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Research Insights into the Genetic Regulation of Root Architecture in Sweet Potato

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Abstract This study offers an in-depth analysis of the genetic regulation of root architecture in sweet potato (*Ipomoea batatas*), focusing on key transcriptional and post-transcriptional mechanisms that govern storage root development. Through dynamic network biomarker analysis, transcription factors such as *IbNAC083* and *IbMYB73* were identified as critical regulators of root initiation and stress response. In addition, the study highlights developmentally regulated genes involved in root thickening, including the receptor-like kinase SRF6, as well as key pathways like anthocyanin biosynthesis mediated by *IbMYB1-2* and tuberous root initiation controlled by *IbMADS1*. RNA-Seq and iTRAQ analyses revealed several vital pathways, such as starch biosynthesis and auxin response factor-mediated differentiation between storage and normal roots. This research provides a valuable foundation for future biotechnological approaches to enhance sweet potato yield and resilience, thereby advancing sustainable cultivation practices.

Keywords Sweet potato (*Ipomoea batatas* L.); Root architecture; Transcription factors; Storage root development; Genetic regulation; Auxin response

1 Introduction

Root architecture plays a crucial role in the overall performance and yield of sweet potato (*Ipomoea batatas*), a staple food crop globally recognized for its nutritional and economic value. The root system's structure, including the development of storage roots, directly impacts the plant's ability to absorb water and nutrients, which are essential for growth and productivity. Efficient root systems can enhance the plant's resilience to environmental stresses, thereby improving yield stability and quality (Joshi et al., 2016; He et al., 2021; Wang et al., 2023). The formation and development of storage roots, which are the primary edible parts of the sweet potato, are particularly significant as they determine the crop's market value and utility (Dong et al., 2019; Tang et al., 2020).

The genetic regulation of root system architecture is a complex process involving numerous genes and regulatory networks. Understanding these genetic mechanisms is vital for improving sweet potato varieties through breeding and biotechnological approaches. Key transcription factors and genes, such as *IbNAC083*, *IbMYB73*, and *IbMADS1*, have been identified as critical regulators in the initiation and development of storage roots (Ku et al., 2008; He et al., 2021; Wang et al., 2023). These genetic elements influence various physiological processes, including hormone signaling, cell division, and metabolic pathways, which collectively shape the root architecture (Tanaka et al., 2005; Dong et al., 2019; Zhang et al., 2020). Advanced techniques like dynamic network biomarker analysis, RNA-Seq, and eQTL mapping have provided deeper insights into the genetic control of root development, revealing potential targets for genetic improvement (Dong et al., 2019; Zhang et al., 2020; He et al., 2021).

This study provides a comprehensive overview of the genetic regulation of root architecture in sweet potato, with a focus on the key genes and regulatory networks controlling storage root development. It summarizes the current understanding of the genetic mechanisms underlying sweet potato root system architecture, highlighting the genes and transcription factors that play critical roles in the initiation and development of storage roots. This study also explores the implications of these genetic discoveries for breeding and biotechnological strategies aimed at improving sweet potato yield and stress tolerance. Its goal is to deepen understanding of the regulation of sweet potato root architecture and propose potential strategies to enhance crop performance through genetic manipulation.

2 Fundamentals of Root Architecture in Sweet Potato

2.1 Key root traits influencing growth and yield

The growth and yield of sweet potato are significantly influenced by various root traits, including the efficiency of ground cover, biomass allocation, and the balance between foliar and root biomass (Figure 1). Studies have shown that genotypes with higher ground cover efficiency during the establishment phase tend to accumulate more root biomass, especially in soils with low water holding capacity (Pérez-Pazos et al., 2021). Additionally, the regulation of starch biosynthesis and the expression of genes involved in carbohydrate metabolism, such as AGPase and GBSSI, play crucial roles in enhancing starch content and overall yield in sweet potato storage roots (Fan et al., 2021). The expression of specific miRNAs and their target genes also contributes to the regulation of storage root development, impacting yield and starch production (Tang et al., 2020).

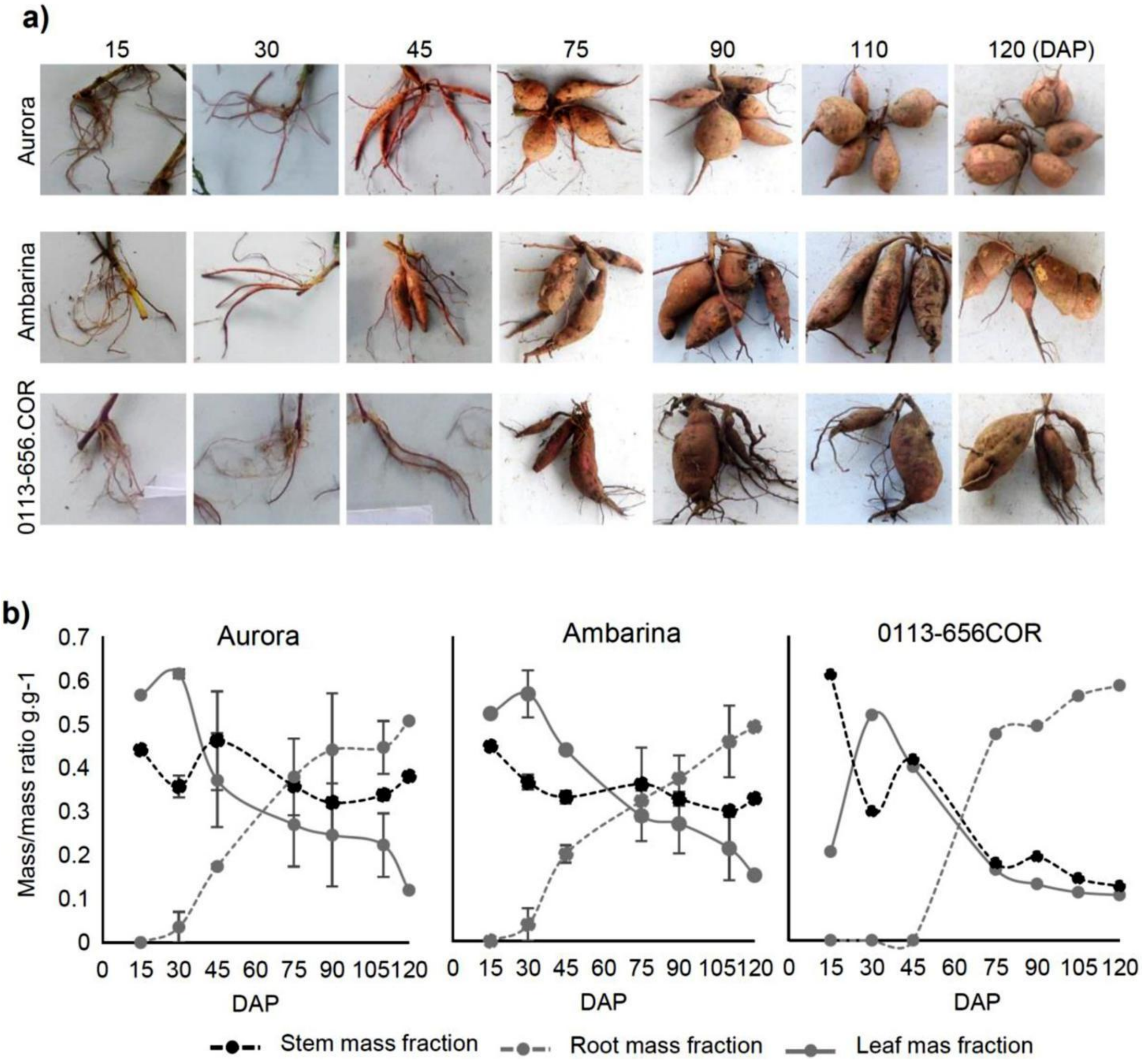

Figure 1 Storage root growth and relation of biomass in three sweet potato genotypes (Adopted from Pérez-Pazos et al., 2021)

Image caption: a) Storage root growth measured until 120 DAP. b) Relation of biomass obtained from leaves, stems and roots with respect to the total biomass during 120 DAP. DAP: days after planting (Adopted from Pérez-Pazos et al., 2021)

2.2 Differences between sweet potato root types

Sweet potato roots can be categorized into two main types: storage roots and fibrous roots. Storage roots are the primary economic part of the plant, characterized by their ability to store large amounts of starch and other nutrients. In contrast, fibrous roots are primarily involved in water and nutrient absorption. The development of storage roots involves a complex genetic and physiological process, including the upregulation of genes and proteins related to meristem development, starch biosynthesis, and phytohormone biosynthesis (Dong et al., 2019). The initiation of storage root swelling is marked by significant morphological and metabolic changes, regulated by key transcription factors such as *IbNAC083* (He et al., 2021). Additionally, the expression of specific genes, such as SRF6, is localized around the primary cambium and meristems, which are crucial for the thickening of storage roots (Tanaka et al., 2005).

2.3 Physiological and morphological importance of root architecture

The root architecture of sweet potato, encompassing both physiological and morphological traits, is vital for its growth, yield, and adaptation to different environments. The root system's ability to efficiently extract water and nutrients from the soil is influenced by the development and branching of adventitious and lateral roots (Joshi et al., 2016). The regulation of carbon flux and starch metabolism in storage roots, mediated by genes like *IbVP1*, is essential for optimizing yield and starch production under various stress conditions (Fan et al., 2021). Furthermore, the genetic regulation of gene expression, as revealed by eQTL analysis, highlights the importance of transcriptional variability in determining root traits and overall plant performance (Zhang et al., 2020). The balance between mother and daughter roots, particularly the ratio of daughter root weight to total root weight, is a critical factor for the acceptance of direct planting cultivation methods.

3 Genetic Factors Influencing Root Development

3.1 Overview of major genes identified in root development

Several key genes have been identified as crucial regulators of root development in sweet potato. One such gene is *IbNAC083*, a NAC-domain transcription factor, which plays a pivotal role in the initiation of storage root swelling. This gene is part of a transcriptional regulatory network that influences the biosynthesis of lignin, flavonol, and starch, thereby driving the transition from pre-swelling to storage roots (He et al., 2021). Another significant gene is *IbMYB1-2*, identified through expression quantitative trait locus (eQTL) analysis, which acts as a master regulator of anthocyanin biosynthesis in storage roots (Zhang et al., 2020). Additionally, the *IbMADS1* gene, a MADS-box transcription factor, has been shown to be involved in the early stages of tuberous root initiation, responding to tuberization-related hormones such as jasmonic acid and cytokinins (Ku et al., 2008).

3.2 Regulatory pathways involved in root morphogenesis

The development of root architecture in sweet potato is governed by complex regulatory pathways. The IbMYB73-IbGER5 module is one such pathway, where the MYB transcription factor *IbMYB73* regulates adventitious root growth and abiotic stress tolerance by modulating the transcription of the abscisic acid-responsive protein IbGER5 (Wang et al., 2023). Another critical pathway involves auxin response factors (ARFs), which are essential for auxin regulation. Specific ARF genes, such as *ItfARF16b* and *ItfARF16c*, are highly expressed in storage roots, indicating their role in root morphogenesis (Pratt and Zhang, 2021). Furthermore, the Ibβfruct2 gene family, particularly *Ibβfruct2-1*, regulates starch and glucose content in sweet potato roots, influencing root development and storage capabilities (Zhang et al., 2023) (Figure 2).

3.3 Role of genetic variations in root trait diversity

Genetic variations play a significant role in the diversity of root traits in sweet potato. The identification of 724 438 high-confidence single nucleotide polymorphisms (SNPs) and 26 026 expressed genes through genome-wide analysis has provided insights into the genetic basis of transcriptomic variations in storage roots (Zhang et al., 2020). These variations are crucial for understanding phenotypic diversity and species evolution. For instance, the differential expression of transcription factors such as *IbMYB1-2* and *IbMADS1* in various sweet potato cultivars highlights the impact of genetic diversity on root traits (Ku et al., 2008; Zhang et al., 2020). Additionally, the regulatory and functional divergence among members of the *Ibβfruct2* gene family further underscores the importance of genetic variations in controlling starch and glucose content, which are vital for root development and storage (Zhang et al., 2023).

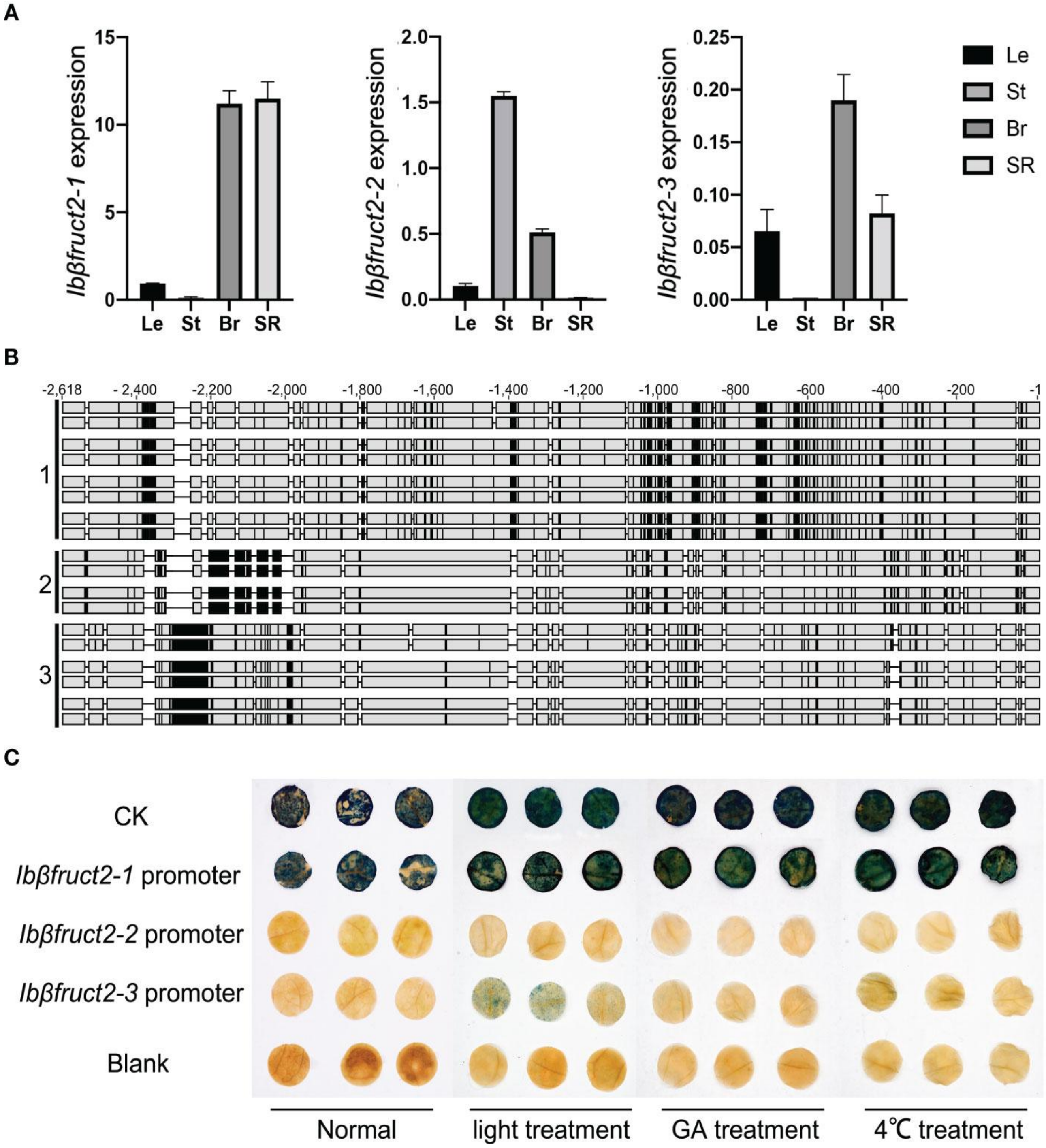

Figure 2 Three *Ibβfruct2* family members show divergence in expression patterns, promoter sequences, and activities (Adopted from Zhang et al., 2023)

Image caption: (A). RT-qPCR detection of *Ibβfruct2-1*, *Ibβfruct2-2*, and *Ibβfruct2-3* expression patterns in leaf (Le), stem (St), branch (Br), and storage root (SR) of sweet potato. Error bar represent SEM calculated from three replicates. (B). Alignment of 2.5-kb *Ibβfruct2* promoter sequences cloned from different sweet potato varieties displaying sequence differences among promoters of the three *Ibβfruct2* family members. 1, 2, and 3: promoter sequences of *Ibβfruct2-1*, *Ibβfruct2-2*, and *Ibβfruct2-3*, respectively. (C) Promoter-GUS fusion assays of promoter activities under normal conditions and light, GA, and low-temperature treatment (Adopted from Zhang et al., 2023)

4 Molecular Mechanisms Governing Root Growth and Patterning

4.1 Transcription factors involved in root architecture

Transcription factors play a crucial role in the regulation of root architecture in sweet potato. The NAC-domain transcription factor *IbNAC083* has been identified as a core regulator in the initiation of storage root swelling. This transcription factor, along with its associated differentially expressed genes, influences metabolic processes such as lignin, flavonol, and starch biosynthesis, which are critical for the transition to swelling roots (He et al., 2021). Another significant transcription factor is *IbMYB73*, which regulates adventitious root growth and abiotic stress tolerance through the abscisic acid (ABA) pathway. Overexpression of *IbMYB73* inhibits root growth, while its suppression enhances root development and stress tolerance (Wang et al., 2023). Additionally, the MADS-box transcription factor *IbMADS1* is involved in the initiation of tuberous root development, responding to hormones like jasmonic acid and cytokinins, and is specifically expressed in meristematic cells within the stele and lateral root primordia (Ku et al., 2008).

4.2 Signaling pathways that influence root growth direction and branching

The direction and branching of root growth in sweet potato are influenced by several signaling pathways. The auxin response factor ARF7 plays a pivotal role in root branching, particularly in response to water availability. ARF7 undergoes posttranslational modification, which regulates its activity and, consequently, the asymmetric expression of target genes like LBD16 in lateral root founder cells. This SUMOylation-dependent regulation of ARF7 is essential for hydropatterning, where roots branch towards water (Orosa-Puente et al., 2018). Furthermore, the ABA signaling pathway, modulated by the IbMYB73-IbGER5 module, significantly impacts adventitious root growth and stress responses. *IbMYB73* activates the transcription of the ABA-responsive protein IbGER5, which in turn affects root growth and stress tolerance (Wang et al., 2023).

4.3 Epigenetic modifications and gene expression related to root architecture

Epigenetic modifications also play a significant role in the regulation of root architecture in sweet potato. The development of storage roots involves complex gene expression patterns regulated by both transcriptional and posttranscriptional mechanisms. For instance, the expression of ARF genes, which are crucial for auxin signaling, varies between storage roots and normal roots, indicating a level of epigenetic control (Pratt and Zhang, 2021). Additionally, the development of tubers in potato, a related species, is governed by photoperiod and epigenetic mechanisms, including histone modifications that regulate key tuberization genes and phytohormone metabolism (Kondhare et al., 2021). These findings suggest that similar epigenetic mechanisms may be at play in sweet potato root development.

5 Role of Environmental Interactions on Root Genetic Regulation

5.1 How environmental factors (e.g., soil type, moisture) impact genetic regulation

Environmental factors such as soil type and moisture significantly influence the genetic regulation of root architecture in sweet potatoes. Soil texture, for instance, affects the efficiency of ground cover and root biomass accumulation, which are critical for the plant's adaptation to sub-humid environments (Pérez-Pazos et al., 2021). Additionally, potassium (K) application and arbuscular mycorrhizal fungi (AMF) inoculation have been shown to synergistically enhance root morphology and nutrient uptake, demonstrating the importance of nutrient availability in root development (Yuan et al., 2023) (Figure 3). The interaction between environmental stressors like drought and genetic factors also plays a crucial role. For example, the expression of the *IbMYB73* gene is suppressed under abiotic stress, affecting root growth and stress tolerance (Wang et al., 2023).

5.2 Gene-environment interactions and root plasticity

Gene-environment interactions are pivotal in determining root plasticity, allowing sweet potatoes to adapt to varying environmental conditions. The dynamic network biomarker (DNB) analysis has identified key transcription factors like *IbNAC083* that regulate the transition from pre-swelling to storage roots, highlighting the genetic basis of root development in response to environmental cues (He et al., 2021). Moreover, the expression of microRNAs (miRNAs) is crucial for modulating root architecture in response to nutrient availability and biotic interactions, further emphasizing the role of gene-environment interactions in root plasticity (Couzigou and Combier, 2016). The regulatory architecture of gene expression variation, as revealed by eQTL analysis, also underscores the complexity of gene-environment interactions in shaping root traits (Zhang et al., 2020).

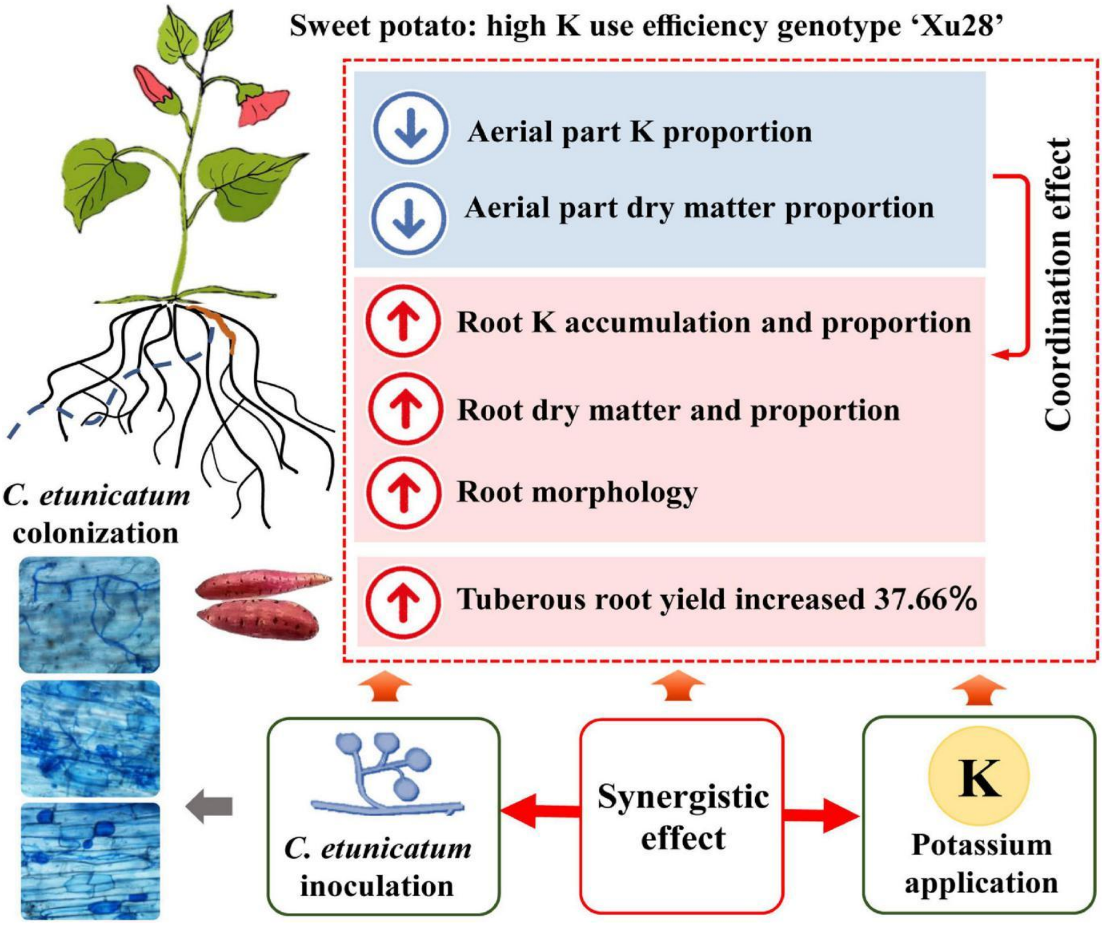

Figure 3 Conceptual diagram depicting the synergistic effect of K and arbuscular mycorrhizal fungi (AMF) on root development and K acquisition of high K use efficiency genotype "Xu28" (Adopted from Yuan et al., 2023)

5.3 Examples of adaptive genetic traits for drought resilience in root architecture

Several adaptive genetic traits have been identified that confer drought resilience in sweet potato root architecture. The overexpression of the WRKY transcription factor ItfWRKY70 enhances drought tolerance by increasing abscisic acid (ABA) content, regulating stomatal aperture, and activating the reactive oxygen species (ROS) scavenging system. Similarly, the IbMYB73-IbGER5 module regulates ABA-dependent adventitious root growth and abiotic stress tolerance, providing a genetic basis for developing drought-resilient sweet potato varieties (Wang et al., 2023). Additionally, the manipulation of root system architecture (RSA) genes, as seen in other crops like potatoes, offers insights into improving drought resilience through enhanced nutrient and water uptake efficiency (Zinta et al., 2022).

6 Recent Advances in Genomic and Biotechnological Tools

6.1 Applications of CRISPR/Cas9, GWAS, and QTL mapping in root architecture studies

Recent advancements in genomic tools such as CRISPR/Cas9, Genome-Wide Association Studies (GWAS), and Quantitative Trait Loci (QTL) mapping have significantly enhanced our understanding of root architecture in sweet potato. CRISPR/Cas9 has been effectively utilized for targeted mutagenesis in sweet potato, demonstrating its potential in modifying starch biosynthetic genes to improve starch quality (Wang et al., 2019). This technology has also been applied in other crops like rice and potato, showcasing its versatility and efficiency in genome editing (Wang et al., 2015; Butt et al., 2018; Ahmad et al., 2022). GWAS and QTL mapping have been instrumental in identifying genetic loci associated with root traits. For instance, a meta-analysis of QTLs in maize has identified numerous QTLs linked to root system architecture, which can be extrapolated to sweet potato research (Karnatam et al., 2023). Additionally, eQTL analysis in sweet potato has revealed key regulatory genes such as *IbMYB1-2*, which plays a crucial role in anthocyanin biosynthesis in storage roots (Zhang et al., 2020).

6.2 Transcriptomic and proteomic studies related to sweet potato root traits

Transcriptomic and proteomic studies have provided deep insights into the genetic regulation of root traits in sweet potato. Dynamic network biomarker analysis has identified stage-specific gene expression patterns and key transcription factors like *IbNAC083*, which are crucial for the initiation and regulation of root tuberization (He et al., 2021). These studies have mapped the transcriptional dynamics during root development, highlighting the importance of coexpressed gene modules in different developmental stages. Furthermore, transcriptomic analyses have uncovered the genetic basis of phenotypic variations in sweet potato storage roots, identifying thousands of expressed genes and eQTLs that regulate their expression (Zhang et al., 2020). These findings are pivotal for understanding the complex regulatory networks governing root architecture and development.

6.3 Integration of multi-omics approaches to understand root architecture genetics

The integration of multi-omics approaches, including genomics, transcriptomics, and proteomics, has been a game-changer in dissecting the genetic architecture of root traits in sweet potato. By combining eQTL mapping with regulatory network analyses, researchers have identified master regulators and key genetic variants affecting root traits (Zhang et al., 2020). Multi-omics approaches have also facilitated the identification of conserved gene models across different species, providing a broader perspective on root architecture genetics (Karnatam et al., 2023). The use of dynamic network biomarker analysis has further refined our understanding of the critical transitions in root development, pinpointing specific genes and regulatory networks involved in these processes (He et al., 2021). These integrative strategies are essential for developing a comprehensive understanding of the genetic regulation of root architecture, paving the way for targeted breeding and genetic improvement of sweet potato.

7 Case Studies in Root Genetic Improvement for Sweet Potato Cultivation

7.1 Specific studies and their findings on improving root traits for yield enhancement

Several studies have focused on enhancing root traits to improve the yield of sweet potato. For instance, a genome-wide analysis of expression quantitative trait loci (eQTLs) identified 4 408 eQTLs regulating the expression of 3 646 genes in sweet potato storage roots. This study highlighted the role of the *IbMYB1-2* gene as a master regulator for anthocyanin biosynthesis, which is crucial for root development and yield (Zhang et al., 2020). Another study utilized computational vision to phenotype root production, demonstrating that image analysis could predict root weight and maintain genotype ranking, thus aiding in the selection of high-yield genotypes (Fernandes et al., 2022). Additionally, the evaluation of orange-fleshed sweet potato (OFSP) genotypes in different agro-climatic zones of Northern Ethiopia revealed that certain genotypes like Ininda, Gloria, and Amelia provided higher yields and better nutritional traits, suggesting the potential for genotype selection to enhance yield (Lamaro et al., 2023).

7.2 Genetic interventions for better root architecture in challenging environments

Genetic interventions have been pivotal in improving root architecture under abiotic stress conditions. The *IbMYB73* gene, for example, was found to regulate root growth and stress tolerance in sweet potato. Overexpression of *IbMYB73* inhibited adventitious root growth and reduced abiotic stress tolerance, while RNAi-mediated suppression of this gene had the opposite effect, enhancing root development and stress resilience (Wang et al., 2023). Another study identified the NAC-domain transcription factor *IbNAC083* as a core regulator of storage root initiation. This gene, along with its associated network, was crucial for the transition from pre-swelling to storage roots, which is essential for root development under varying environmental conditions (He et al., 2021) (Figure 4). Furthermore, the influence of morpho-physiological traits on root yield was studied, showing that genotypes with efficient ground cover and lower foliar biomass accumulation adapted better to sub-humid environments, thus improving root biomass accumulation (Pérez-Pazos et al., 2021).

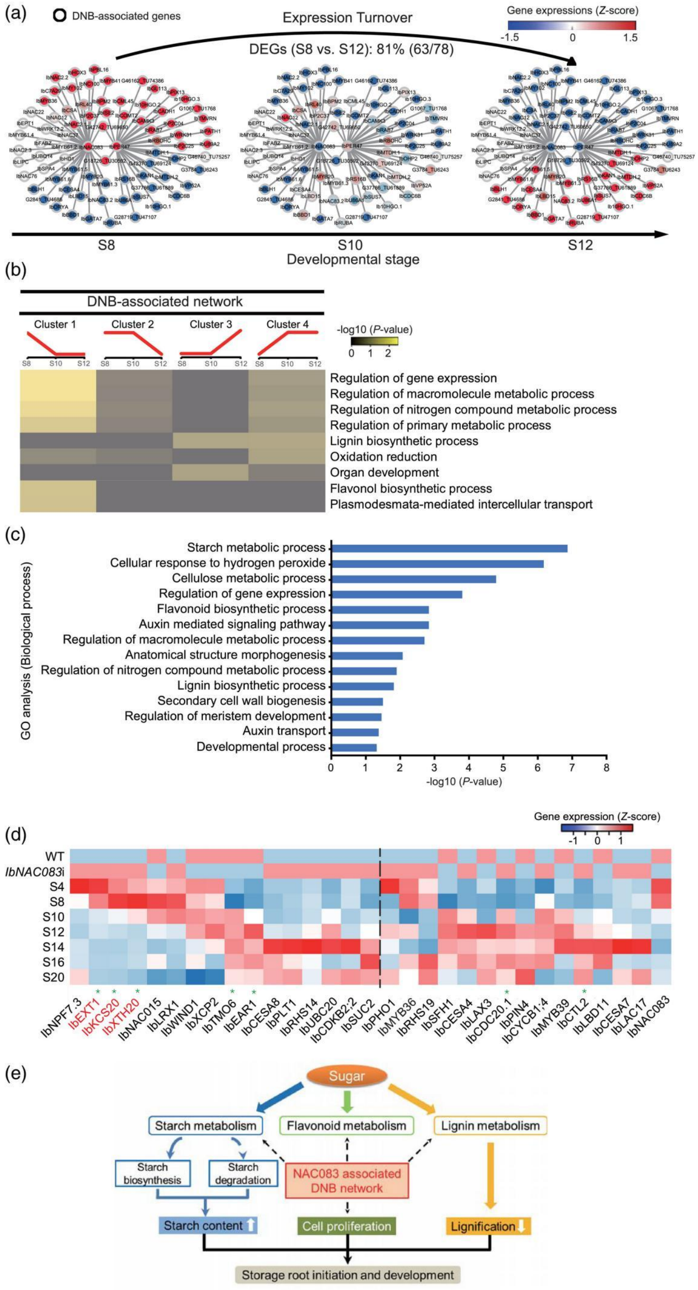

Figure 4 Dynamic network analysis of *Ipomoea batatas* (sweet potato) root developmental transcriptome (Adopted from He et al., 2021)

Image caption: (a) Dynamics of *IbNAC083*-associated genes in terms of expression before and after the critical period. Expression of *IbNAC083* and its 63 neighboring differentially expressed genes (DEGs) changes significantly (or inversed) from low (or high) at stage S8 to high (or low) at stage S12 (i.e. the expression levels of those genes are reversed before and after the critical period, at stage S10), implying key roles of dynamic network biomarker (DNB) members in coordinating the critical transition to root swelling at stage S10. (b) Dynamic activity of the relative gene ontology (GO) terms that involved *IbNAC083* and its neighboring DEGs in different dynamic patterns. (c) GO enrichment analysis of the DEGs in the initial swelling roots of *IbNAC083*-RNAi transgenic plants relative to the wild type (WT). The GO terms of biological processes with statistical significance ($P \leq 0.05$) are shown. Three biological replicates were performed for each genotype. (d) A heat map illustrated the co-expression of *IbNAC083* and typical root development-related genes. The 16 genes listed on the left of the dashed line were also DEGs in the root developmental series transcriptomic data; seven genes labeled by a green star had co-expression relationships with *IbNAC083* by analysis of both the root developmental series transcriptomic expression profiling and the RNA-seq data of WT and *IbNAC083*-RNAi transgenic plants. Genes in red showed positive co-expression with *IbNAC083* (Pearson correlation coefficient, PCC>0.8), whereas genes in black showed negative co-expression with *IbNAC083* (PCC<-0.8). (e) A molecular model of *IbNAC083*-associated DNB network function in sweet potato initiation and development (Adopted from He et al., 2021)

7.3 Potential for developing varieties with optimal root structures

The potential for developing sweet potato varieties with optimal root structures is significant, given the advancements in genetic and phenotypic analyses. The dynamic network biomarker analysis identified *IbNAC083* as a key regulator in root tuberization, providing a target for genetic manipulation to enhance root structure (He et al., 2021). The use of computational vision for phenotyping has also shown promise in accurately predicting root weight and maintaining genotype rankings, which is crucial for breeding programs aimed at improving root traits (Fernandes et al., 2022). Additionally, the agronomic characterization of sweet potato genotypes obtained through crossbreeding identified several promising genotypes with high productivity of commercial roots, indicating the potential for developing high-yield varieties (Oliveira et al., 2022). These studies collectively underscore the feasibility of using genetic and phenotypic tools to develop sweet potato varieties with optimal root structures, tailored for both yield enhancement and environmental resilience.

8 Future Perspectives and Challenges

8.1 Emerging research directions in root architecture genetics

The genetic regulation of root architecture in sweet potato is a burgeoning field with significant potential for advancing crop productivity and resilience. Recent studies have highlighted the importance of root system architecture (RSA) in plant fitness and stress tolerance, emphasizing the need for a deeper understanding of the genetic and environmental factors that influence root growth (Rogers and Benfey, 2015; Khan et al., 2016). For instance, dynamic network biomarker analysis has identified key transcription factors, such as *IbNAC083*, that play crucial roles in the initiation and regulation of root tuberization in sweet potato (He et al., 2021). Additionally, genome-wide expression quantitative trait loci (eQTL) analyses have uncovered the regulatory architecture of gene expression variation in sweet potato storage roots, providing insights into the genetic basis of phenotypic traits (Zhang et al., 2020). Future research should focus on integrating high-throughput phenotyping and genotyping techniques to map RSA traits more precisely and explore their potential for improving crop resilience under various stress conditions (Khan et al., 2016; Maqbool et al., 2022).

8.2 Challenges in applying root architecture research to breeding programs

Despite the promising advances in understanding the genetic regulation of RSA, several challenges remain in translating this knowledge into practical breeding programs. One major hurdle is the difficulty in phenotyping root traits due to their hidden nature and the complexity of root-soil interactions (Joshi et al.,, 2016; Maqbool et al., 2022). High-throughput and non-invasive phenotyping methods, such as X-ray CT and MRI, are still under development and need to be optimized for routine use in breeding programs (Maqbool et al., 2022). Additionally, the genetic manipulation of root traits often requires sophisticated techniques and can lead to unintended genomic changes, complicating the breeding process (Zhang et al., 2022). Another challenge is the limited availability of robust databases and analytical pipelines that can handle the vast amount of data generated from RSA studies (Khan et al., 2016). Addressing these challenges will require a multidisciplinary approach, combining advances in molecular biology, bioinformatics, and agronomy to develop more efficient and targeted breeding strategies.

8.3 Potential implications for sustainable sweet potato production

Understanding and manipulating the genetic regulation of RSA in sweet potato holds significant promise for enhancing sustainable agricultural practices. Improved root systems can lead to better nutrient and water uptake, increased tolerance to abiotic stresses such as drought and salinity, and ultimately higher yields. For example, the identification of genes that regulate root architecture can be used to develop sweet potato varieties with more efficient root systems, reducing the need for chemical fertilizers and irrigation (Rogers and Benfey, 2015; Zinta et al., 2022). Moreover, the ability to breed sweet potato varieties with optimized root traits can contribute to food security by ensuring stable production under changing climatic conditions (Khan et al., 2016; Dong et al., 2019). The integration of RSA research into breeding programs can thus play a pivotal role in achieving sustainable sweet potato production, benefiting both farmers and the environment.

9 Concluding Remarks

The genetic regulation of root architecture in sweet potato has uncovered several key regulators critical to root development and stress response. Dynamic network biomarker (DNB) analysis identified *IbNAC083* as a central regulator involved in initiating storage root swelling, highlighting its significant role in the transcriptional network during root development. Genome-wide expression quantitative trait loci (eQTL) analysis further revealed *IbMYB1-2* as a master regulator of anthocyanin biosynthesis in storage roots, enriching our understanding of the genetic architecture behind gene expression variation. Additionally, the IbMYB73-IbGER5 module was found to play a role in regulating ABA-dependent adventitious root growth and in supporting abiotic stress tolerance, underscoring the impact of transcription factors in root structure and environmental resilience. The MADS-box gene *IbMADS1*, crucial for tuberous root initiation and influenced by hormones like jasmonic acid and cytokinins, further emphasizes the role of hormonal regulation in root formation.

These findings offer substantial promise for sweet potato breeding strategies. Key transcription factors like *IbNAC083*, *IbMYB1-2*, and *IbMADS1* are valuable targets for genetic manipulation aimed at optimizing root architecture and storage root development. With these genetic markers, breeders can work toward developing sweet potato varieties with stronger root systems that enhance nutrient uptake, resilience to stress, and overall productivity. Understanding the role of the IbMYB73-IbGER5 module in stress tolerance further opens doors to breeding sweet potato varieties capable of withstanding environmental challenges, ensuring consistent yields in variable conditions. The use of eQTL analysis in breeding programs can also streamline the selection of desirable traits tied to specific genetic variants, facilitating the creation of high-performance sweet potato cultivars.

Continued research on the genetic regulation of root architecture in sweet potato and other crops is crucial to tackling global food security challenges. A detailed understanding of transcriptional regulatory networks and critical genetic regulators sets a strong foundation for innovative breeding strategies. Future work should emphasize functional validation of these genes and their interactions, as well as exploring gene-editing technologies like CRISPR/Cas9 for precise trait modification. Additionally, integrating multi-omics approaches—including transcriptomics, proteomics, and metabolomics—will shed further light on the complex regulatory mechanisms that govern root development. Collaboration among researchers, breeders, and policymakers is essential to transform these insights into practical applications, ultimately advancing the cultivation of crops with optimized root systems for sustainable agricultural productivity.

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Conflict of Interest Disclosure

The authors affirm that this research was conducted without any commercial or financial relationships that could be construed as a potential conflict of interest.

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