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Case Study **Open Access**

Case Study of Sweet Potato Breeding for Enhanced Agronomic Traits

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Abstract This study comprehensively examines the latest advances in sweet potato (*Ipomoea batatas* L.) breeding to improve agronomic traits such as yield, disease resistance, and nutritional quality. Focus on developing varieties that meet market needs and consumer preferences, using both traditional and modern breeding techniques; Explored genetic diversity and adopted molecular breeding approaches to address biotic and abiotic stresses, highlighting significant increases in yield and nutrient content through targeted breeding programs. The findings highlight the potential of combining phenotypic selection with advanced genomic tools to accelerate the development of high-quality sweet potato varieties that contribute to food security and economic growth, especially in areas vulnerable to climate change and resource constraints.

Keywords Sweet potato breeding; Agronomic traits; Genetic diversity; Molecular breeding; Biotic and abiotic stress

1 Introduction

Sweet potato (*Ipomoea batatas* L.) is a vital crop globally, ranking as the sixth most important food crop worldwide. It is particularly significant in regions such as Sub-Saharan Africa and Mozambique, where it plays a crucial role in food security and economic stability (Swanckaert et al., 2021). The crop's adaptability to diverse environmental conditions, including drought-prone areas, further underscores its importance (Maquia et al., 2013). Sweet potato is rich in essential nutrients, including vitamins, minerals, and bioactive compounds, which contribute to its health benefits and market value (Escobar-Puentes et al., 2022).

Sweet potato breeding faces several challenges, primarily due to the crop's high genetic diversity and the complex nature of its hexaploid genome (Swanckaert et al., 2021). Traditional breeding methods, which rely on phenotypic selection and recombination, are time-consuming and often hindered by the variability in quality traits such as color, texture, and taste. Moreover, the need for improved resistance to biotic and abiotic stresses, such as pathogens and drought, adds another layer of complexity to breeding programs (Lebot et al., 2021). Despite these challenges, advancements in molecular breeding and biotechnology offer promising avenues for developing high-yielding, disease-resistant, and nutritionally superior sweet potato varieties.

This study focuses on the development of new varieties that meet market needs and consumer preferences by utilizing traditional and modern breeding techniques to improve yield, disease resistance, and nutritional quality. It has the potential to make recommendations for food security, especially in areas vulnerable to climate change and resource constraints, while also boosting economic growth through the cultivation of high-value sweet potato varieties.

2 Agronomic Traits and Genetic Basis of Sweet Potato

2.1 Key agronomic traits of sweet potato

Sweet potato (*Ipomoea batatas* L.) is a vital crop for food security, particularly in regions prone to drought and other climatic stresses. Key agronomic traits of sweet potato include tuber yield, drought tolerance, and nutritional composition. Tuber yield is influenced by several factors such as vine length, vine weight, biological yield per plant, and harvest index, which have been shown to have positive correlations with tuber yield (Jha, 2014; Qin et al., 2022). Drought tolerance is another critical trait, as sweet potato is often grown in regions with limited water availability. Drought tolerance mechanisms include changes in antioxidant enzyme activities, chlorophyll and proline concentrations, and nitrate reductase activity, which are correlated with root yield under stress conditions (Laurie et al., 2022). Nutritional composition, particularly the content of essential minerals and dietary fiber, is also a significant trait, with certain cultivars like *Bophelo* and *Ndou* showing superior nutritional profiles.

2.2 Genetic diversity of sweet potato

The genetic diversity of sweet potato is substantial, with significant variations observed across different regions and cultivars. The sweet potato germplasm collection in Mozambique exhibits high genetic, morphological, and agronomic diversity, comparable to primary centers of origin and other African collections (Hong, 2024). This diversity is crucial for breeding programs aimed at improving drought tolerance and other agronomic traits. The Mozambican germplasm includes genotypes with high potential for drought-prone regions, such as *Admarc*, *Chingova*, and *NASPOT-5*, which can be utilized in breeding programs to enhance drought resistance and yield stability (Maquia et al., 2013). The genetic variability among sweet potato cultivars is also evident in their response to drought stress, with some cultivars showing significant changes in physiological and biochemical traits that contribute to drought tolerance (Laurie et al., 2022).

2.3 Genetic mechanisms of agronomic traits

The genetic mechanisms underlying key agronomic traits in sweet potato involve complex interactions between various genes and environmental factors. Drought tolerance, is regulated through multiple signaling pathways that modify growth patterns, activate antioxidants, and accumulate stress proteins (Sapakhova et al., 2023). Marker-assisted selection (MAS) and genome-wide association studies (GWAS) have identified specific genetic markers associated with drought tolerance and other agronomic traits. For instance, transcript and metabolite markers have been used to predict drought tolerance in potato, a related crop, with high accuracy (Sprenger et al., 2017). In sweet potato, similar approaches can be employed to identify and select for drought-tolerant genotypes. The genetic basis of traits like tuber yield involves the interplay of genes controlling vine length, vine weight, and harvest index, which have been shown to have direct and indirect effects on yield (Gervais et al., 2021). Understanding these genetic mechanisms is essential for developing improved sweet potato varieties with enhanced agronomic traits.

3 Overview of Sweet Potato Breeding Methods

3.1 Conventional breeding methods

Conventional breeding methods for sweet potatoes typically involve targeted outcrossing followed by phenotypic recurrent selection over multiple generations to identify superior cultivars. This approach relies heavily on field-based phenotyping to evaluate traits such as yield, disease resistance, and quality. Despite its effectiveness, conventional breeding is time-consuming and labor-intensive, often taking several years to develop new cultivars (Slater et al., 2017).

3.2 Molecular breeding methods

3.2.1 Marker-assisted selection (MAS): application examples in sweet potato

Marker-assisted selection (MAS) uses DNA markers linked to desirable traits to facilitate the selection process. MAS has been particularly effective for traits controlled by a few major genes, such as disease resistance, MAS has been used to track resistance genes against pathogens like Phytophthora infestans in potatoes, demonstrating its potential for similar applications in sweet potatoes (Beketova et al., 2021). By integrating MAS with conventional breeding, the breeding cycle can be significantly shortened, and the efficiency of selecting superior lines can be improved (Sandhu et al., 2022).

3.2.2 Genomic selection (GS): application of genomic information in sweet potato breeding

Genomic selection (GS) is an advanced molecular breeding method that uses genome-wide markers to predict the breeding values of individuals. Unlike MAS, which focuses on specific markers, GS incorporates all available marker information to capture the effects of both major and minor genes. This approach has shown promise in improving complex traits such as yield and stress tolerance in various crops, including sweet potatoes (Varshney et al., 2017; Budhlakoti et al., 2022). GS can accelerate the breeding cycle by reducing the need for extensive phenotyping and allowing for the selection of superior genotypes based on their genomic estimated breeding values (GEBVs) (Sverrisdóttir et al., 2018; Merrick et al., 2022).

3.2.3 Gene editing techniques: potential applications of CRISPR and other tools in sweet potato

Gene editing techniques, such as CRISPR-Cas9, offer unprecedented precision in modifying specific genes associated with desirable traits. These tools can be used to introduce or knock out genes to enhance traits like disease resistance, drought tolerance, and nutritional quality. While gene editing is still in its early stages for sweet potatoes, its potential applications are vast. For example, CRISPR has been successfully used in other crops to improve traits rapidly and accurately, suggesting similar possibilities for sweet potatoes (Meiyalaghan et al., 2019). The integration of gene editing with other molecular breeding methods could further accelerate the development of superior sweet potato cultivars (Sandhu et al., 2022).

4 Case Study of Sweet Potato Breeding for Enhanced Yield

4.1 Selection and improvement of high-yield traits

The selection and improvement of high-yield traits in sweet potato breeding programs have been pivotal in enhancing crop productivity. The high genetic variability present in sweet potato populations offers significant opportunities for genetic gains through selective breeding, the use of selection indexes, such as the one proposed by Mulamba & Mock, has been effective in identifying superior individuals for root production and dual-aptitude traits, as demonstrated by the evaluation of 95 accessions and two commercial cultivars, leading to the recommendation of specific clones for further testing (Vargas et al., 2020). Additionally, the assessment of genotype × environment interactions (G × E) and stability analysis has been crucial in identifying genotypes that not only yield high but also exhibit stability across diverse environments. This approach has been successfully applied in Nigeria, where genotypes G13, G11, and G14 were identified as promising candidates due to their high mean root yield and stability (Ebem et al., 2021). The evaluation of genetic parameters and the use of multi-trait selection indexes have facilitated the identification of genotypes with high genetic variability and potential for significant genetic advances, such as the CERAT31-01, CERAT21-02, and CERAT51-30 genotypes (Otoboni et al., 2020). These methodologies underscore the importance of integrating genetic variability, selection indexes, and stability analysis in breeding programs to achieve enhanced yield traits in sweet potato.

4.2 Case analysis: development of high-yield sweet potato varieties in Nigeria

The development of high-yield sweet potato varieties in Nigeria has been a focal point of breeding programs aimed at improving productivity and food security. In a study conducted to evaluate the agronomic performance of sweet potato genotypes across different agro-ecological regions in Nigeria, significant genetic variability was observed among the genotypes, which is essential for effective crop development. For example, genotype PYT/12/074 exhibited the highest root yield in both the rainforest belt and the humid guinea savannah, highlighting its potential as a superior variety (Agbim et al., 2022). Another study focused on the evaluation of selected sweet potato landraces for high harvest index and root yield indices, identified accessions such as Kwara, Agege, and Buttermilk as high-yielding varieties suitable for inclusion in breeding programs (Nwankwo et al., 2018). The use of multi-trait selection indexes and stability analysis in multi-environmental evaluations has proven effective in selecting genotypes with superior agronomic performance and stability. The CropInd tool, facilitated the selection of the 0113-672COR variety for the Colombian Caribbean region (Figure 1), demonstrating the applicability of such methodologies in different contexts (Rosero et al., 2023). These case studies illustrate the successful application of advanced breeding techniques and the importance of selecting genotypes with high yield potential and stability to enhance sweet potato production in Nigeria.

5 Improvement of Sweet Potato Quality Traits

5.1 Breeding strategies for increasing starch content

Enhancing the starch content in sweet potatoes is a critical objective for breeding programs aimed at improving the crop’s agronomic traits. One effective strategy involves the use of polyploid genome-wide association studies (GWAS) to identify genetic markers associated with high starch content. For instance, a study identified significant single-nucleotide polymorphisms (SNPs) linked to starch content in a mapping population of purple-fleshed sweet potatoes. These markers, particularly those located on homologous group 15, were found to have a positive effect on starch accumulation, with the gene *IbGBSSI* playing a crucial role in amylose biosynthesis (Haque et al., 2023). Additionally, somaclonal variation has been employed to create genetic variability, leading to the development of somaclones with significantly higher starch content compared to their parent varieties. This method has proven effective in increasing both the fresh and dry weights of tubers, as well as upregulating key starch-synthesis-related genes (Adly et al., 2023). These advanced breeding techniques, including the use of molecular markers and somaclonal variation, provide a robust framework for enhancing starch content in sweet potatoes.

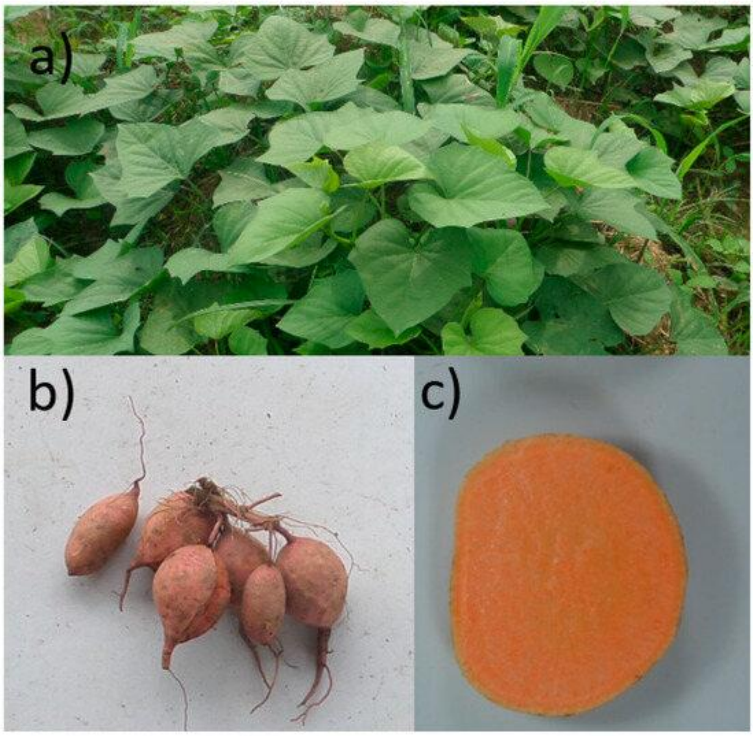

Figure 1 Morphological characteristics of Agrosavia Aurora (0113-672COR), (a) plant morphology, (b) storage root shape, (c) root flesh (Adopted from Rosero et al., 2023)

5.2 Breeding for increased vitamin A content

Increasing the vitamin A content in sweet potatoes is another vital breeding goal, particularly for addressing malnutrition in regions with high vitamin A deficiency. Orange-fleshed sweet potatoes (OFSP) are a primary focus due to their high beta-carotene content, a precursor of vitamin A. Studies have shown that genotype selection plays a significant role in enhancing beta-carotene levels. For example, certain OFSP genotypes, such as *Ininda*, *Gloria*, and *Amelia*, have demonstrated higher yields and beta-carotene content across different agro-climatic zones, indicating their potential to alleviate vitamin A deficiency (Lamaro et al., 2023). Furthermore, breeding programs that are responsive to market segment needs and demographic changes have been recommended to maximize the impact of these nutritional improvements. By targeting regions with high stunting rates and vitamin A deficiency, breeding programs can develop varieties that not only meet nutritional needs but also address gender inequalities and poverty (Ojwang et al., 2023). These strategies underscore the importance of a multifaceted approach in breeding sweet potatoes for enhanced vitamin A content, combining genotype selection with socio-economic considerations.

6 Case Studies of Sweet Potato Breeding for Environmental Adaptability and Stress Resistance

6.1 Genetic basis of adaptability traits

The genetic basis of adaptability traits in sweet potato is crucial for developing varieties that can withstand environmental stresses such as drought. Sweet potato, being a key crop for food security, especially in developing countries, faces significant challenges due to osmotic stress, which impacts its agronomic and economic productivity. Plants respond to water stress through various signaling pathways that modify growth patterns, activate antioxidants, accumulate suitable solutes and chaperones, and produce stress proteins. These physiological, metabolic, and genetic modifications serve as indicators for selecting drought-tolerant genotypes (Figure 2). The main objective of sweet potato breeding in drought-affected regions is to develop varieties that combine drought tolerance with high yields. This involves studying the physiological and biochemical features of certain varieties to implement effective drought resistance measures. By regulating genetics, the creation of drought-resistant varieties can become cost-effective for smallholder farmers (Sapakhova et al., 2023). The use of multi-trait selection indices, stability, and genetic gain analysis in multi-environmental evaluations has proven effective in selecting superior sweet potato genotypes that exhibit better profiles and stability (Rosero et al., 2023). Transcriptomic analyses have also revealed mechanisms for different drought tolerance levels in sweet potato cultivars, identifying new genes and transcripts that play roles in drought response (Liu et al., 2023).

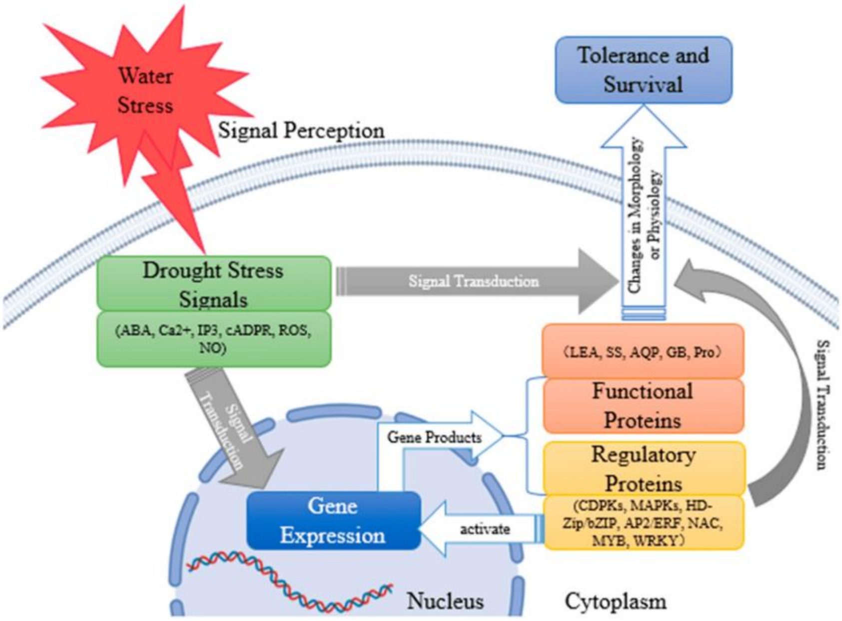

Figure 2 Mechanism of plant tolerance to drought stress (Adopted from Sapakhova et al., 2023)

6.2 Case analysis: promotion of drought-resistant sweet potato in northern China

In Northern China, where drought is a frequent environmental stress during the sweet potato growing season, the promotion of drought-resistant sweet potato varieties has been a significant focus. China, having the largest sweet potato planting area worldwide, faces challenges in maintaining growth and yield under drought conditions. Studies have shown that the application of salicylic acid (SA) can mitigate drought stress in sweet potato by enhancing antioxidant defense systems and modulating abscisic acid-related gene expression (Zhao, 2024). This approach has been effective in reducing oxidative damage and maintaining optimized osmotic environments in drought-stressed plants. For instance, foliar spraying of SA on drought-stressed sweet potato varieties has been shown to induce resistance, thereby increasing growth and crop yield (Huang et al., 2022). Transcriptomic analyses have provided insights into the molecular mechanisms underlying drought tolerance in different sweet potato cultivars, revealing that drought-tolerant cultivars regulate various metabolic pathways to cope with stress. These findings are crucial for selecting and promoting drought-resistant sweet potato varieties in regions like Northern China, where drought conditions are prevalent (Liu et al., 2023).

7 Summary of Case Analyses and Evaluation of Breeding Effectiveness

7.1 Comprehensive analysis of case studies

The case studies on sweet potato breeding have demonstrated significant advancements in addressing key agronomic traits such as drought tolerance, yield improvement, and nutritional enhancement. The study by the

International Potato Center (CIP) highlighted the importance of developing varieties that cater to specific market segments, focusing on poverty alleviation, nutrition, and gender responsiveness (Ojwang et al., 2023). Similarly, research conducted in Mozambique identified genotypes with high drought tolerance, which are crucial for regions frequently experiencing drought. The agronomic characterization of sweet potato accessions collected from diverse regions has provided valuable insights into the genetic diversity and potential for breeding programs (Vargas et al., 2017). These comprehensive analyses underscore the effectiveness of targeted breeding strategies in enhancing the agronomic performance of sweet potatoes.

7.2 Cost-benefit analysis of breeding projects

The cost-benefit analysis of sweet potato breeding projects reveals a favorable return on investment, particularly when breeding efforts are aligned with specific agronomic and environmental challenges. For example, the development of drought-tolerant varieties not only improves yield stability but also reduces the economic risks for smallholder farmers in drought-prone areas (Sapakhova et al., 2023). The integration of genetic, morphological, and agronomic data in breeding programs has proven to be cost-effective, as it allows for the selection of high-performing genotypes with desirable traits (Maquia et al., 2013). The use of advanced breeding techniques, such as clonal selection and molecular characterization, has streamlined the breeding process, reducing the time and resources required to develop new varieties (Kai et al., 2013). Overall, the economic benefits of these breeding projects are substantial, contributing to increased productivity and resilience in sweet potato cultivation.

7.3 Impact of breeding effectiveness on industry development

The effectiveness of sweet potato breeding programs has had a profound impact on the development of the sweet potato industry. The introduction of high-yielding and stress-tolerant varieties has significantly boosted production, thereby enhancing food security and economic stability in many regions (Ebem et al., 2021). The focus on traits such as high starch yield and improved nutritional content has also opened new market opportunities, particularly in the food processing and biofuel industries. Additionally, the emphasis on gender-responsive breeding programs has promoted greater inclusivity and equity within the agricultural sector, empowering women farmers and contributing to broader social development goals (Ojwang et al.,2023). The cumulative effect of these breeding efforts has been the transformation of the sweet potato industry, making it more resilient, productive, and inclusive.

8 Conclusion

The case study on sweet potato breeding for enhanced agronomic traits has yielded several significant findings. The use of multi-trait selection indices, such as the CropInd tool, has proven effective in identifying superior genotypes by incorporating variables like total and commercial fresh root yield and survival percentage across multiple environments. Additionally, the study highlighted the importance of targeting market segment needs, emphasizing the necessity for breeding programs to be demand-driven and responsive to changing customer preferences, poverty alleviation, nutrition, and gender considerations. The agronomic characterization of sweet potato accessions collected from traditional communities revealed specific accessions suitable for various uses, including human consumption, industrial applications, and animal feed. Furthermore, the evaluation of experimental white-fleshed sweet potato genotypes demonstrated the potential of certain genotypes, such as UZBD-L1-04, to perform well in commercial fields. The application of new breeding technologies, such as CRISPR/Cas9, has also been identified as a promising approach for improving the nutritional value and overall agronomic profile of sweet potatoes.

Future breeding efforts should continue to leverage multi-trait selection indices and stability analyses to identify and develop genotypes with superior agronomic traits across diverse environmental conditions. It is also recommended that breeding programs adopt a more market-oriented approach, focusing on the specific needs of different market segments, including those related to poverty alleviation, nutrition, and gender equity. The genetic variability observed in sweet potato accessions should be further explored to enhance root production and dual-aptitude traits, with particular attention to accessions like VR13-61, VR13-11, and VR13-22. Additionally, the integration of new breeding technologies, such as CRISPR/Cas9, should be prioritized to achieve precise and efficient genetic improvements without the regulatory challenges associated with transgenic products. Understanding the genetic divergence and interrelationships among various agronomic traits will be crucial for planning effective breeding programs aimed at increasing tuber yield and quality.

The advancements in sweet potato breeding for enhanced agronomic traits hold great promise for addressing food security, nutrition, and economic challenges. The successful identification and development of superior genotypes through multi-trait selection and stability analyses, combined with a market-oriented breeding approach, can lead to the release of new varieties that meet the diverse needs of different regions and populations. The incorporation of new breeding technologies will further accelerate the development of high-yielding, nutritionally enhanced, and environmentally resilient sweet potato varieties. Continued research and collaboration among breeders, researchers, and stakeholders will be essential to realize the full potential of sweet potato breeding programs and contribute to sustainable agricultural development.

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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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