BioSci Publisher©
**Bioscience Methods 2025, Vol.16, No.1, 23-32**
http://bioscipublisher.com/index.php/bm

**Research Insight** **Open Access**

# Recent Insights into Molecular Breeding for High Yield Sweet Potato Cultivars

Liang Zhang, Honghu Ji, Meiqiao Jiang, Ziyu Zhong, Linrun Cheng ✉
Jinhua Academy of Agricultural Sciences/Jinhua Key Laboratory of Innovative Utilization of Special Grain Crops Resources in Central Zhejiang Province 321017, Jinhua, Zhejiang, China
✉ Corresponding email: clrjh@126.com

Bioscience Methods, 2025, Vol.16, No.1 doi: 10.5376/bm.2025.16.0003
Received: 06 Nov., 2024
Accepted: 18 Jan., 2025
Published: 06 Feb., 2025

**Preferred citation for this article**:
Zhang L., Ji H.H., Jiang M.Q., Zhong Z.Y., and Chen L.R., 2025, Recent insights into molecular breeding for high yield sweet potato cultivars, Bioscience Methods, 16(1): 23-32 (doi: 10.5376/bm.2025.16.0003)

**Abstract** Sweet potato is a vital staple crop with significant potential to address global food security challenges. Developing high-yield cultivars is essential to enhance productivity and meet increasing demand, and molecular breeding has emerged as a promising approach for achieving these goals. This study explores recent advancements in molecular breeding techniques applied to sweet potato, with a focus on understanding its unique genomic architecture and genetic diversity. Key methods such as marker-assisted selection (MAS), genomic selection (GS), CRISPR-based gene editing, and RNA interference (RNAi) are examined for their role in improving yield-related traits, photosynthetic efficiency, storage root development, and stress tolerance. A case study on breeding programs in China highlights successful cultivar development and lessons for global breeding efforts. This study also addresses challenges in molecular breeding, including polyploidy complexities and limitations in genomic tools, while outlining future opportunities such as the integration of artificial intelligence (AI) and international collaborations. This study emphasizes the need for targeted breeding strategies and policy support to ensure the development of resilient, high-yield cultivars capable of contributing to food security and sustainable agriculture.

**Keywords** Sweet potato; Molecular breeding; CRISPR; Marker-assisted selection; Yield improvement

## 1 Introduction

Sweet potato (*Ipomoea batatas* L.) is a vital root crop globally, known for its adaptability to diverse environmental conditions and its nutritional benefits. It ranks as one of the most important crops in many countries, including Mozambique, where it is the third most significant root crop after cassava and maize (Maquia et al., 2013). The crop's versatility allows it to be cultivated in various climates, from tropical to temperate regions, making it a staple food source in many parts of the world (Karan and Şanli, 2021).

High-yield sweet potato cultivars are crucial for enhancing food security, especially in regions prone to food shortages. The ability to produce more food per unit area can significantly impact the availability of nutritious food, particularly in developing countries. For instance, in Turkey, expanding sweet potato cultivation to new regions has been suggested to meet the increasing domestic demand (Karan and Şanli, 2021). High-yield cultivars not only ensure a stable food supply but also contribute to economic stability by providing farmers with a reliable source of income (Swanckaert et al., 2021).

Molecular breeding has emerged as a powerful tool in crop improvement, enabling the development of cultivars with desirable traits such as high yield, drought tolerance, and disease resistance. By utilizing genetic, morphological, and agronomic diversity, researchers can identify and select genotypes that are best suited for specific environmental conditions. This approach has been particularly effective in characterizing sweet potato germplasm and identifying genotypes with high agronomic potential, which can be used in breeding programs to develop superior cultivars (Maquia et al., 2013; Teshome et al., 2020).

This study aims to provide recent insights into the molecular breeding of sweet potato for high-yield cultivars. It will explore the genetic diversity within sweet potato germplasm, the assessment of yield and quality traits in different environmental conditions, and the potential of molecular breeding techniques to enhance sweet potato production. By examining these aspects, the study seeks to highlight the importance of molecular breeding in ensuring food security and improving the livelihoods of farmers globally.

## 2 Sweet Potato Genetics and Genomics: Foundation for Molecular Breeding

### 2.1 Genomic architecture of sweet potato (hexaploidy and challenges)

Sweet potato (*Ipomoea batatas*) is a hexaploid species, meaning it has six sets of chromosomes. This complex genomic structure poses significant challenges for genetic and genomic studies. The hexaploid nature of sweet potato results in a wide range of meiotic configurations and linkage phases, complicating gene action and genotype data quality (Gemenet et al., 2020). Additionally, the high level of heterozygosity and the presence of multiple homologous chromosomes make it difficult to develop accurate genetic maps and perform genome-wide association studies (Hirakawa et al., 2015; Kim et al., 2017).

### 2.2 Recent advancements in sweet potato genome sequencing

Recent advancements in genome sequencing technologies have significantly improved our understanding of the sweet potato genome. Single-molecule real-time sequencing has enabled the identification of massive full-length cDNAs and alternative splicing events, facilitating comparative and functional genomics studies in sweet potato (Figure 1) (Ding et al., 2019). Moreover, the development of a half haplotype-resolved genome has provided insights into the hexaploidization history of sweet potato, allowing for a more detailed analysis of its genomic structure. These advancements have paved the way for more precise and efficient molecular breeding strategies.

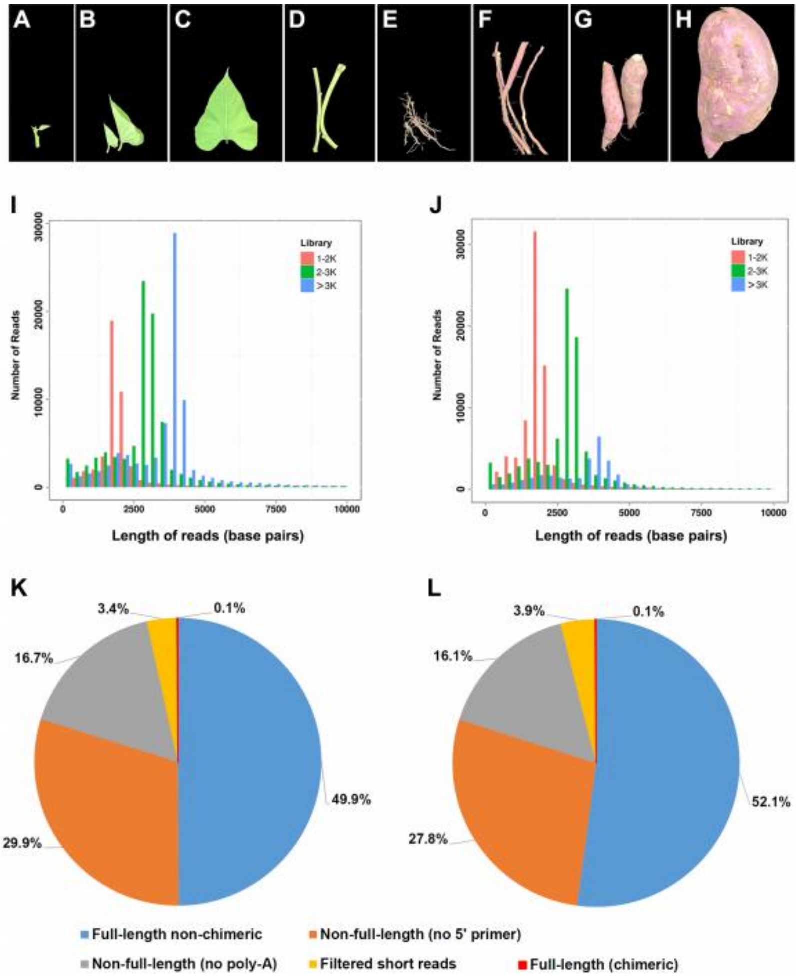

Figure 1 Plant materials used in this study and summary of PacBio RS II single-molecule real-time (SMRT) sequencing (Adopted from Ding et al., 2019)

Image caption: (A-H) Photos showing the developmental stages and overall morphology of eight tissues in *I. batatas* used for SMRT sequencing in this study. (A) Young leaves; (B) mature leaves; (C) apical shoots; (D) mature stems; (E) fibrous roots; (F) initiating tuberous roots; (G) expanding tuberous roots; (H) mature tuberous roots. The photos were adopted from our previous report (Ding et al., 2017). Number and length distributions of 220 035 reads in *I. batatas* (I) and 195,188 reads in *I. trifida* (J) from different PacBio libraries (fractionated size: 1-2, 2-3, >3 kb); Proportion of different types of PacBio reads in *I. batatas* (K) and *I. trifida* (L) (Adopted from Ding et al., 2019)

### 2.3 Identification of key genes linked to yield traits

The identification of key genes linked to yield traits is crucial for the development of high-yield sweet potato cultivars. Quantitative trait loci (QTL) mapping using whole-genome next-generation sequencing (NGS) has been employed to identify clusters of single nucleotide polymorphisms (SNPs) linked to important agronomic traits, such as storage root anthocyanin content (Yamakawa et al., 2021). Additionally, the construction of genetic maps using EST-SSR markers has facilitated the identification of QTLs associated with major agronomic characters in hexaploid sweet potato (Kim et al., 2017). These efforts have led to the development of tightly linked DNA markers that can be used in marker-assisted selection for yield improvement (Zhang, 2024).

### 2.4 Genetic diversity and its implications for molecular breeding

Genetic diversity is a critical factor in the success of molecular breeding programs. Studies on the genetic diversity of sweet potato and its diploid ancestor, *Ipomoea trifida*, have revealed a wealth of genetic variation that can be harnessed for breeding purposes (Hirakawa et al., 2015). The comprehensive analysis of intraspecific and interspecific sequence data has provided valuable insights into the genetic makeup of sweet potato, enabling the identification of diverse alleles and haplotypes that can be targeted for trait improvement (Ding et al., 2019; Amundson et al., 2020). Understanding and utilizing this genetic diversity is essential for the development of robust and high-yield sweet potato cultivars through molecular breeding. By leveraging these recent insights into the genetics and genomics of sweet potato, researchers can develop more effective molecular breeding strategies to enhance yield and other desirable traits in this important crop.

## 3 Techniques and Tools in Molecular Breeding for Sweet Potato

### 3.1 Marker-assisted selection (MAS) in sweet potato breeding

Marker-assisted selection (MAS) has been a cornerstone in modern plant breeding, enabling the identification and selection of desirable traits with greater precision and efficiency. MAS utilizes molecular markers that are closely linked to target genes, facilitating the selection process. In sweet potato breeding, MAS has been instrumental in mapping and introgressing genes associated with high yield and disease resistance. The development of high-throughput sequencing technologies, such as genotyping-by-sequencing (GBS), has further enhanced the efficiency of MAS by allowing the simultaneous discovery and genotyping of single nucleotide polymorphisms (SNPs) across the genome (Figure 2) (He et al., 2014; Hasan et al., 2021). This approach has significantly shortened the breeding cycle and increased the accuracy of selecting superior cultivars (Jannink et al., 2010; Tiwari et al., 2022).

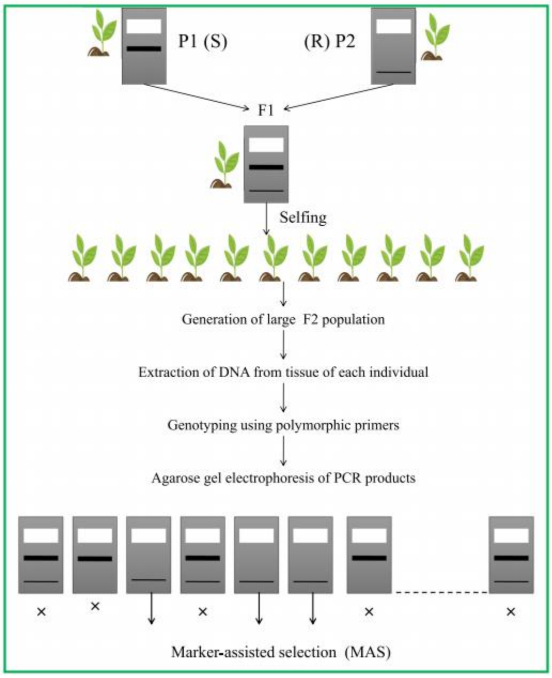

Figure 2 The figure explains the basic procedure of marker-assisted selection (Adopted from Hasan et al., 2021)

### 3.2 Genomic selection (GS) strategies for yield improvement

Genomic selection (GS) represents a paradigm shift in plant breeding, particularly for complex traits controlled by multiple genes with small effects. Unlike MAS, which focuses on individual loci, GS uses genome-wide marker data to predict the performance of breeding lines. This method has shown great promise in accelerating genetic gains and improving yield in crops like sweet potato. By incorporating high-throughput phenotyping and genotyping, GS can enhance the accuracy of selection and reduce the breeding cycle time (Merrick et al., 2022; Sandhu et al., 2022). The integration of machine learning and advanced statistical models further refines the prediction accuracy, making GS a powerful tool for sweet potato yield improvement (Jannink et al., 2010).

### 3.3 CRISPR-based gene editing for targeted trait enhancement

CRISPR-Cas9 technology has revolutionized the field of genetic engineering by providing a precise and efficient method for genome editing. In sweet potato breeding, CRISPR-based gene editing can be used to introduce or modify specific genes associated with desirable traits such as increased yield, disease resistance, and improved nutritional content. This technology allows for targeted modifications without the introduction of foreign DNA, making it a more acceptable approach for developing genetically modified organisms (GMOs) (Dheer et al., 2020; Ahmad et al., 2022). The application of CRISPR in sweet potato breeding holds great potential for creating high-yield cultivars with enhanced traits in a relatively short time frame (Sandhu et al., 2022).

### 3.4 RNA interference (RNAi) in modifying metabolic pathways

RNA interference (RNAi) is a powerful tool for silencing specific genes and has been widely used to study gene function and develop crops with improved traits. In sweet potato, RNAi can be employed to modify metabolic pathways that influence yield and quality. For instance, silencing genes involved in starch biosynthesis or degradation can lead to increased starch content and improved tuber quality. RNAi has also been used to enhance resistance to pests and diseases by targeting genes essential for pathogen survival or virulence (Ahmad et al., 2022). The use of RNAi in sweet potato breeding offers a versatile approach to fine-tune metabolic pathways and achieve desired phenotypic outcomes (Dheer et al., 2020). By leveraging these advanced molecular breeding techniques, sweet potato breeders can develop high-yield cultivars more efficiently and effectively, addressing the growing demand for this important staple crop.

## 4 Trait-Based Molecular Approaches for High Yield Cultivars

### 4.1 Yield-related traits and their molecular regulation

Yield-related traits in sweet potatoes, such as tuber size, number, and overall biomass, are critical for achieving high yield cultivars. Molecular regulation of these traits involves identifying and manipulating key genetic markers associated with high yield. Advanced plant breeding tools, including genetic mapping and transgenic approaches, have been instrumental in pinpointing these markers. Techniques such as TALENS, CRISPR-Cas9, RNAi, and cisgenesis have been successfully employed to enhance yield-related traits by modifying specific genes responsible for tuber development and growth (Ahmar et al., 2020; Ahmad et al., 2022).

### 4.2 Improvement of photosynthetic efficiency through gene modification

Photosynthetic efficiency is a pivotal factor in determining the overall yield of sweet potato cultivars. Enhancing this efficiency can be achieved through gene modification techniques that optimize the photosynthetic pathways. Recent advances in genome editing, particularly using CRISPR-Cas9, have enabled precise modifications in genes that regulate photosynthesis. These modifications can lead to improved light absorption, carbon fixation, and overall energy conversion efficiency, thereby boosting the yield potential of sweet potato plants (Ahmar et al., 2020; Ahmad et al., 2022).

### 4.3 Molecular approaches to increase storage root development

The development of storage roots is a key determinant of sweet potato yield. Molecular approaches to enhance storage root development include the use of genetic selection and mutagenic breeding to identify and propagate desirable traits. Additionally, whole-genome sequencing and functional genomic tools have been employed to understand the genetic basis of storage root formation. By targeting specific genes involved in root development, researchers can manipulate these pathways to increase the size and number of storage roots, ultimately leading to higher yields (Gebhardt, 2013).

### 4.4 Enhancing stress tolerance (drought, salinity, and pest resistance) for stable yields

Stress tolerance is crucial for maintaining stable yields in sweet potato cultivars, especially under adverse environmental conditions. Molecular breeding techniques have been utilized to enhance tolerance to drought, salinity, and pests. Genetic selection and genome editing tools, such as CRISPR-Cas9, have been used to introduce or modify genes that confer resistance to these stresses. By improving the plant's ability to withstand environmental challenges, these molecular approaches ensure consistent and high yields even in suboptimal growing conditions (Otoboni et al., 2020; Tiwari et al., 2020).

In summary, the integration of advanced molecular techniques in sweet potato breeding programs holds significant promise for developing high yield cultivars. By focusing on yield-related traits, photosynthetic efficiency, storage root development, and stress tolerance, researchers can create robust sweet potato varieties capable of meeting the growing food demand (Basu et al., 2018).

## 5 Case Study: Genetic Resource Utilization for Sweet Potato Breeding in China

### 5.1 Overview of molecular breeding projects in China

China has been actively involved in molecular breeding projects to enhance the yield and quality of sweet potato cultivars. These projects leverage advanced biotechnological tools such as SSR markers and RNA-seq to identify and utilize genetic diversity within sweet potato germplasm. For instance, the phenotypic and genetic diversity analysis of potato cultivars in China has provided a framework for similar studies in sweet potatoes, highlighting the importance of molecular markers in breeding programs (Hu et al., 2022). Additionally, the integration of market segment needs into breeding strategies has been emphasized to ensure that new cultivars meet the demands of various stakeholders, including those focused on poverty alleviation and nutrition (Ojwang' et al., 2023).

### 5.2 Key high-yield cultivars developed through molecular techniques

Several high-yield sweet potato cultivars have been developed through molecular breeding techniques in China. For example, the use of selection indexes and genetic parameters has led to the identification of promising genotypes such as CERAT31-01, CERAT21-02, and CERAT51-30, which exhibit high beta-carotene content and significant yield potential (Otoboni et al., 2020). Moreover, the evaluation of sweet potato genotypes through crossbreeding has resulted in the development of cultivars like CERAT16-20 and CERAT31-1, which are noted for their high productivity and suitability for both household consumption and industrial use (Oliveira et al., 2022).

### 5.3 Challenges and achievements in breeding programs

Breeding programs in China have faced several challenges, including the need to balance genetic diversity with the selection of high-yield traits. The high genetic variability within sweet potato populations has been both a challenge and an opportunity, requiring sophisticated selection strategies to achieve genetic gains (Vargas et al., 2020). Despite these challenges, significant achievements have been made, such as the development of genotypes with high dry matter content and resistance to sweet potato virus disease (SPVD), which are crucial for stable and high yields. Additionally, the use of genotype-by-environment interaction analysis has been instrumental in identifying genotypes that perform well across diverse environmental conditions (Ngailo et al., 2019).

### 5.4 Lessons learned for global sweet potato breeding initiatives

The experiences from China's molecular breeding projects offer valuable lessons for global sweet potato breeding initiatives. One key lesson is the importance of integrating molecular techniques with traditional breeding methods to enhance the efficiency and effectiveness of breeding programs. The success of using SSR markers and RNA-seq in identifying valuable genetic traits can be replicated in other regions to improve sweet potato cultivars (Hu et al., 2022; Wei et al., 2023). Furthermore, the focus on market-driven breeding strategies ensures that new cultivars meet the specific needs of different regions, thereby maximizing their impact on food security and nutrition (Ojwang et al., 2023). Lastly, the emphasis on genetic diversity and the use of advanced statistical tools for genotype evaluation can help other countries develop robust and high-yield sweet potato cultivars (Ngailo et al., 2019; Otoboni et al., 2020; Vargas et al., 2020).

## 6 Challenges and Opportunities in Molecular Breeding of Sweet Potato

### 6.1 Polyploidy and its complexity in molecular breeding

Polyploidy presents a significant challenge in the molecular breeding of sweet potato due to the complexity of its genome. Sweet potato is an autopolyploid species, meaning it has multiple sets of chromosomes, which complicates genetic analysis and breeding efforts. The presence of multiple homologous chromosomes can lead to difficulties in SNP identification and validation, as well as in the development of molecular markers (You et al., 2018; Yamakawa et al., 2021; Haque et al., 2023). For instance, the polyploid genome-wide association study (GWAS) has been used to dissect the genetic basis of complex traits such as starch content, but the polyploid nature of sweet potato adds layers of complexity to these analyses. Despite these challenges, advancements in high-throughput genotyping tools, such as SNP arrays, are helping to overcome some of these obstacles by providing more accurate and efficient genotyping methods for polyploid crops.

### 6.2 Limitations of current genomic tools and datasets

The current genomic tools and datasets available for sweet potato breeding are still limited, which hampers the progress of molecular breeding programs. Although sequencing technologies have advanced, the assembly and analysis of polyploid genomes remain challenging. The lack of comprehensive and high-quality reference genomes for sweet potato limits the ability to perform detailed genetic analyses and develop effective molecular markers (Visser et al., 2014). Additionally, the high cost and technical complexity of next-generation sequencing and other genomic tools can be prohibitive for many breeding programs (Slater et al., 2017; Pandey et al., 2023). There is a need for more robust and cost-effective genomic tools that can handle the complexity of polyploid genomes and provide reliable data for breeding purposes.

### 6.3 Integration of high-throughput phenotyping with molecular breeding

Integrating high-throughput phenotyping with molecular breeding offers a promising opportunity to accelerate the development of high-yield sweet potato cultivars. High-throughput phenotyping technologies, such as automated imaging systems and sensor-based field phenotyping, can provide large-scale and precise phenotypic data that are essential for effective selection in breeding programs (Slater et al., 2017). These technologies enable the rapid assessment of multiple traits, including those related to yield, disease resistance, and quality, thereby enhancing the efficiency of breeding efforts. Combining high-throughput phenotyping with genomic selection and marker-assisted selection can significantly reduce the breeding cycle and improve the accuracy of selecting superior cultivars (Sverrisdóttir et al., 2017; Pandey et al., 2022).

### 6.4 Opportunities for international collaboration and technology sharing

International collaboration and technology sharing present significant opportunities to advance the molecular breeding of sweet potato. Collaborative efforts can facilitate the exchange of genetic resources, knowledge, and technologies, thereby overcoming some of the limitations faced by individual breeding programs. For example, sharing high-quality genomic datasets and advanced phenotyping tools can help standardize breeding practices and improve the overall efficiency of sweet potato breeding (Visser et al., 2014; Slater et al., 2017). Additionally, international partnerships can provide access to funding and technical expertise, which are crucial for developing and implementing cutting-edge breeding technologies. By working together, researchers and breeders can accelerate the development of high-yield, resilient sweet potato cultivars that can contribute to global food security (Guo et al., 2023).

## 7 Future Directions and Recommendations

### 7.1 Need for deeper understanding of sweet potato functional genomics

To advance the molecular breeding of sweet potatoes, a deeper understanding of functional genomics is essential. Functional genomics approaches, such as transcriptomics and allele mining, can identify functional markers (FMs) closely associated with phenotypic traits, thereby increasing selection efficiencies for developing elite cultivars (Salgotra and Stewart, 2020). Additionally, the development of genetic maps and quantitative trait loci (QTL) analysis can facilitate the identification of key genes involved in desirable traits such as yield, disease resistance, and nutritional content (Kim et al., 2017). The integration of these genomic tools will provide a robust platform for the precise selection of high-yield sweet potato cultivars.

### 7.2 Potential of AI and machine learning in molecular breeding

Artificial intelligence (AI) and machine learning (ML) hold significant potential in revolutionizing molecular breeding. These technologies can analyze large datasets generated from genomic studies to predict the performance of breeding lines and identify optimal breeding strategies. For instance, high-throughput sequencing data combined with AI algorithms can enhance the prediction accuracy of genomic selection models, thereby accelerating the breeding process (Caruana et al., 2019). The application of AI and ML can also optimize the identification of SNP markers and their association with complex traits, leading to more efficient breeding programs (Haque et al., 2023).

### 7.3 Policy recommendations to support molecular breeding research

To support the advancement of molecular breeding in sweet potatoes, several policy recommendations are necessary. Governments and funding agencies should prioritize investments in genomic research and the development of advanced breeding technologies. Policies should also encourage public-private partnerships to facilitate the transfer of technology and knowledge from research institutions to breeding programs. Additionally, regulatory frameworks need to be updated to accommodate the use of genome editing tools such as CRISPR-Cas9, ensuring that new cultivars can be developed and commercialized efficiently (Ahmad et al., 2022). Support for training programs in molecular breeding techniques will also be crucial to build the necessary human resource capacity.

### 7.4 Vision for the next generation of high-yield sweet potato cultivars

The next generation of high-yield sweet potato cultivars will be characterized by enhanced nutritional content, disease resistance, and adaptability to diverse environmental conditions. By leveraging advanced molecular techniques such as genome editing, marker-assisted selection, and functional genomics, breeders can develop cultivars with optimized traits for both yield and quality (Peng, 2011; Vargas et al., 2020). The integration of AI and ML in breeding programs will further streamline the selection process, enabling the rapid development of superior cultivars. Ultimately, these advancements will contribute to global food security by providing resilient and high-yielding sweet potato varieties that can meet the demands of a growing population (Ngailo et al., 2019; Otoboni et al., 2020).

## 8 Concluding Remarks

Recent advancements in molecular breeding have significantly contributed to the development of high-yield sweet potato cultivars. Key findings from various studies highlight the importance of integrating traditional and modern breeding techniques to enhance drought tolerance, yield, and nutritional quality. For instance, the use of molecular markers and genetic mapping has been instrumental in identifying traits associated with drought resistance and high yield. Additionally, genome editing tools such as CRISPR-Cas9 have opened new avenues for rapid and precise genetic improvements. Studies have also emphasized the need for breeding programs to be demand-driven, addressing specific market needs and socio-economic factors such as poverty, malnutrition, and gender inequality.

Molecular breeding holds immense promise for enhancing global food security, particularly in the context of climate change and increasing food demand. By employing advanced genetic tools, researchers can develop sweet potato varieties that are not only high-yielding but also resilient to environmental stresses such as drought. This is crucial for smallholder farmers in developing countries who rely on sweet potato as a staple crop. Moreover, the ability to rapidly develop new cultivars through techniques like speed breeding and genome editing can significantly shorten the breeding cycle, making it possible to meet the urgent food needs of a growing global population. The integration of molecular breeding with traditional methods also ensures that the new varieties are well-adapted to local conditions and farmer preferences.

Future research in sweet potato breeding should focus on several key areas to maximize the benefits of molecular breeding. First, there is a need for more comprehensive studies on the genetic basis of complex traits such as starch content and drought tolerance, which can be facilitated by polyploid genome-wide association studies (GWAS). Second, breeding programs should continue to prioritize the development of varieties that address specific socio-economic challenges, including poverty alleviation and nutritional deficiencies. Third, the adoption of advanced breeding technologies like CRISPR-Cas9 and speed breeding should be expanded to accelerate the development of new cultivars. Finally, collaborative efforts between researchers, policymakers, and farmers are essential to ensure that the benefits of molecular breeding are widely disseminated and adopted, ultimately contributing to global food security and sustainable agriculture.

## Acknowledgments

We are grateful to Dr. Huang for critically reading the manuscript and providing valuable feedback that improved the clarity of the text. We express our heartfelt gratitude to the two anonymous reviewers for their valuable comments on the manuscript.

## 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.

## References

Ahmad D., Zhang Z., Rasheed H., Xu X., and Bao J., 2022, Recent advances in molecular improvement for potato tuber traits, International Journal of Molecular Sciences, 23(17): 9982.
https://doi.org/10.3390/ijms23179982

Ahmar S., Gill R., Jung K., Faheem A., Qasim M., Mubeen M., and Zhou W., 2020, Conventional and molecular techniques from simple breeding to speed breeding in crop plants: recent advances and future outlook, International Journal of Molecular Sciences, 21(7): 2590.
https://doi.org/10.3390/ijms21072590

Amundson K., Ordoñez B., Santayana M., Tan E., Henry I., Mihovilovich E., Bonierbale M., and Comai L., 2020, Genomic outcomes of haploid induction crosses in potato (*Solanum tuberosum* L.), Genetics, 214(2): 369-380.
https://doi.org/10.1534/genetics.119.302843

Basu U., Bajaj D., Sharma A., Malik N., Daware A., Narnoliya L., Thakro V., Upadhyaya H., Kumar R., Tripathi S., Bharadwaj C., Tyagi A., and Parida S., 2018, Genetic dissection of photosynthetic efficiency traits for enhancing seed yield in chickpea, Plant, Cell and Environment, 42(1): 158-173.
https://doi.org/10.1111/pce.13319

Caruana B., Pembleton L., Constable F., Rodoni B., Slater A., and Cogan N., 2019, Validation of genotyping by sequencing using transcriptomics for diversity and application of genomic selection in tetraploid potato, Frontiers in Plant Science, 10: 670.
https://doi.org/10.3389/fpls.2019.00670

Dheer P., Rautela I., Sharma V., Dhiman M., Sharma A., Sharma N., and Sharma M., 2020, Evolution in crop improvement approaches and future prospects of molecular markers to CRISPR/Cas9 system, Gene, 753: 144795.
https://doi.org/10.1016/j.gene.2020.144795

Ding N., Cui H., Miao Y., Tang J., Cao Q., and Luo Y., 2019, Single-molecule real-time sequencing identifies massive full-length cDNAs and alternative-splicing events that facilitate comparative and functional genomics study in the hexaploid crop sweet potato, PeerJ, 7: e7933.
https://doi.org/10.7717/peerj.7933

Gebhardt C., 2013, Bridging the gap between genome analysis and precision breeding in potato, Trends in genetics, 29(4): 248-256.
https://doi.org/10.1016/j.tig.2012.11.006

Gemenet D., Gemenet D., Lindqvist-Kreuze H., Boeck B., Pereira G., Pereira G., Mollinari M., Zeng Z., Yencho G., and Campos H., 2020, Sequencing depth and genotype quality: accuracy and breeding operation considerations for genomic selection applications in autopolyploid crops, Theoretical and Applied Genetics, 133: 3345-3363.
https://doi.org/10.1007/s00122-020-03673-2

Guo H., Zhou M., Zhang G., He L., Yan C., Wan M., Hu J., He W., Zeng D., Zhu B., and Zeng Z., 2023, Development of homozygous tetraploid potato and whole genome doubling-induced the enrichment of H3K27ac and potentially enhanced resistance to cold-induced sweetening in tubers, Horticulture Research, 10(3): uhad017.
https://doi.org/10.1093/hr/uhad017

Haque E., Shirasawa K., Suematsu K., Tabuchi H., Isobe S., and Tanaka M., 2023, Polyploid GWAS reveals the basis of molecular marker development for complex breeding traits including starch content in the storage roots of sweet potato, Frontiers in Plant Science, 14: 1181909.
https://doi.org/10.3389/fpls.2023.1181909

Hasan N., Choudhary S., Naaz N., Sharma N., and Laskar R., 2021, Recent advancements in molecular marker-assisted selection and applications in plant breeding programmes, Journal of Genetic Engineering and Biotechnology, 19(1): 128.
https://doi.org/10.1186/s43141-021-00231-1

He J., Zhao X., Laroche A., Lu Z., Liu H., and Li Z., 2014, Genotyping-by-sequencing (GBS), an ultimate marker-assisted selection (MAS) tool to accelerate plant breeding, Frontiers in Plant Science, 5: 484.
https://doi.org/10.3389/fpls.2014.00484

Hirakawa H., Okada Y., Tabuchi H., Shirasawa K., Watanabe A., Tsuruoka H., Minami C., Nakayama S., Sasamoto S., Kohara M., Kishida Y., Fujishiro T., Kato M., Nanri K., Komaki A., Yoshinaga M., Takahata Y., Tanaka M., Tabata S., and Isobe S., 2015, Survey of genome sequences in a wild sweet potato, *Ipomoea trifida* (H. B. K.) G. Don, DNA Research, 22(2): 171-179.
https://doi.org/10.1093/dnares/dsv002

Hu J., Mei M., Jin F., Xu J., Duan S., Bian C., Li G., Wang X., and Jin L., 2022, Phenotypic variability and genetic diversity analysis of cultivated potatoes in China, Frontiers in Plant Science, 13: 954162.
https://doi.org/10.3389/fpls.2022.954162

Jannink J., Lorenz A., and Iwata H., 2010, Genomic selection in plant breeding: from theory to practice, Briefings in Functional Genomics, 9(2): 166-177.
https://doi.org/10.1093/bfgp/elq001

Karan Y., and Şanli Ö., 2021, The assessment of yield and quality traits of sweet potato (*Ipomoea batatas* L.) genotypes in middle Black Sea region, Turkey, PLoS ONE, 16(9): e0257703.
https://doi.org/10.1371/journal.pone.0257703

Kim J., Chung I., and Kim K., 2017, Construction of a genetic map using EST-SSR markers and QTL analysis of major agronomic characters in hexaploid sweet potato (*Ipomoea batatas* (L.) Lam), PLoS ONE, 12(10): e0185073.
https://doi.org/10.1371/journal.pone.0185073

Maquia I., Muocha I., Naico A., Martins N., Gouveia M., Andrade I., Goulao L., and Ribeiro A., 2013, Molecular, morphological and agronomic characterization of the sweet potato (*Ipomoea batatas* L.) germplasm collection from Mozambique: genotype selection for drought prone regions, South African Journal of Botany, 88: 142-151.
https://doi.org/10.1016/J.SAJB.2013.07.008

Merrick L., Herr A., Sandhu K., Lozada D., and Carter A., 2022, Optimizing plant breeding programs for genomic selection, Agronomy, 12(3): 714.
https://doi.org/10.20944/preprints202202.0048.v1

Ngailo S., Shimelis H., Sibiya J., Mtunda K., and Mashilo J., 2019, Genotype-by-environment interaction of newly-developed sweet potato genotypes for storage root yield, yield-related traits and resistance to sweet potato virus disease, Heliyon, 5(3): e01448.
https://doi.org/10.1016/j.heliyon.2019.e01448

Ojwang' S., Okello J., Otieno D., Mutiso J., Lindqvist-Kreuze H., Coaldrake P., Mendes T., Andrade M., Sharma N., Gruneberg W., Makunde G., Ssali R., Yada B., Mayanja S., Polar V., Oloka B., Chelangat D., Ashby J., Hareau G., and Campos H., 2023, Targeting market segment needs with public-good crop breeding investments: A case study with potato and sweetpotato focused on poverty alleviation, nutrition and gender, Frontiers in Plant Science, 14: 1105079.
https://doi.org/10.3389/fpls.2023.1105079

Oliveira D., Otoboni M., Pavan B., Fernandes A., and Vargas P., 2022, Agronomic characterization of sweet potato genotypes obtained through crossbreeding, Revista Caatinga, 35(4): 839-847.
https://doi.org/10.1590/1983-21252022v35n411rc

Otoboni M., Oliveira D., Vargas P., Pavan B., and Andrade M., 2020, Genetic parameters and gain from selection in sweet potato genotypes with high beta-carotene content, Crop Breeding and Applied Biotechnology, 20(3): e31632038.
https://doi.org/10.1590/1984-70332020v20n3a42

Pandey J., Scheuring D., Koym J., and Vales M., 2022, Genomic regions associated with tuber traits in tetraploid potatoes and identification of superior clones for breeding purposes, Frontiers in Plant Science, 13: 952263.
https://doi.org/10.3389/fpls.2022.952263

Pandey J., Scheuring D., Koym J., Endelman J., and Vales M., 2023, Genomic selection and genome-wide association studies in tetraploid chipping potatoes, The Plant Genome, 16(1): e20297.
https://doi.org/10.1002/tpg2.20297

Peng Z., 2011, Genetic transformation of sweet potato and its application in molecular breeding, Plant Physiology, 47(5): 427-436.

Salgotra R., and Stewart C., 2020, Functional markers for precision plant breeding, International Journal of Molecular Sciences, 21(13): 4792.
https://doi.org/10.3390/ijms21134792

Sandhu K., Shiv A., Kaur G., Meena M., Raja A., Vengavasi K., Mall A., Kumar S., Singh P., Singh J., Hemaprabha G., Pathak A., Krishnappa G., and Kumar S., 2022, Integrated approach in genomic selection to accelerate genetic gain in sugarcane, Plants, 11(16): 2139.
https://doi.org/10.3390/plants11162139

Slater A., Cogan N., Rodoni B., Daetwyler H., Hayes B., Caruana B., Badenhorst P., Spangenberg G., and Forster J., 2017, Breeding differently—the digital revolution: high-throughput phenotyping and genotyping, Potato Research, 60: 337-352.
https://doi.org/10.1007/S11540-018-9388-X

Sverrisdóttir E., Byrne S., Sundmark E., Johnsen H., Kirk H., Asp T., Janss L., and Nielsen K., 2017, Genomic prediction of starch content and chipping quality in tetraploid potato using genotyping-by-sequencing, Theoretical and Applied Genetics, 130: 2091-2108.
https://doi.org/10.1007/s00122-017-2944-y

Swanckaert J., Gemenet D., Anglin N., and Grüneberg W., 2021, Sweet potato (*Ipomoea batatas* (L.) Lam.) breeding, In: Advances in Plant Breeding Strategies: Vegetable Crops, pp.513-546.
https://doi.org/10.1007/978-3-030-66965-2_12

Teshome S., Amide A., and Bobo T., 2020, Adaptability and evaluation of improved orange fleshed sweet potato (*Ipomoea batatas* L. ) varieties in the Mid Altitude of Guji Zone, Southern Ethiopia, Archives of Biochemistry and Biophysics, 8(3): 35-41.
https://doi.org/10.11648/j.abb.20200802.14

Tiwari J., Devi S., Buckseth T., Ali N., Singh R., Zinta R., Dua V., and Chakrabarti S., 2020, Precision phenotyping of contrasting potato (*Solanum tuberosum* L.) varieties in a novel aeroponics system for improving nitrogen use efficiency: in search of key traits and genes, Journal of Integrative Agriculture, 19(1): 51-61.
https://doi.org/10.1016/s2095-3119(19)62625-0

Tiwari J., Yerasu S., Rai N., Singh D., Singh A., Karkute S., Singh P., and Behera T., 2022, Progress in marker-assisted selection to genomics-assisted breeding in tomato, Critical Reviews in Plant Sciences, 41(5): 321-350.
https://doi.org/10.1080/07352689.2022.2130361

Vargas P., Otoboni M., Lopes B., and Pavan B., 2020, Prediction of genetic gains through selection of sweet potato accessions, Horticultura Brasileira, 38: 387-393.
https://doi.org/10.1590/s0102-0536202004008

Visser R., Bachem C., Borm T., Boer J., Eck H., Finkers R., Linden G., Maliepaard C., Uitdewilligen J., Voorrips R., Vos P., and Wolters A., 2014, Possibilities and challenges of the potato genome sequence, Potato Research, 57: 327-330.
https://doi.org/10.1007/s11540-015-9282-8

Wei Q., Yin Y., Deng B., Song X., Gong Z., and Shi Y., 2023, Transcriptome analysis of nitrogen-deficiency-responsive genes in two potato cultivars, Agronomy, 13(8): 2164.
https://doi.org/10.3390/agronomy13082164

Yamakawa H., Haque E., Tanaka M., Takagi H., Asano K., Shimosaka E., Akai K., Okamoto S., Katayama K., and Tamiya S., 2021, Polyploid QTL-seq towards rapid development of tightly linked DNA markers for potato and sweetpotato breeding through whole-genome resequencing, Plant Biotechnology Journal, 19(10): 2040-2051.
https://doi.org/10.1111/pbi.13633

You Q., Yang X., Peng Z., Xu L., and Wang J., 2018, Development and applications of a high throughput genotyping tool for polyploid crops: single nucleotide polymorphism (SNP) array, Frontiers in Plant Science, 9: 104.
https://doi.org/10.3389/fpls.2018.00104

Zhang X., 2024, Breeding high-yield and disease-resistant carrot varieties using marker-assisted selection, International Journal of Horticulture, 14(4): 263-274.
https://doi.org/10.5376/ijh.2024.14.0028