R. From Conservation Genetics to Conservation Genomics. *Ann. N. Y. Acad. Sci.* **2009**, *1162*, 357–368, doi:https://doi.org/10.1111/j.1749-6632.2009.04444.x.
42. Marmey, P.; Beeching, J.R.; Hamon, S.; Charrier, A. Evaluation of Cassava (*Manihot Esculenta* Crantz) Germplasm Collections Using RAPD Markers. *Euphytica* **1993**, *74*, 203–209, doi:10.1007/BF00040402.
43. Wong, H.-L.; Yeoh, H.-H.; Lim, S.-H.; Lionel Looi, K.-C. Design of Primers for Rapid Analyses of Cassava, *Manihot Esculenta*. *Phytochemistry* **1997**, *46*, 805–810, doi:https://doi.org/10.1016/S0031-9422(97)00394-4.
44. Colombo, C.; Second, G.; Valle, T.L.; Charrier, A. Genetic Diversity Characterization of Cassava Cultivars (*Manihot Esculenta* Crantz): I) RAPD Markers. *Genet. Mol. Biol.* **1999**, *21*.
45. Roa, A.C.; Maya, M.M.; Duque, M.C.; Tohme, J.; Allem, A.C.; Bonierbale, M.W. AFLP Analysis of Relationships among Cassava and Other *Manihot* Species. *Theor. Appl. Genet.* **1997**, *95*, 741–750, doi:10.1007/s001220050620.

46. Elias, M.; Panaud, O.; Robert, T. Assessment of Genetic Variability in a Traditional Cassava (*Manihot Esculenta* Crantz) Farming System, Using AFLP Markers. *Heredity (Edinb)*. **2000**, *85*, 219–230, doi:10.1046/j.1365-2540.2000.00749.x.
47. Asante, I.K.; Offei, S.K. RAPD-Based Genetic Diversity Study of Fifty Cassava (*Manihot Esculenta* Crantz) Genotypes. *Euphytica* **2003**, *131*, 113–119, doi:10.1023/A:1023056313776.
48. Syvänen, A.-C. Accessing Genetic Variation: Genotyping Single Nucleotide Polymorphisms. *Nat. Rev. Genet.* **2001**, *2*, 930–942, doi:10.1038/35103535.
49. Ferguson, M.; Rabbi, I.; Kim, D.-J.; Gedil, M.; Lopez-Lavalle, L.A.B.; Okogbenin, E. Molecular Markers and Their Application to Cassava Breeding: Past, Present and Future. *Trop. Plant Biol.* **2012**, *5*, 95–109, doi:10.1007/s12042-011-9087-0.
50. Amelework, A.B.; Bairu, M.W. Advances in Genetic Analysis and Breeding of Cassava (*Manihot Esculenta* Crantz): A Review. *Plants* **2022**, *11*.
51. Colombo, C.; Second, G.; Charrier, A. Diversity within American Cassava Germ Plasm Based on RAPD Markers. *Genet. Mol. Biol.* **2000**, *23*, 189–199.
52. Herzberg, F.; Mahungu, N.M.; Mignouna, J.; Kullaya, A. Assessment of Genetic Diversity of Local Varieties of Cassava in Tanzania Using Molecular Markers. *African Crop Sci. J.* **2004**, *12*, 171–187.
53. Zaldivar, M.E.; Rocha, O.J.; Aguilar, G.; Castro, L.; Castro, E.; Barrantes, R. Genetic Variation of Cassava (*Manihot Esculenta* Crantz) Cultivated by Chibchan Amerindians of Costa Rica. *Econ. Bot.* **2004**, *58*, 204–213.
54. Elias, M.; Mühlen, G.S.; McKey, D.; Roa, A.C.; Tohme, J. Genetic Diversity of Traditional South American Landraces of Cassava (*Manihot Esculenta* Crantz): An Analysis Using Microsatellites. *Econ. Bot.* **2004**, *58*, 242–256.
55. Montero-Rojas, M.; Correa, A.M.; 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*, plr010, doi:10.1093/aobpla/plr010.
56. Esuma, W.; Kawuki, R.S.; Herselman, L.; Labuschagne, M.T. Stability and Genotype by Environment Interaction of Provitamin A Carotenoid and Dry Matter Content in Cassava in Uganda. *Breed. Sci.* **2016**, *66*, 434–443, doi:10.1270/jsbbs.16004.
57. Turyagyenda, L.F.; Kizito, E.B.; Ferguson, M.E.; Baguma, Y.; Harvey, J.W.; Gibson, P.; Wanjala, B.W.; Osiru, D.S.O. Genetic Diversity among Farmer-Preferred Cassava Landraces in Uganda. *African Crop Sci. J.* **2012**, *20*, 15–30.
58. Kawuki, R.S.; Herselman, L.; Labuschagne, M.T.; Nzuki, I.; Ralimanana, I.; Bidiaka, M.; Kanyange, M.C.; Gashaka, G.; Masumba, E.; Mkamilo, G. Genetic Diversity of Cassava (*Manihot Esculenta* Crantz) Landraces and Cultivars from Southern, Eastern and Central Africa. *Plant Genet. Resour.* **2013**, *11*, 170–181.
59. Beovides, Y.; Fregene, M.; Gutiérrez, J.P.; Milián, M.D.; Coto, O.; Buitrago, C.; Cruz, J.A.; Ruiz, E.; Basail, M.; Rayas, A.; et al. Molecular Diversity of Cuban Cassava (*Manihot Esculenta* Crantz) Cultivars Assessed by Simple Sequences Repeats (SSR) [Diversité Moléculaire de Cultivars Cubains de Manioc (*Manihot Esculenta* Crantz) Analysés Par Séquences Simples Répétées (SSR)]. *Biotechnol. Agron. Soc. Environ.* **2015**, *19*, 364–377.
60. Tiago, A. V.; Rossi, A.A.B.; Tiago, P. V.; Carpejani, A.A.; Silva, B.M.; Hoogerheide, E.S.S.; Yamashita, O.M. Genetic Diversity in Cassava Landraces Grown on Farms in Alta Floresta-MT, Brazil. *Genet. Mol. Res* **2016**, *15*, 1–10.
61. Alves-Pereira, A.; Clement, C.R.; Picanço-Rodrigues, D.; Veasey, E.A.; Dequigiovanni, G.; Ramos, S.L.F.; Pinheiro, J.B.; Zucchi, M.I. Patterns of Nuclear and Chloroplast Genetic Diversity and Structure of Manioc along Major Brazilian Amazonian Rivers. *Ann. Bot.* **2018**, *121*, 625–639, doi:10.1093/aob/mcx190.
62. de Albuquerque, H.Y.G.; Carmo, C.D. do; Brito, A.C.; Oliveira, E.J. de Genetic Diversity of *Manihot Esculenta* Crantz Germplasm Based on Single-nucleotide Polymorphism Markers. *Ann. Appl. Biol.* **2018**, *173*, 271–284.
63. Pedri, E.C.M.; Hoogerheide, E.S.S.; Tiago, A. V.; Cardoso, E. dos S.; Pinto, J.M.A.; Santos, L.L.; Yamashita, O.M.; Rossi, A.A.B. Genetic Diversity of Cassava Landraces Cultivated in Northern Mato Grosso State, Brazil, Using Microsatellite Markers. *Genet. Mol. Res* **2019**, *18*.

64. Tiago, A. V.; Hoogerheide, E.S.S.; Pedri, E.C.M.; Rossi, F.S.; Cardoso, E.S.; Pinto, J.M.A.; Pena, G.F.; Rossi, A.A.B. Genetic Diversity and Population Structure of Cassava Ethno-Varieties Grown in Six Municipalities in the State of Mato Grosso, Brazil. *Gene Conserv.* **2019**, *18*.
65. Kamanda, I.; Blay, E.T.; Asante, I.K.; Danquah, A.; Ifie, B.E.; Parkes, E.; Kulakow, P.; Rabbi, I.; Conteh, A.; Kamara, J.S. Genetic Diversity of Provitamin-A Cassava (*Manihot Esculenta* Crantz) in Sierra Leone. *Genet. Resour. Crop Evol.* **2020**, *67*, 1193–1208.
66. Prempeh, R.N.A.; Manu-aduening, J.A.; Quain, M.D.; Asante, I.K.; Offei, S.K.; Danquah, E.Y. Assessment of Genetic Diversity among Cassava Landraces Using Single Nucleotide Polymorphic Markers. *African J. Biotechnol.* **2020**, *19*, 383–391, doi:10.5897/AJB2018.16420.
67. Adjebeng-Danquah, J.; Asante, I.K.; Manu-Aduening, J.; Agyare, R.Y.; Gracen, V.E.; Offei, S.K. Genotypic Variability in Some Morpho-Physiological Traits in Different Environments and Their Relationship with Cassava (*Manihot Esculenta* Crantz) Root Yield. *Int. J. Agron.* **2020**, *2020*, 5871351, doi:https://doi.org/10.1155/2020/5871351.
68. Karim, K.Y.; Ifie, B.; Dzidzienyo, D.; Danquah, E.Y.; Blay, E.T.; Whyte, J.B.A.; Kulakow, P.; Rabbi, I.; Parkes, E.; Omoigui, L. Genetic Characterization of Cassava (*Manihot Esculenta* Crantz) Genotypes Using Agro-Morphological and Single Nucleotide Polymorphism Markers. *Physiol. Mol. Biol. Plants* **2020**, *26*, 317–330.
69. Aizat, W.M.; Ismail, I.; Noor, N.M. Recent Development in Omics Studies. *Adv. Exp. Med. Biol.* **2018**, *1102*, 1–9, doi:10.1007/978-3-319-98758-3_1.
70. Muthamilarasan, M.; Singh, N.K.; Prasad, M. Multi-Omics Approaches for Strategic Improvement of Stress Tolerance in Underutilized Crop Species: A Climate Change Perspective. *Adv. Genet.* **2019**, *103*, 1–38, doi:10.1016/bs.adgen.2019.01.001.
71. Salt, D.E.; Baxter, I.; Lahner, B. Ionomics and the Study of the Plant Ionome. *Annu. Rev. Plant Biol.* **2008**, *59*, 709–733, doi:10.1146/annurev.arplant.59.032607.092942.
72. Houle, D.; Govindaraju, D.R.; Omholt, S. Phenomics: The next Challenge. *Nat. Rev. Genet.* **2010**, *11*, 855–866, doi:10.1038/nrg2897.
73. Talukdar, D.; Sinjushin, A. Cytogenomics and Mutagenomics in Plant Functional Biology and Breeding BT - PlantOmics: The Omics of Plant Science. In: Barh, D., Khan, M.S., Davies, E., Eds.; Springer India: New Delhi, 2015; pp. 113–156 ISBN 978-81-322-2172-2.
74. Wu, S.; Ning, F.; Zhang, Q.; Wu, X.; Wang, W. Enhancing Omics Research of Crop Responses to Drought under Field Conditions. *Front. Plant Sci.* **2017**, *8*, 174, doi:10.3389/fpls.2017.00174.
75. Amer, B.; Baidoo, E.E.K. Omics-Driven Biotechnology for Industrial Applications. *Front. Bioeng. Biotechnol.* **2021**, *9*, 613307, doi:10.3389/fbioe.2021.613307.
76. Yang, Y.; Saand, M.A.; Huang, L.; Abdelaal, W.B.; Zhang, J.; Wu, Y.; Li, J.; Sirohi, M.H.; Wang, F. Applications of Multi-Omics Technologies for Crop Improvement. *Front. Plant Sci.* **2021**, *12*, 563953, doi:10.3389/fpls.2021.563953.
77. Govindaraj, M.; Vetriventhan, M.; Srinivasan, M. Importance of Genetic Diversity Assessment in Crop Plants and Its Recent Advances: An Overview of Its Analytical Perspectives. *Genet. Res. Int.* **2015**, *2015*, 431487, doi:10.1155/2015/431487.
78. Isobe, S.; Shirasawa, K.; Hirakawa, H. Current Status in Whole Genome Sequencing and Analysis of *Ipomoea* Spp. *Plant Cell Rep.* **2019**, *38*, 1365–1371, doi:10.1007/s00299-019-02464-4.
79. Riechmann, J.L.; Heard, J.; Martin, G.; Reuber, L.; Jiang, C.-Z.; Keddie, J.; Adam, L.; Pineda, O.; Ratcliffe, O.J.; Samaha, R.R.; et al. Arabidopsis Transcription Factors: Genome-Wide Comparative Analysis Among Eukaryotes. *Science (80-.)*. **2000**, *290*, 2105–2110, doi:10.1126/science.290.5499.2105.
80. Prochnik, S.; Marri, P.R.; Desany, B.; Rabinowicz, P.D.; Kodira, C.; Mohiuddin, M.; Rodriguez, F.; Fauquet, C.; Tohme, J.; Harkins, T.; et al. The Cassava Genome: Current Progress, Future Directions. *Trop. Plant Biol.* **2012**, *5*, 88–94, doi:10.1007/s12042-011-9088-z.
81. Daniell, H.; Wurdack, K.J.; Kanagaraj, A.; Lee, S.-B.; Saski, C.; Jansen, R.K. The Complete Nucleotide Sequence of the Cassava (*Manihot Esculenta*) Chloroplast Genome and the Evolution of AtpF in Malpighiales: RNA Editing and Multiple Losses of a Group II Intron. *Theor. Appl. Genet.* **2008**, *116*, 723–737, doi:10.1007/s00122-007-0706-y.

82. Goodstein, D.M.; Shu, S.; Howson, R.; Neupane, R.; Hayes, R.D.; Fazo, J.; Mitros, T.; Dirks, W.; Hellsten, U.; Putnam, N.; et al. Phytozome: A Comparative Platform for Green Plant Genomics. *Nucleic Acids Res.* **2012**, *40*, D1178-86, doi:10.1093/nar/gkr944.
83. Sakurai, T.; Mochida, K.; Yoshida, T.; Akiyama, K.; Ishitani, M.; Seki, M.; Shinozaki, K. Genome-Wide Discovery and Information Resource Development of DNA Polymorphisms in Cassava. *PLoS One* **2013**, *8*, e74056, doi:10.1371/journal.pone.0074056.
84. Wang, W.; Feng, B.; Xiao, J.; Xia, Z.; Zhou, X.; Li, P.; Zhang, W.; Wang, Y.; Möller, B.L.; Zhang, P.; et al. Cassava Genome from a Wild Ancestor to Cultivated Varieties. *Nat. Commun.* **2014**, *5*, 5110, doi:10.1038/ncomms6110.
85. Bredeson, J. V.; Lyons, J.B.; Prochnik, S.E.; Wu, G.A.; Ha, C.M.; Edsinger-Gonzales, E.; Grimwood, J.; Schmutz, J.; Rabbi, I.Y.; Egesi, C. Sequencing Wild and Cultivated Cassava and Related Species Reveals Extensive Interspecific Hybridization and Genetic Diversity. *Nat. Biotechnol.* **2016**, *34*, 562–570.
86. Hu, W.; Ji, C.; Shi, H.; Liang, Z.; Ding, Z.; Ye, J.; Ou, W.; Zhou, G.; Tie, W.; Yan, Y.; et al. Allele-Defined Genome Reveals Biallelic Differentiation during Cassava Evolution. *Mol. Plant* **2021**, *14*, 851–854.
87. Zhang, Y.; Ma, X.; Xie, X.; Liu, Y.-G. Chapter Eight - CRISPR/Cas9-Based Genome Editing in Plants. In *Gene Editing in Plants*; Weeks, D.P., Yang, B.B.T.-P. in M.B. and T.S., Eds.; Academic Press, 2017; Vol. 149, pp. 133–150 ISBN 1877-1173.
88. Chen, K.; Wang, Y.; Zhang, R.; Zhang, H.; Gao, C. CRISPR/Cas Genome Editing and Precision Plant Breeding in Agriculture. *Annu. Rev. Plant Biol.* **2019**, *70*, 667–697.
89. Symington, L.S.; Gautier, J. Double-Strand Break End Resection and Repair Pathway Choice. *Annu. Rev. Genet.* **2011**, *45*, 247–271, doi:10.1146/annurev-genet-110410-132435.
90. Lloyd, A.; Plaisier, C.L.; Carroll, D.; Drews, G.N. Targeted Mutagenesis Using Zinc-Finger Nucleases in Arabidopsis. *Proc. Natl. Acad. Sci. U. S. A.* **2005**, *102*, 2232–2237, doi:10.1073/pnas.0409339102.
91. Zhang, F.; Maeder, M.L.; Unger-Wallace, E.; Hoshaw, J.P.; Reyon, D.; Christian, M.; Li, X.; Pierick, C.J.; Dobbs, D.; Peterson, T.; et al. High Frequency Targeted Mutagenesis in Arabidopsis Thaliana Using Zinc Finger Nucleases. *Proc. Natl. Acad. Sci. U. S. A.* **2010**, *107*, 12028–12033, doi:10.1073/pnas.0914991107.
92. Zhang, F.; Voytas, D.F. Targeted Mutagenesis in Arabidopsis Using Zinc-Finger Nucleases. *Methods Mol. Biol.* **2011**, *701*, 167–177, doi:10.1007/978-1-61737-957-4_9.
93. Petolino, J.F. Genome Editing in Plants via Designed Zinc Finger Nucleases. *Vitr. Cell. Dev. Biol. Plant J. Tissue Cult. Assoc.* **2015**, *51*, 1–8, doi:10.1007/s11627-015-9663-3.
94. Kumar, V.; Jain, M. The CRISPR-Cas System for Plant Genome Editing: Advances and Opportunities. *J. Exp. Bot.* **2015**, *66*, 47–57, doi:10.1093/jxb/eru429.
95. Smith, J.; Bibikova, M.; Whitby, F.G.; Reddy, A.R.; Chandrasegaran, S.; Carroll, D. Requirements for Double-Strand Cleavage by Chimeric Restriction Enzymes with Zinc Finger DNA-Recognition Domains. *Nucleic Acids Res.* **2000**, *28*, 3361–3369, doi:10.1093/nar/28.17.3361.
96. Bibikova, M.; Golic, M.; Golic, K.G.; Carroll, D. Targeted Chromosomal Cleavage and Mutagenesis in Drosophila Using Zinc-Finger Nucleases. *Genetics* **2002**, *161*, 1169–1175, doi:10.1093/genetics/161.3.1169.
97. Ghosh, D.; Kumar, A.; Sinha, N. Targeted Genome Editing: A New Era in Molecular Biology. In *Advances in animal genomics*; Elsevier, 2021; pp. 75–89.
98. Juma, B.S.; Mweu, C.; Piero, M.; Mbinda, W. CRISPR/Cas Genome Editing: A Frontier for Transforming Precision Cassava Breeding. *African J. Biotechnol.* **2021**, *20*, 237–250.
99. Mehta, D.; Stürchler, A.; Anjanappa, R.B.; Zaidi, S.S.-A.; Hirsch-Hoffmann, M.; Grussem, W.; Vanderschuren, H. Linking CRISPR-Cas9 Interference in Cassava to the Evolution of Editing-Resistant Geminiviruses. *Genome Biol.* **2019**, *20*, 80, doi:10.1186/s13059-019-1678-3.
100. Odipio, J.; Alicai, T.; Ingelbrecht, I.; Nusinow, D.A.; Bart, R.; Taylor, N.J. Efficient CRISPR/Cas9 Genome Editing of Phytoene Desaturase in Cassava. *Front. Plant Sci.* **2017**, *Volume 8*-.
101. Gomez, M.A.; Berkoff, K.C.; Gill, B.K.; Iavarone, A.T.; Lieberman, S.E.; Ma, J.M.; Schultink, A.; Karavolias, N.G.; Wyman, S.K.; Chauhan, R.D. CRISPR-Cas9-Mediated Knockout of CYP79D1 and CYP79D2 in Cassava Attenuates Toxic Cyanogen Production. *Front. Plant Sci.* **2023**, *13*, 1079254.

102. Qin, G.; Gu, H.; Ma, L.; Peng, Y.; Deng, X.W.; Chen, Z.; Qu, L.-J. Disruption of Phytoene Desaturase Gene Results in Albino and Dwarf Phenotypes in Arabidopsis by Impairing Chlorophyll, Carotenoid, and Gibberellin Biosynthesis. *Cell Res.* **2007**, *17*, 471–482, doi:10.1038/cr.2007.40.
103. Kashala-Abotnes, E.; Okitundu, D.; Mumba, D.; Boivin, M.J.; Tylleskär, T.; Tshala-Katumbay, D. Konzo: A Distinct Neurological Disease Associated with Food (Cassava) Cyanogenic Poisoning. *Brain Res. Bull.* **2019**, *145*, 87–91, doi:https://doi.org/10.1016/j.brainresbull.2018.07.001.
104. Ani, D.; Ojila, H.; Abu, O. Profitability of Cassava Processing: A Case Study of Otukpo Lga, Benue State, Nigeria. *Sustain Food Prod* **2019**, *6*, 12–23.
105. Juma, B.S.; Mukami, A.; Mweu, C.; Ngugi, M.P.; Mbinda, W. Targeted Mutagenesis of the CYP79D1 Gene via CRISPR/Cas9-Mediated Genome Editing Results in Lower Levels of Cyanide in Cassava. *Front. Plant Sci.* **2022**, *13*, 1009860, doi:10.3389/fpls.2022.1009860.
106. Luo, S.; Ma, Q.; Zhong, Y.; Jing, J.; Wei, Z.; Zhou, W.; Lu, X.; Tian, Y.; Zhang, P. Editing of the Starch Branching Enzyme Gene SBE2 Generates High-Amylose Storage Roots in Cassava. *Plant Mol. Biol.* **2022**, *108*, 429–442, doi:10.1007/s11103-021-01215-y.
107. Wang, Z.; Gerstein, M.; Snyder, M. RNA-Seq: A Revolutionary Tool for Transcriptomics. *Nat. Rev. Genet.* **2009**, *10*, 57–63, doi:10.1038/nrg2484.
108. An, D.; Yang, J.; Zhang, P. Transcriptome Profiling of Low Temperature-Treated Cassava Apical Shoots Showed Dynamic Responses of Tropical Plant to Cold Stress. *BMC Genomics* **2012**, *13*, 64, doi:10.1186/1471-2164-13-64.
109. Utsumi, Y.; Tanaka, M.; Morosawa, T.; Kurotani, A.; Yoshida, T.; Mochida, K.; Matsui, A.; Umemura, Y.; Ishitani, M.; Shinozaki, K.; et al. Transcriptome Analysis Using a High-Density Oligomicroarray under Drought Stress in Various Genotypes of Cassava: An Important Tropical Crop. *DNA Res. an Int. J. rapid Publ. reports genes genomes* **2012**, *19*, 335–345, doi:10.1093/dnares/dss016.
110. Hu, W.; Yang, H.; Yan, Y.; Wei, Y.; Tie, W.; Ding, Z.; Zuo, J.; Peng, M.; Li, K. Genome-Wide Characterization and Analysis of BZIP Transcription Factor Gene Family Related to Abiotic Stress in Cassava. *Sci. Rep.* **2016**, *6*, 22783.
111. Yan, Y.; Zhao, S.; Ding, Z.; Tie, W.; Hu, W. Comparative Transcriptomic Analysis of Storage Roots in Cassava During Postharvest Physiological Deterioration. *Plant Mol. Biol. Report.* **2021**, *39*, 607–616, doi:10.1007/s11105-020-01274-3.
112. Li, R.; Yuan, S.; Zhou, Y.; Wang, S.; Zhou, Q.; Ding, Z.; Wang, Y.; Yao, Y.; Liu, J.; Guo, J. Comparative Transcriptome Profiling of Cassava Tuberous Roots in Response to Postharvest Physiological Deterioration. *Int. J. Mol. Sci.* **2023**, *24*.
113. Wilson, M.C.; Mutka, A.M.; Hummel, A.W.; Berry, J.; Chauhan, R.D.; Vijayaraghavan, A.; Taylor, N.J.; Voytas, D.F.; Chitwood, D.H.; Bart, R.S. Gene Expression Atlas for the Food Security Crop Cassava. *New Phytol.* **2017**, *213*, 1632–1641, doi:https://doi.org/10.1111/nph.14443.
114. Ding, Z.; Fu, L.; Tie, W.; Yan, Y.; Wu, C.; Hu, W.; Zhang, J. Extensive Post-Transcriptional Regulation Revealed by Transcriptomic and Proteomic Integrative Analysis in Cassava under Drought. *J. Agric. Food Chem.* **2019**, *67*, 3521–3534.
115. Behnam, B.; Higo, A.; Yamaguchi, K.; Tokunaga, H.; Utsumi, Y.; Selvaraj, M.G.; Seki, M.; Ishitani, M.; Ceballos, H.; Lopez-Lavalle, L.A.B.; et al. Field-Transcriptome Analyses Reveal Developmental Transitions during Flowering in Cassava (*Manihot Esculenta* Crantz). *Plant Mol. Biol.* **2021**, *106*, 285–296, doi:10.1007/s11103-021-01149-5.
116. Song, J.; Fan, B.; Shao, X.; Zang, Y.; Wang, D.; Min, Y. Single-Cell Transcriptome Sequencing Atlas of Cassava Tuberous Root. *Front. Plant Sci.* **2023**, *Volume 13*.
117. Oliver, S.G.; Winson, M.K.; Kell, D.B.; Baganz, F. Systematic Functional Analysis of the Yeast Genome. *Trends Biotechnol.* **1998**, *16*, 373–378, doi:10.1016/s0167-7799(98)01214-1.
118. Hall, R.D.; Hardy, N.W. Practical Applications of Metabolomics in Plant Biology. In *Plant metabolomics: Methods and protocols*; Springer, 2012; pp. 1–10.
119. Chen, H.; Cui, F.; Li, H.; Sheng, J.; Lv, J. Metabolic Changes during the Pu-erh Tea Pile-fermentation Revealed by a Liquid Chromatography Tandem Mass-spectrometry-based Metabolomics Approach. *J. Food Sci.* **2013**, *78*, C1665–C1672.

120. Fernie, A.R.; Pichersky, E. Focus Issue on Metabolism: Metabolites, Metabolites Everywhere. *Plant Physiol.* **2015**, *169*, 1421–1423.
121. Fang, C.; Fernie, A.R.; Luo, J. Exploring the Diversity of Plant Metabolism. *Trends Plant Sci.* **2019**, *24*, 83–98.
122. Fang, C.; Luo, J.; Wang, S. The Diversity of Nutritional Metabolites: Origin, Dissection, and Application in Crop Breeding. *Front. Plant Sci.* **2019**, *10*, 1028.
123. Rosado-Souza, L.; David, L.C.; Drapal, M.; Fraser, P.D.; Hofmann, J.; Klemens, P.A.W.; Ludewig, F.; Neuhaus, H.E.; Obata, T.; Perez-Fons, L.; et al. Cassava Metabolomics and Starch Quality. *Curr. Protoc. plant Biol.* **2019**, *4*, e20102, doi:10.1002/cppb.20102.
124. Wang, S.; Alseekh, S.; Fernie, A.R.; Luo, J. The Structure and Function of Major Plant Metabolite Modifications. *Mol. Plant* **2019**, *12*, 899–919, doi:https://doi.org/10.1016/j.molp.2019.06.001.
125. Uarrota, V.G.; Moresco, R.; Coelho, B.; Nunes, E. da C.; Peruch, L.A.M.; Neubert, E. de O.; Rocha, M.; Maraschin, M. Metabolomics Combined with Chemometric Tools (PCA, HCA, PLS-DA and SVM) for Screening Cassava (*Manihot Esculenta* Crantz) Roots during Postharvest Physiological Deterioration. *Food Chem.* **2014**, *161*, 67–78, doi:10.1016/j.foodchem.2014.03.110.
126. Xiao, L.; Cao, S.; Shang, X.; Xie, X.; Zeng, W.; Lu, L.; Kong, Q.; Yan, H. Metabolomic and Transcriptomic Profiling Reveals Distinct Nutritional Properties of Cassavas with Different Flesh Colors. *Food Chem. Mol. Sci.* **2021**, *2*, 100016, doi:10.1016/j.fochms.2021.100016.
127. Fu, L.; Ding, Z.; Tie, W.; Yang, J.; Yan, Y.; Hu, W. Integrated Metabolomic and Transcriptomic Analyses Reveal Novel Insights of Anthocyanin Biosynthesis on Color Formation in Cassava Tuberous Roots. *Front. Nutr.* **2022**, *9*, 842693, doi:10.3389/fnut.2022.842693.
128. James, P. Protein Identification in the Post-Genome Era: The Rapid Rise of Proteomics. *Q. Rev. Biophys.* **1997**, *30*, 279–331, doi:10.1017/s0033583597003399.
129. Baginsky, S. Plant Proteomics: Concepts, Applications, and Novel Strategies for Data Interpretation. *Mass Spectrom. Rev.* **2009**, *28*, 93–120, doi:10.1002/mas.20183.
130. Wu, L.; Hwang, S.-I.; Rezaul, K.; Lu, L.J.; Mayya, V.; Gerstein, M.; Eng, J.K.; Lundgren, D.H.; Han, D.K. Global Survey of Human T Leukemic Cells by Integrating Proteomics and Transcriptomics Profiling. *Mol. Cell. Proteomics* **2007**, *6*, 1343–1353, doi:10.1074/mcp.M700017-MCP200.
131. Komatsu, S.; Kajiwara, H.; Hirano, H. A Rice Protein Library: A Data-File of Rice Proteins Separated by Two-Dimensional Electrophoresis. *Theor. Appl. Genet.* **1993**, *86*, 935–942, doi:10.1007/BF00211044.
132. Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A. Separation and Characterization of Arabidopsis Thaliana Proteins by Two-Dimensional Gel Electrophoresis. *Electrophoresis* **1995**, *16*, 423–430, doi:10.1002/elps.1150160169.
133. Vanderschuren, H.; Nyaboga, E.; Poon, J.S.; Baerenfaller, K.; Grossmann, J.; Hirsch-Hoffmann, M.; Kirchgessner, N.; Nanni, P.; Gruissem, W. Large-Scale Proteomics of the Cassava Storage Root and Identification of a Target Gene to Reduce Postharvest Deterioration. *Plant Cell* **2014**, *26*, 1913–1924, doi:10.1105/tpc.114.123927.
134. Wang, X.; Chang, L.; Tong, Z.; Wang, D.; Yin, Q.; Wang, D.; Jin, X.; Yang, Q.; Wang, L.; Sun, Y.; et al. Proteomics Profiling Reveals Carbohydrate Metabolic Enzymes and 14-3-3 Proteins Play Important Roles for Starch Accumulation during Cassava Root Tuberization. *Sci. Rep.* **2016**, *6*, 19643, doi:10.1038/srep19643.
135. Chang, L.; Wang, L.; Peng, C.; Tong, Z.; Wang, D.; Ding, G.; Xiao, J.; Guo, A.; Wang, X. The Chloroplast Proteome Response to Drought Stress in Cassava Leaves. *Plant Physiol. Biochem. PPB* **2019**, *142*, 351–362, doi:10.1016/j.plaphy.2019.07.025.
136. Santanoo, S.; Vongcharoen, K.; Banterng, P.; Vorasoot, N.; Jogloy, S.; Roytrakul, S.; Theerakulpisut, P. Physiological and Proteomic Responses of Cassava to Short-Term Extreme Cool and Hot Temperature. *Plants (Basel, Switzerland)* **2022**, *11*, doi:10.3390/plants11172307.

Disclaimer/Publisher's Note: The statements, opinions and data contained in all publications are solely those of the individual author(s) and contributor(s) and not of MDPI and/or the editor(s). MDPI and/or the editor(s) disclaim responsibility for any injury to people or property resulting from any ideas, methods, instructions or products referred to in the content.