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Feature Review **Open Access**

Figure Review of Genetic Approaches to Improve Yield and Starch Content in Sweet Potato

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Abstract Sweet potato (*Ipomoea batatas*) is a globally significant crop for both food and industrial use, with high yield and starch content playing crucial roles in meeting demands for food, feed, and bioenergy. However, improving sweet potato yield and starch content poses challenges due to its genetic complexity and environmental sensitivity. This study summarizes genetic improvement methods for enhancing sweet potato yield and starch content, focusing on traditional breeding, marker-assisted selection (MAS), genomic selection (GS), gene editing, and multi-omics integration strategies. In recent years, MAS and GS have shown distinct advantages in accelerating the selection of high-yield and high-starch traits in sweet potato. Gene editing technologies, such as CRISPR/Cas9, provide precise approaches for the targeted regulation of key genes. Additionally, multi-omics techniques, including transcriptomics, metabolomics, and proteomics, help elucidate the biological pathways and regulatory mechanisms that influence yield and starch synthesis, offering strong support for optimizing breeding strategies. This study provides a clear direction for sweet potato breeding research, advancing progress toward high-yield and high-starch content varieties and carrying profound implications for global agricultural production and sustainability.

Keywords Sweet potato; Genetic improvement; Yield; Starch content; Gene editing

1 Introduction

Sweet potato (*Ipomoea batatas*) is a vital crop with significant economic and nutritional value worldwide. It is a staple food in many developing countries and serves as a crucial source of carbohydrates, vitamins, and minerals. The crop's adaptability to diverse climatic conditions and its ability to thrive in poor soils make it an essential food security crop, particularly in regions prone to food scarcity. Additionally, sweet potato is increasingly recognized for its industrial applications, including its use in food derivatives, dietary supplements, and as a raw material in various industrial processes (Lyu et al., 2021).

Despite its importance, sweet potato cultivation faces several challenges, particularly in terms of yield and starch content. Traditional breeding methods have been employed to address these issues, focusing on traits such as root yield, starch content, and disease resistance (Kar et al., 2022). However, the complex polyploid nature of sweet potato and its long breeding cycle have limited the effectiveness of these conventional approaches (Lyu et al., 2021). Recent advancements in genetic engineering and biotechnological techniques, such as CRISPR/Cas9-mediated genome editing, have shown promise in overcoming these challenges by enabling precise modifications to the sweet potato genome (Wang et al., 2019; Lyu et al., 2021).

Enhancing the yield and starch content of sweet potato is crucial for meeting the growing global food demand and supporting sustainable agriculture. Increased yield and improved starch quality can significantly contribute to food security, particularly in regions where sweet potato is a staple crop (Lamaro et al., 2023). Moreover, higher starch content and better starch properties can enhance the crop's industrial value, making it more suitable for various applications, including biofuel production and food processing (Lyu et al., 2021). Genetic improvements that increase yield and starch content can also help in developing sweet potato varieties that are more resilient to environmental stresses, thereby supporting sustainable agricultural practices (Ren et al., 2018; Fan et al., 2021).

This study will analyze the advancements in genetic improvement techniques for enhancing sweet potato yield and starch content, delving into recent achievements in genetic engineering, genome editing, and traditional breeding methods. It aims to provide a comprehensive overview of the current state of research while identifying potential future directions. The ultimate goal is to highlight effective strategies for increasing sweet potato yield and starch content, thereby contributing to food security and sustainable agriculture.

2 Genetic Basis of Sweet Potato Yield and Starch Content

2.1 Genetic background of yield traits in sweet potato

The yield traits in sweet potato are influenced by multiple quantitative trait loci (QTL) and genetic factors. For instance, a study identified two major QTL on linkage groups 3 and 12 that affect starch content, β-carotene, dry matter, and flesh color. These QTL regions act pleiotropically, reducing starch content while increasing β-carotene in genotypes carrying specific haplotypes (Gemenet et al., 2019). Another study using a polyploid genome-wide association study (GWAS) identified significant SNPs associated with starch content, dry matter, and storage root fresh weight, highlighting the complex genetic architecture of these traits (Haque et al., 2023). Additionally, QTL mapping in potato, a close relative of sweet potato, has revealed that QTLs for tuber yield and starch content are often linked, suggesting shared genetic control.

2.2 Starch synthesis pathways and related genes

Starch synthesis in sweet potato involves several key biochemical pathways and genes. The primary enzymes include ADP-glucose pyrophosphorylase (AGPase), soluble starch synthase (SSS), and starch branching enzyme (SBE). AGPase catalyzes the first step in starch biosynthesis, converting glucose-1-phosphate and ATP to ADP-glucose, which is then used by SSS to elongate the starch chain. SBE introduces branch points into the starch molecule, creating a more complex structure (Menéndez et al., 2002). In sweet potato, genes such as granule-bound starch synthase I (IbGBSSI) have been identified as crucial for amylose biosynthesis, with consistent expression during starch accumulation (Haque et al., 2023). Additionally, the physical linkage of phytoene synthase with sucrose synthase has been shown to negatively correlate β-carotene and starch content, indicating a complex interplay between these pathways (Gemenet et al., 2019)

2.3 Gene expression and environmental interactions

Environmental factors such as soil quality and climate significantly influence gene expression, impacting yield and starch content in sweet potato. High heritability and genetic advance for traits like vine length, number of branches, and root yield per plant suggest that these traits are less influenced by environmental factors and are governed by additive genes (Kar et al., 2022). However, the expression of genes involved in starch metabolism can be modulated by environmental conditions. For example, cold storage conditions in potato tubers lead to the accumulation of reducing sugars due to the activity of genes like invertase, which are also relevant in sweet potato (Li et al., 2005). Furthermore, QTLs for traits like cold-induced sweetening and reconditioning in potato have been mapped to specific chromosomes, indicating that environmental interactions can have a significant genetic basis (Xiao et al., 2018).

3 Role of Traditional Breeding in Sweet Potato Improvement

3.1 Phenotypic selection and hybrid breeding

Traditional breeding methods, such as phenotypic selection and hybrid breeding, have been instrumental in improving sweet potato yield and starch content. Phenotypic selection involves choosing plants with desirable traits based on observable characteristics. This method has been effective in identifying high-yield and high-starch varieties, as demonstrated by the significant genetic variability and potential for genetic gains in sweet potato populations (Otoboni et al., 2020; Vargas et al., 2020). For instance, the study by Otoboni et al. (2020) showed that 81.25% of the traits had genotypic coefficients of variation above 20%, indicating favorable conditions for selection with considerable genetic advances.

However, phenotypic selection has its limitations. The process is labor-intensive and time-consuming, requiring multiple generations to achieve significant improvements. Additionally, the selection is often influenced by environmental factors, which can mask the true genetic potential of the plants. The study by Visalakshi et al. (2021) highlighted the high variability in traits such as vine length, number of branches per plant, and root yield per plant, which are influenced by environmental conditions, making it challenging to achieve consistent results.

3.2 Mutation breeding

Mutation breeding is another traditional approach that has been used to create genetic diversity in sweet potato. This method involves inducing mutations through physical or chemical agents to generate new genetic variations. Mutation breeding has been successful in developing sweet potato varieties with improved starch properties. For example, the study by Katayama et al. (2006) demonstrated that crossing and mutagenesis could increase the variations of amylose content in sweet potato, leading to the selection of variants with low or high amylose content.

The application of mutation breeding has led to the development of new sweet potato cultivars with desirable traits. The "Quick Sweet" cultivar, developed through mutation breeding, features low gelatinization temperatures and altered starch fine structure, making it suitable for various industrial applications (Katayama et al., 2006). This cultivar's starch properties, such as lower gelatinization temperatures and higher proportions of short amylopectin chains, provide excellent cold storage stability, which is beneficial for food processing industries.

3.3 Successful cases: examples and applications of high-yield and high-starch sweet potato variety development

Several successful cases of high-yield and high-starch sweet potato variety development have been reported. One notable example is the study by Lin et al. (2007), which investigated the maternal effects on yield and quality traits in sweet potato through reciprocal crosses. The results showed significant positive correlations between top weight, storage root weight, and starch content, indicating the potential for selecting high-yield and high-starch varieties through hybrid breeding.

Another successful case is the identification of promising sweet potato genotypes with high genetic variability and potential for selection gains. The study by Otoboni et al. (2020) identified genotypes CERAT31-01, CERAT21-02, and CERAT51-30 as the most promising for high yield and starch content. Similarly, the study by Vargas et al. (2020) recommended the VR13-61 accession for root production and VR13-11 and VR13-22 for dual-aptitude, highlighting the effectiveness of traditional breeding methods in improving sweet potato traits.

4 Application of Marker-Assisted Selection (MAS) in Sweet Potato Breeding

4.1 Principles of marker-assisted selection and its advantages in efficient sweet potato breeding

Marker-assisted selection (MAS) is a modern plant breeding technique that leverages molecular markers to select desirable traits in crops. The principle behind MAS is the identification and use of DNA markers that are closely linked to genes of interest, allowing breeders to select plants with favorable traits at the seedling stage, thus bypassing the need for phenotypic selection in mature plants (Francia et al, 2005; Collard and Mackill, 2008; Singh and Singh, 2015). This method significantly accelerates the breeding process by enabling the selection of traits that are difficult to measure directly, such as yield and stress tolerance (Collard and Mackill, 2008; Singh and Singh, 2015).

MAS offers several advantages over traditional breeding methods. It allows for the precise transfer of genomic regions of interest, improving the efficiency of breeding programs (Babu et al., 2004; Huang and Hong, 2024). Additionally, MAS can be used for both simply inherited traits and complex polygenic traits, although its application in the latter has been more challenging (Babu et al., 2004; Francia et al, 2005). The integration of MAS with conventional breeding can lead to the development of new cultivars with improved traits in a shorter time frame (Collard and Mackill, 2008; Singh and Singh, 2015).

4.2 Important molecular markers related to yield and starch accumulation and their applications

The identification of key molecular markers associated with yield and starch accumulation is crucial for the successful application of MAS in sweet potato breeding. Quantitative trait loci (QTL) mapping studies have identified several markers linked to these traits, which can be used to select high-yielding and high-starch varieties (Babu et al., 2004; Francia et al, 2005; Collard and Mackill, 2008; Li, 2024). For instance, markers linked to genes controlling starch biosynthesis pathways can be used to enhance starch content in sweet potatoes (Babu et al., 2004; Collard and Mackill, 2008).

The application of these markers involves genotyping breeding populations to identify individuals carrying the desirable alleles. This process can be done using various molecular techniques, such as single nucleotide polymorphisms (SNPs) and sequence-characterized amplified regions (SCAR) markers (Babu et al., 2004; Beketova et al., 2021). By selecting individuals with favorable marker profiles, breeders can efficiently develop new sweet potato varieties with enhanced yield and starch content (Babu et al., 2004; Collard and Mackill, 2008).

4.3 Case studies: performance of high-yield, high-starch sweet potato varieties developed through mas

Several case studies have demonstrated the effectiveness of MAS in developing high-yield and high-starch sweet potato varieties. For example, the use of MAS in maize has shown significant improvements in grain yield under drought conditions, which can be analogous to improving yield in sweet potatoes under various stress conditions (Ribaut and Ragot, 2006). Similarly, MAS has been successfully used to develop potato cultivars with resistance to late blight, showcasing the potential of this technique in improving complex traits (Beketova et al., 2021).

In sweet potatoes, the application of MAS has led to the development of varieties with enhanced starch content and yield. These varieties have been evaluated under different environmental conditions, showing consistent performance and higher productivity compared to traditional varieties (Babu et al., 2004; Collard and Mackill, 2008). The integration of MAS with conventional breeding methods has thus proven to be a powerful approach in sweet potato improvement, enabling the rapid development of superior cultivars (Babu et al., 2004; Collard and Mackill, 2008; Singh and Singh, 2015).

5 Genomic Selection (GS) for Enhanced Yield and Starch Content in Sweet Potato

5.1 Application of genomic selection in sweet potato breeding

Genomic selection (GS) leverages genome-wide molecular markers to predict the performance of individuals, allowing for selection without direct phenotyping. This approach accelerates genetic gain in breeding programs by enabling early and more accurate selection of desirable traits (Sverrisdóttir et al., 2017; Stich and Inghelandt, 2018). The principles of GS involve using statistical models to estimate the genetic value of individuals based on their genotypic data, which can significantly reduce the breeding cycle time and increase the efficiency of selecting high-yield and high-starch content sweet potato varieties (Slater et al., 2016; Haque et al., 2023). The feasibility of GS in crops like tetraploid potato has shown promising results, suggesting its potential application in sweet potato breeding as well (Sverrisdóttir et al., 2017; Stich and Inghelandt, 2018).

5.2 Development of multi-trait selection models

Multi-trait genomic selection models are essential for optimizing the selection process in sweet potato breeding, as they allow breeders to consider multiple traits simultaneously, such as yield, starch content, disease resistance, and plant architecture (Moeinizade et al., 2020; Rosero et al., 2023). Strategies for multi-trait selection include index selection, which assigns weights to different traits based on their economic importance, and multi-objective optimization, which identifies trade-offs across traits to achieve a balanced selection. Advanced methods like the look-ahead selection (LAS) algorithm have been proposed to maximize certain traits while keeping others within desirable ranges, demonstrating superior performance compared to conventional index selection (Moeinizade et al., 2020). These models help in identifying genotypes that exhibit a better overall profile and stability across different environments (Moeinizade et al., 2020; Rosero et al., 2023).

5.3 Success stories: achievements in improving sweet potato yield and starch content using genomic selection

Several studies have reported successful applications of genomic selection in improving sweet potato yield and starch content. For instance, the use of a multi-trait index in the CropInd tool facilitated the selection of superior sweet potato genotypes based on their agronomic performance across multiple environments, leading to the identification of a new variety, 0113-672COR, for the Colombian Caribbean region (Figure 1) (Rosero et al., 2023). *Agrosavia Aurora* (0113-672COR) is a newly developed sweet potato variety with enhanced disease resistance and adaptability, particularly suited for growth in tropical and subtropical regions. Studies indicate that *Agrosavia Aurora* demonstrates high and stable yield performance, achieving substantial productivity across diverse soil conditions, making it a promising genetic resource for staple crop improvement.

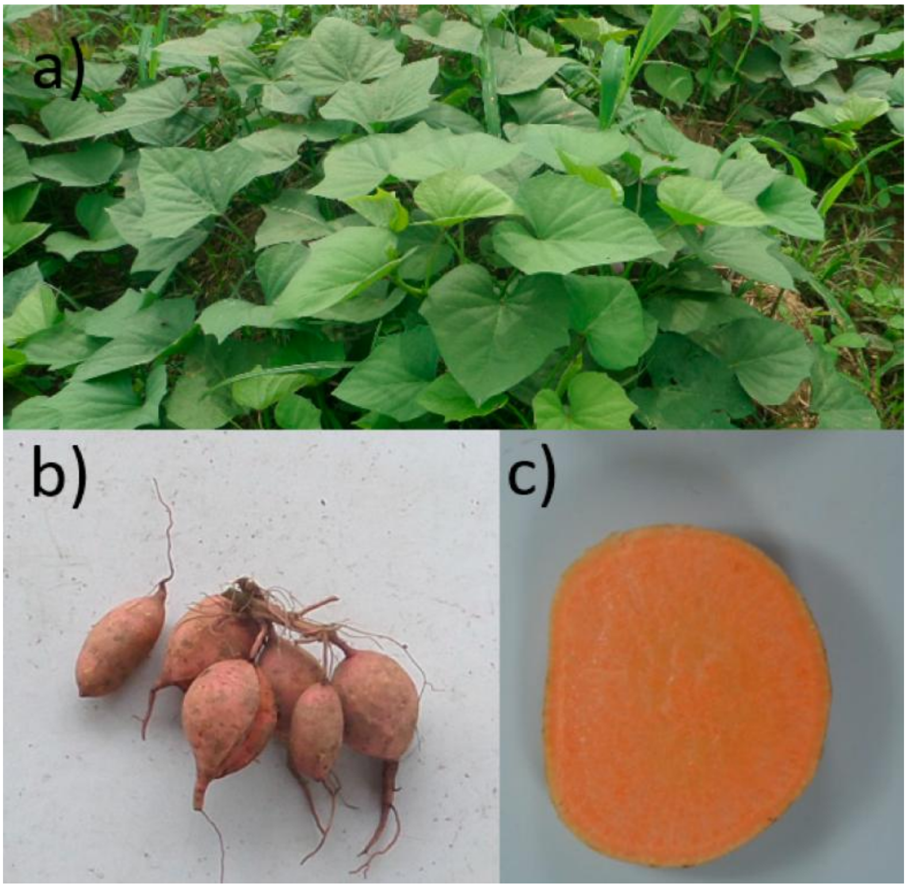

Figure 1 Morphological characteristics of sweet potato variety *Agrosavia Aurora* (0113-672COR) (Adapted from Rosero et al., 2023)
Image caption: a) Plant morphology, featuring broad, dense leaves; b) Tuber shape, spindle-shaped and moderately sized; c) Cross-section of the tuber flesh, displaying orange-colored flesh characteristics (Adapted from Rosero et al., 2023)

Additionally, the development of genomic prediction models for starch content in tetraploid potato has shown that GS can be a feasible breeding strategy, with significant genetic gains achieved through the selection of high-starch-containing lines (Sverrisdóttir et al., 2017; Stich and Inghelandt, 2018). These success stories highlight the potential of GS to enhance the efficiency and effectiveness of sweet potato breeding programs, ultimately leading to the development of high-yielding and high-starch varieties (Sverrisdóttir et al., 2017; Stich and Inghelandt, 2018; Rosero et al., 2023).

6 Prospects of Gene Editing Technology in Sweet Potato Breeding

6.1 Application of the CRISPR/Cas9 system in sweet potato

The CRISPR/Cas9 system, a revolutionary genome editing tool, has significantly advanced the field of plant genetics by enabling precise and efficient modifications of target genes. The system operates by utilizing a single-guide RNA (sgRNA) to direct the Cas9 nuclease to a specific DNA sequence, where it induces double-stranded breaks (DSBs). These breaks are subsequently repaired by the cell's natural repair mechanisms, leading to targeted mutations such as insertions, deletions, or substitutions (Bortesi and Fischer, 2015; Wang et al., 2015; Chen et al., 2019). This technology has been successfully applied to various crops, including sweet potato (*Ipomoea batatas*), to enhance desirable traits such as starch content and yield (Wang et al., 2019; Tussipkan and Manabayeva, 2021).

6.2 Targeted editing of key genes

In sweet potato, key genes involved in starch biosynthesis, such as *IbGBSSI* (granule-bound starch synthase I) and *IbSBEII* (starch branching enzyme II), have been targeted using CRISPR/Cas9 to directly regulate starch synthesis pathways. For instance, CRISPR/Cas9-mediated knockout of *IbGBSSI* and *IbSBEII* in sweet potato cultivars resulted in significant alterations in amylose content, demonstrating the potential of this technology to modify starch quality (Wang et al., 2019). Such targeted editing allows for the precise manipulation of metabolic pathways, thereby improving both the yield and nutritional quality of sweet potatoes (Andersson et al., 2018; Wang et al., 2019; Li et al., 2021).

6.3 Challenges and successes in gene editing

Despite the promising applications of CRISPR/Cas9 in sweet potato breeding, several technical challenges remain. One major challenge is the efficient delivery of the CRISPR/Cas9 components into sweet potato cells, which are often recalcitrant to transformation (Andersson et al., 2018; Tussipkan and Manabayeva, 2021). Additionally, the polyploid nature of sweet potato complicates the editing process, as multiple alleles of a gene must be simultaneously targeted to achieve the desired phenotype (Wang et al., 2015; Wang et al., 2019). However, successes have been reported, such as the high mutation efficiency (62%-92%) achieved in sweet potato cultivars, leading to significant changes in starch composition without affecting total starch content (Table 1) (Wang et al., 2019). These successes underscore the potential of CRISPR/Cas9 to revolutionize sweet potato breeding by enabling precise genetic modifications that enhance crop traits (Abdelrahman et al., 2018; Chen et al., 2019; Wang et al., 2019).

Table 1 Mutation rates of CRISPR/Cas9 in sweet potato (Adopted from Wang et al., 2019)

Cultivar	Target gene	No. of plants with Cas9 gene	No. of plants with mutation	Mutation rates of transgenic plants
Xushu22	*IbGBSSI*	25	23	92.0%
Xushu22	*IbSBEII*	47	40	85.1%
Taizhong6	*IbGBSSI*	24	15	62.5%
Taizhong6	*IbSBEII*	11	7	63.6%

7 Multi-Omics Approaches for Studying Yield and Starch Content in Sweet Potato

7.1 Transcriptomics

Transcriptomics involves the comprehensive analysis of RNA transcripts to understand gene expression patterns. In sweet potato, transcriptomic studies have identified key genes involved in starch biosynthesis and yield improvement. For instance, the gene *IbGBSSI*, which encodes granule-bound starch synthase I, has been shown to play a crucial role in starch accumulation. Elevated expression of *IbGBSSI* during starch accumulation phases was observed, indicating its importance in enhancing starch content in sweet potato (Haque et al., 2023). Additionally, CRISPR/Cas9-mediated mutagenesis targeting starch biosynthetic genes such as *IbGBSSI* and *IbSBEII* has demonstrated the potential to modify starch quality, further emphasizing the role of transcriptomics in identifying and manipulating key genes for improved yield and starch content (Wang et al., 2019).

7.2 Metabolomics

Metabolomics focuses on the comprehensive profiling of metabolites within a biological system. In sweet potato, metabolomic studies have been instrumental in elucidating the starch synthesis pathway and identifying key metabolites involved in starch accumulation. For example, the study of metabolites in the starch synthesis pathway has revealed the accumulation of specific metabolites that are crucial for starch biosynthesis. The integration of metabolomics with other omics approaches has provided insights into the regulatory mechanisms governing starch accumulation. This approach has been successfully applied in other crops, such as potato, where the simultaneous boosting of source and sink capacities led to a significant increase in tuber starch yield (Jonik et al., 2012). These findings highlight the potential of metabolomics in identifying key metabolites and regulatory mechanisms that can be targeted for improving starch content in sweet potato.

7.3 Proteomics and epigenomics

Proteomics and epigenomics offer valuable insights into the roles of proteins and epigenetic modifications in regulating yield and starch synthesis. Proteomic analyses have identified numerous proteins associated with starch metabolism and yield traits. For instance, a study on potato tubers identified over 300 protein spots associated with various quality traits, including starch content (Acharjee et al., 2018). These proteins can serve as potential targets for improving starch synthesis and yield in sweet potato. Additionally, epigenetic modifications, such as DNA methylation and histone modifications, play a crucial role in regulating gene expression and can influence starch biosynthesis and yield. Integrating proteomics and epigenomics with other omics approaches can provide a comprehensive understanding of the molecular mechanisms underlying yield and starch content in sweet potato (Ritchie et al., 2015; Yang et al., 2021).

8 Integrated Breeding Strategies for Sweet Potato Improvement

8.1 Integration of traditional and modern techniques

A multi-level breeding strategy that combines traditional breeding, marker-assisted selection (MAS), genomic selection, and gene editing is essential for the improvement of sweet potato yield and starch content. Traditional breeding methods have been foundational in selecting desirable traits such as high yield and disease resistance (Kar et al., 2022). However, integrating modern techniques like CRISPR/Cas9-based genome editing has shown significant promise. For instance, CRISPR/Cas9-mediated mutagenesis of starch biosynthetic genes in sweet potato has been effective in modifying starch quality without significantly altering total starch content (Wang et al., 2019). Additionally, the overexpression of genes like *IbVP1* and *IbSnRK1* has been shown to enhance starch content and yield by regulating carbohydrate metabolism and starch biosynthesis pathways (Ren et al., 2018; Fan et al., 2021). These modern techniques, when combined with traditional breeding, can accelerate the development of superior sweet potato cultivars.

8.2 Multi-trait selection strategy

Optimizing additional traits alongside yield and starch content is crucial for the holistic improvement of sweet potato. Traits such as disease resistance, stress tolerance, and nutritional quality should be considered. For example, the overexpression of *IbVP1* not only improves starch content but also enhances photosynthesis and sucrose transport, which are vital under stress conditions (Fan et al., 2021). Similarly, the selection of genotypes with high beta-carotene content can address nutritional deficiencies while maintaining high yield and starch content (Lamaro et al., 2023). The use of polyploid genome-wide association studies (GWAS) has also been instrumental in identifying molecular markers associated with complex traits, enabling the selection of genotypes with a combination of desirable traits (Haque et al., 2023).

8.3 Case studies in integrated breeding

Real-life examples of applying integrated breeding methods in sweet potato improvement highlight the effectiveness of these strategies. One notable case is the use of CRISPR/Cas9 to target starch biosynthetic genes, resulting in modified starch quality in sweet potato cultivars Xushu22 and Taizhong6 (Wang et al., 2019). Another example is the overexpression of the *IbVP1* gene, which significantly increased starch content and yield by enhancing photosynthesis and sucrose transport (Figure 2) (Fan et al., 2021). Overexpression of the *IbVP1* gene significantly increased the yield and inorganic phosphorus content in the storage roots of sweet potato, with particularly outstanding results in transgenic lines IA7 and IA8. Phosphorus is an essential nutrient for plant growth and development. This study demonstrates that regulating phosphorus metabolism-related genes can effectively enhance crop yield and nutritional value, providing potential genetic resources and theoretical support for the genetic improvement of high-yield sweet potato cultivation.

Additionally, the development of the "Quick Sweet" cultivar through traditional breeding and selection for specific starch properties demonstrates the potential of combining traditional and modern techniques (Katayama et al., 2006). These case studies underscore the importance of an integrated approach in achieving substantial improvements in sweet potato yield and starch content.

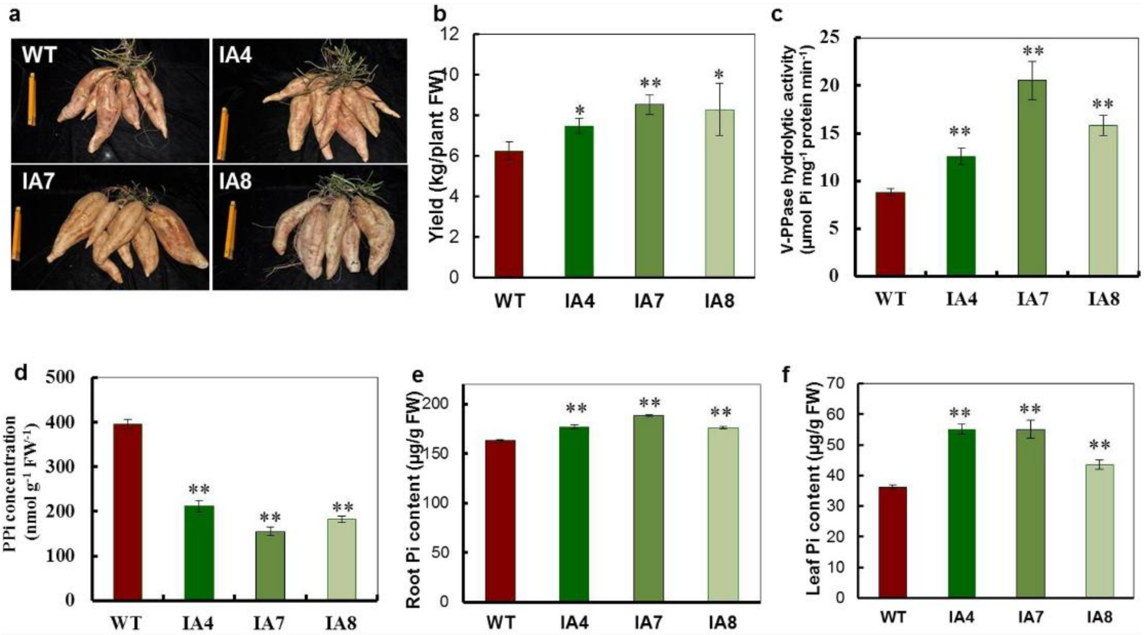

Figure 2 Analysis of storage root yield and inorganic phosphorus content in transgenic sweet potato (*IbVP1* overexpression) (Adapted from Fan et al., 2021)

Image caption: a: Storage root morphology of different sweet potato plants; b: Comparison of storage root yield, with IA lines significantly higher than WT; c: Pyrophosphatase activity in storage roots; d: Pyrophosphate concentration in storage roots; e: Phosphorus content in roots; f: Phosphorus content in leaves (Adapted from Fan et al., 2021)

9 Future Directions for Increasing Sweet Potato Yield and Starch Content

9.1 Application of high-throughput phenotyping

High-throughput phenotyping (HTP) platforms have revolutionized the efficiency of phenotypic data collection in crop breeding. These platforms utilize advanced imaging technologies, such as hyperspectral cameras and thermal sensors, to capture detailed plant responses to environmental stimuli non-destructively (Araus and Cairns, 2014; Yang et al., 2020; Tiwari et al., 2021). The integration of HTP with aeroponic culture systems allows for precise phenotyping of both above- and below-ground plant parts, which is particularly beneficial for root crops like sweet potatoes (Tiwari et al., 2021). Field-based HTP platforms, which combine remote sensing methods with automated environmental data collection, are paving the way for more efficient crop genetic improvement (Araus and Cairns, 2014; Shakoor et al., 2017). These advancements in HTP can significantly enhance the selection efficacy for traits such as yield potential, tuber quality, and stress tolerance, thereby accelerating the development of high-yield and high-starch sweet potato varieties (Shakoor et al., 2017; Yang et al., 2020; Tiwari et al., 2021).

9.2 Adaptive breeding under climate change

Climate change poses significant challenges to crop production, necessitating the development of stress-tolerant varieties. Breeding for stress tolerance in sweet potatoes can benefit from large-scale phenotyping, which enables continuous monitoring of plant growth under various stress conditions. For instance, X-ray computed tomography (CT) has been used to monitor potato tuber development under combined heat and drought stress, revealing the potential for similar applications in sweet potatoes (Harsselaar et al., 2021). Additionally, the identification of genetic markers associated with key traits, such as starch content and stress tolerance, can facilitate the development of sweet potato varieties that are better adapted to changing environmental conditions (Kar et al., 2022; Haque et al., 2023). By leveraging these genetic insights and advanced phenotyping techniques, breeders can enhance the adaptability of sweet potatoes to diverse environments, ensuring stable yields and improved starch content under climate stress (Harsselaar et al., 2021; Kar et al., 2022; Haque et al., 2023).

9.3 Data-driven precision breeding

The advent of big data and machine learning offers unprecedented opportunities for precision breeding in sweet potatoes. High-throughput phenotyping generates vast amounts of data that, when combined with genomic information, can be analyzed using advanced statistical and machine learning techniques to identify optimal breeding strategies (Lin et al., 2007; Moreira et al., 2020). For example, polyploid genome-wide association studies (GWAS) have been used to dissect the genetic basis of complex traits, such as starch content, in sweet potatoes, identifying key genetic markers that can be targeted in breeding programs (Haque et al., 2023). Integrating these data-driven approaches with traditional breeding methods can enhance the efficiency and accuracy of selecting high-yield and high-starch sweet potato lines (Lin et al., 2007; Moreira et al., 2020; Haque et al., 2023). Moreover, the use of machine learning algorithms to analyze phenotypic and genotypic data can help predict the performance of breeding lines under different environmental conditions, further optimizing breeding strategies for improved yield and starch content (Lin et al., 2007; Moreira et al., 2020).

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Conflict of Interest Disclosure

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