Utilizing Sweet Potato Genetic Diversity and Molecular Breeding Techniques for Resistance Breeding and Quality Improvement

Gongkai Chen, Hong Wang ✉, Lingli Wang, Yong'an Liu, Fanglei Hong, Hongshuang Yang

Wenzhou Vocational College of Science and Technology, Wenzhou, 325006, Zhejiang, China

✉ Corresponding email: 1850076351@qq.com

Abstract This study comprehensively explores the importance of genetic diversity in sweet potato breeding and crop improvement. As a globally significant crop, sweet potato offers abundant genetic resources for developing high-yielding, stress-tolerant, and nutritionally enhanced varieties. By evaluating genetic variation and population structure in sweet potato germplasm across different geographical regions, the study identifies key traits associated with yield, disease resistance, and nutritional quality. Modern breeding techniques, including marker-assisted selection and gene editing, were applied to accelerate the development of superior sweet potato varieties. Additionally, case studies, such as the identification of disease-resistant germplasm and the development of biofortified varieties, demonstrate the critical role of genetic diversity in addressing food security and sustainable agriculture. The findings highlight that integrating advanced molecular techniques with traditional breeding approaches can maximize the genetic potential of sweet potato, effectively tackling agricultural challenges posed by climate change, and support global agricultural innovation and socio-economic development.

Keywords Sweet potato; Genetic diversity; Molecular breeding; Disease resistance; Biofortification; Climate adaptability; Genetic resource utilization

1 Introduction

Sweet potato (*Ipomoea batatas*) is a vital crop globally, known for its adaptability to diverse environmental conditions and its high nutritional value. The genetic diversity within sweet potato is extensive, providing a rich resource for breeding and crop improvement efforts. Genetic diversity is crucial for the success of breeding programs as it provides the raw material for selection and improvement (Zhou and Chen, 2024). In sweet potato, genetic variability has been shown to influence key traits such as tuber yield, carotene content, and disease resistance (Mohammed et al., 2015; Solankey et al., 2015; Vargas et al., 2018). Understanding and utilizing this diversity can lead to the development of superior cultivars that meet the demands of food security and nutritional needs (Rodríguez-Bonilla et al., 2014; Vargas et al., 2020). Moreover, the genetic diversity within sweet potato populations can help in the conservation of genetic resources, ensuring the sustainability of breeding programs (Hardigan et al., 2017; Vargas et al., 2018).

Crop improvement in sweet potato has traditionally relied on the selection of superior genotypes from diverse populations. Studies have demonstrated significant genetic variation among sweet potato accessions, which can be harnessed for breeding purposes (Mohammed et al., 2015; Solankey et al., 2015; Vargas et al., 2018). For instance, genetic diversity assessments in Ethiopia and Puerto Rico have revealed substantial variability in agro-morphological and physicochemical traits, indicating the potential for selecting high-performing genotypes (Rodríguez-Bonilla et al., 2014; Mohammed et al., 2015). Additionally, modern breeding technologies, such as genome sequencing and marker-assisted selection, have facilitated the identification of key loci associated with desirable traits, further enhancing the efficiency of breeding programs (Springer and Schmitz, 2017; Hameed et al., 2018).

This study will assess the genetic variation and population structure of sweet potato germplasm resources in different geographical regions, identify key genetic traits associated with high yield, nutritional quality and disease resistance, develop breeding strategies incorporating genetic diversity to develop high-quality sweet

potato varieties, and evaluate the potential of modern breeding techniques to enhance sweet potato improvement efforts. By harnessing the genetic diversity of sweet potatoes, this study aims to facilitate the development of improved varieties to meet global food security challenges and meet the nutritional needs of a growing population.

2 Genetic Diversity in Sweet Potato

2.1 Sources of genetic diversity

Sweet potato (*Ipomoea batatas* L.) exhibits significant genetic diversity, which is crucial for breeding and crop improvement. The sources of this diversity include natural genetic variation, human intervention, and the plant's out-crossing nature. Studies have shown that sweet potato landraces from different regions, such as Puerto Rico, display high levels of genetic diversity due to these factors (Rodríguez-Bonilla et al., 2014). Additionally, the presence of long terminal repeat (LTR) retrotransposons in the sweet potato genome contributes significantly to its genetic diversity (Meng et al., 2021). These retrotransposons are highly abundant and play a crucial role in the genetic makeup of sweet potato, making them valuable markers for genetic diversity studies.

2.2 Evolutionary history and domestication

The evolutionary history and domestication of sweet potato are complex and involve multiple events of selection and adaptation. Sweet potato is believed to have been domesticated in Central or South America and subsequently spread to other parts of the world. The genetic diversity observed in sweet potato today is a result of both ancient domestication events and more recent human-mediated dispersal. For instance, the genetic diversity of sweet potato in Puerto Rico can be traced back to pre-Columbian times, indicating a long history of cultivation and selection (Rodríguez-Bonilla et al., 2014). Furthermore, studies using chloroplast SSR markers have shown that sweet potato accessions from different regions, including Korea, Japan, Taiwan, and the USA, exhibit distinct genetic clusters, reflecting their unique evolutionary paths (Lee et al., 2019).

2.3 Assessment of genetic diversity

Assessing the genetic diversity of sweet potato is essential for effective breeding and conservation strategies. Various molecular markers, such as SSR, SNP, and retrotransposon-based markers, have been employed to evaluate the genetic diversity of sweet potato germplasm. For example, an assessment using SSR markers in Puerto Rico revealed a high level of genetic diversity among 167 sweet potato samples, with observed heterozygosity of 0.71 (Rodríguez-Bonilla et al., 2014). Similarly, a genome-wide assessment using SNP markers identified significant genetic variation among 197 sweet potato accessions, which were grouped into three major clusters based on their genetic relationships (Su et al., 2017). Retrotransposon-based insertion polymorphism (RBIP) markers have also been used to study the genetic diversity of sweet potato, revealing significant intergroup genetic variation (Meng et al., 2021). These assessments provide valuable insights into the genetic structure of sweet potato populations and inform breeding programs aimed at improving this important crop.

3 Key Traits for Sweet Potato Improvement

3.1 Yield and biomass

Yield and biomass are critical traits for sweet potato improvement, as they directly impact the economic viability and food security potential of the crop. Genetic variability in sweet potato genotypes for traits such as tuber yield per plant, fresh weight of tubers, and the number of branches per plant has been observed, indicating significant potential for breeding programs to enhance these traits. The positive phenotypic correlation between fresh weight of tubers per plant and the number of tubers per plant, as well as days to maturity, suggests that selecting for these traits can lead to improved yield outcomes (Solankey et al., 2015). Additionally, the application of genetic transformation techniques has shown promise in enhancing yield and stress tolerance simultaneously, which is crucial for maintaining productivity under varying environmental conditions (Imbo et al., 2016).

3.2 Abiotic stress tolerance

Abiotic stress tolerance is essential for the resilience of sweet potato crops, especially in the face of climate change. Various strategies have been employed to improve tolerance to stresses such as drought, salinity, and temperature extremes. For instance, the overexpression of the betaine aldehyde dehydrogenase (BADH) gene from spinach in sweet potato has been shown to enhance tolerance to multiple abiotic stresses, including salt,

oxidative stress, and low temperature, without causing phenotypic defects. This genetic modification leads to increased glycine betaine accumulation, which helps maintain cell membrane integrity and reduces reactive oxygen species (ROS) production under stress conditions (Fan et al., 2012). Moreover, the use of crop wild relatives (CWRs) has been identified as a valuable approach to introduce genetic diversity and improve abiotic stress tolerance in sweet potato (Kapazoglou et al., 2023).

3.3 Nutritional quality and biofortification

Improving the nutritional quality of sweet potato is a key objective for breeding programs, particularly in regions where the crop is a staple food. Biofortification efforts have focused on increasing the content of essential nutrients such as carotene, vitamins, and minerals. For example, genetic variability in carotene content among sweet potato genotypes has been documented, with significant associations between carotene content and other agronomic traits like vine length and number of leaves per plant (Solankey et al., 2015). Advances in genomic tools and technologies have facilitated the identification and transfer of genomic regions responsible for desirable nutritional traits, accelerating the development of biofortified sweet potato varieties (Figure 1) (Medina-Lozano and Díaz, 2022). These efforts are crucial for addressing micronutrient deficiencies and improving the overall health benefits of sweet potato consumption.
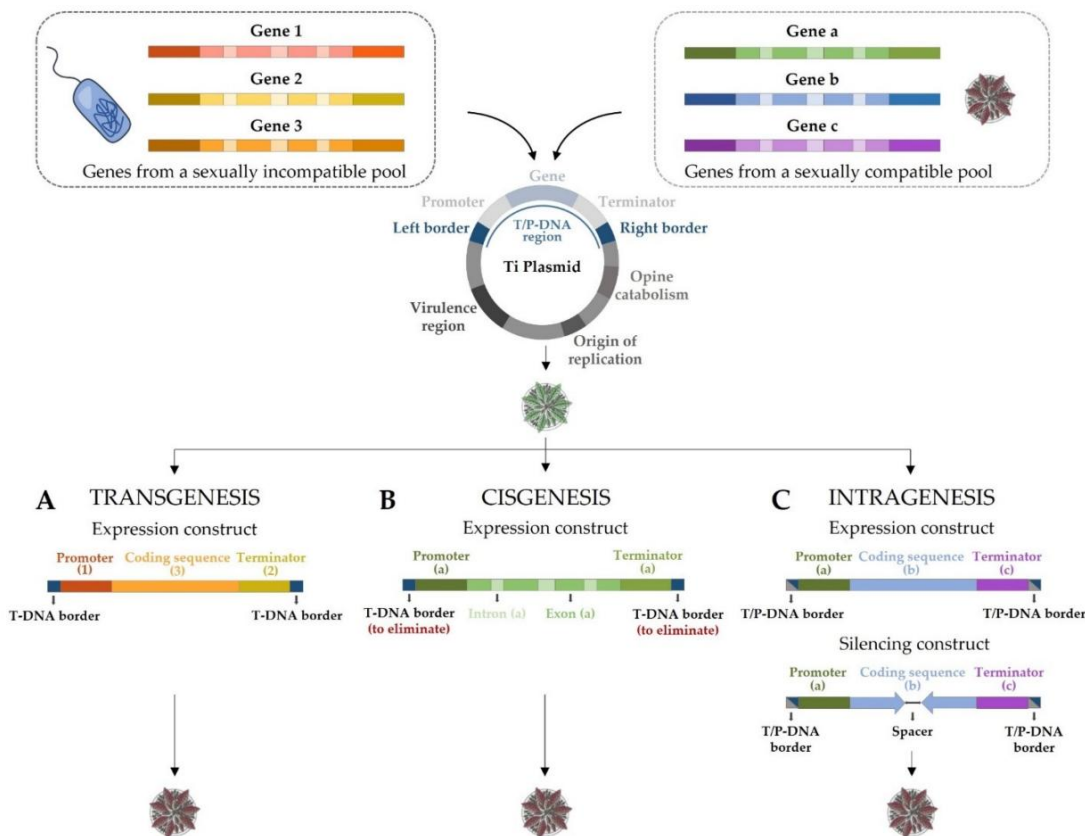

Figure 1 Schematic representation of three modern biotechnology techniques to introduce allelic variants of interest in a recipient organism: (A) transgeneis; (B) cisgenesis; and (C) intragenesis (Adopted from Medina-Lozano and Díaz, 2022)

4 Techniques and Technologies for Breeding

4.1 Conventional breeding approaches

Conventional breeding approaches in sweet potato involve the selection and cross-breeding of plants with desirable traits to produce improved cultivars. This method relies heavily on phenotypic selection and has been the cornerstone of crop improvement for centuries. The process involves selecting parent plants with favorable characteristics, cross-pollinating them, and then selecting the best offspring over several generations. This approach, while effective, is time-consuming and labor-intensive, often requiring many years to develop a new cultivar with the desired traits.

4.2 Marker-assisted selection (MAS) and genomic selection (GS)

Marker-assisted selection (MAS) and genomic selection (GS) are advanced breeding techniques that utilize molecular markers to accelerate the breeding process. MAS involves the use of DNA markers linked to specific traits of interest, allowing for the selection of plants carrying these markers without the need for extensive phenotypic evaluation. This method has been particularly useful for traits that are difficult to measure or have low heritability (Tiwari et al., 2022; Huang and Hong, 2024). Genomic selection (GS), on the other hand, uses genome-wide marker data to predict the breeding value of individuals. This approach allows for the simultaneous selection of multiple traits, including those controlled by many small-effect genes, which are often challenging to improve through MAS alone. GS has shown promise in increasing the accuracy and efficiency of selection, thereby accelerating genetic gains in breeding programs (Varshney et al., 2017; Merrick et al., 2022; Sandhu et al., 2022).

4.3 Gene editing and biotechnology applications

Gene editing and biotechnology applications represent the frontier of modern plant breeding. Techniques such as CRISPR/Cas9 allow for precise modifications of the plant genome, enabling the introduction, deletion, or alteration of specific genes. This technology offers the potential to develop sweet potato varieties with enhanced traits such as disease resistance, improved nutritional content, and better adaptability to environmental stresses (Nahirñak et al., 2022). Biotechnological methods also include genetic transformation techniques, such as Agrobacterium-mediated transformation and particle bombardment, which have been widely used in other crops like potatoes. These methods allow for the introduction of new genes into the plant genome, providing opportunities to enhance traits that are difficult to achieve through conventional breeding (Nahirñak et al., 2022). The integration of these advanced biotechnological tools with traditional breeding methods holds great promise for the future of sweet potato improvement.

5 Case Studies in Sweet Potato Breeding

5.1 Case study: establishing a sweet potato resistance identification nursery

To address the challenge of sweet potato basal rot in high-risk areas, the Wenzhou Academy of Agricultural Sciences in Zhejiang of China established a resistance identification nursery in a key region heavily affected by sweet potato blight. The primary goal was to identify and promote blight-resistant sweet potato varieties to combat the devastating impact of the disease and improve crop yield and sustainability in the region.

The institute collected approximately approximately 350 breeding materials and 110 sweet potato germplasm resources (Table 1; Figure 2) for resistance identification from across the country. Field evaluations were conducted, focusing on agronomic traits and resistance to root rot (a critical disease for sweet potatoes).

Ultimately, over 10 superior sweet potato resources were selected, including CH60, CP37, CP158, CJ3056, and QX3009, all of which demonstrated excellent disease resistance with infection rates consistently below 25% (Table 2). The average infection rates for these varieties were as follows: CH60 at 3.2%, CP37 at 3.8%, CP158 at 2.9%, CJ3056 at 2.6%, and QX3009 at 1.6%. These resources are ideal candidates for further breeding and large-scale promotion.

5.2 Case study: breeding for virus resistance

Sweet potato virus disease (SPVD) is one of the most significant biotic constraints affecting sweet potato production, causing yield reductions ranging from 50% to 98%. Breeding for resistance to SPVD has been a primary focus to mitigate these losses. Traditional breeding methods face challenges such as reduced flowering, fertility issues, and self- or cross-incompatibility. Despite these challenges, the development of resistant varieties remains the most effective and economical method for small-scale farmers. Non-conventional breeding techniques, including marker-assisted selection and genetic engineering, offer promising complementary roles in enhancing resistance to SPVD (Ngailo et al., 2013).

Table 1 Sweet potato germplasm resources

Number		BX series	CH series	CJ series	CJ series	CP series	CS series	FJ series	FJ series	PT series	PT series	QX series	TP series	XX series
1	2020A4	BX3001	CH14	CJ3002	CJ3033	CP37	CS3002	FJ3001	FJ3034	PT	PT64	QX3009	TP3	XX3002
2	AD2025	BX3002	CH15	CJ3003	CJ3034	CP81	CS3003	FJ3002	FJ3035	PT1	PT70	QX3010	TP6	XX3003
3	CD9348	BX3003	CH35	CJ3004	CJ3035	CP108	CS3006	FJ3005	FJ3036	PT11	PT76	QX3013	TP25	XX3004
4	TC04	BX3004	CH45	CJ3006	CJ3036	CP142	CS3007	FJ3006	FJ3037	PT13	PT76 Big Potato	QX3016	TP30	XX3009
5	W-10	BX3006	CH54	CJ3008	CJ3037	CP158	CS3008	FJ3008	FJ3038	PT16	PT80	QX3021	TP37	XX3010
6	Chaoshu No.1	BX3007	CH59	CJ3009	CJ3038	CP162	CS3010	FJ3010	FJ3039	PT20	PT81	QX3023	TP41	XX3011
7	Longshu 116	BX3013	CH60	CJ3010	CJ3040	CP167	CS3021	FJ3011	FJ3041	PT24	PT84	QX3024	TP48	XX3012
8	Ning C2-6	BX3017	CH67	CJ3011	CJ3041	CP181	-	FJ3012	FJ3042	PT35	PT92	QX3025	TP50	XX3013
9	Ningzishu No.1	BX3020	CH86	CJ3013	CJ3042	CP201	-	FJ3015	FJ3043	PT38	PT104	QX3026	TP56	XX3014
10	xu 22	BX3022	CH109	CJ3014	CJ3043	CP250	-	FJ3016	FJ3044	PT40	PT120	QX3027	TP57	XX3015
11	Zheshu 38	BX3023	CH600	CJ3015	CJ3045	CP379	-	FJ3017	FJ3045	PT45	PT122	QX3028	TP62	XX3016
12	Wenshu No.1	BX3024	CH605	CJ3016	CJ3046	CP407	-	FJ3018	FJ3047	PT47	PT135	QX3029	TP84	XX3017
13	Fushu 604	BX3027	CH609	CJ3018	CJ3047	CP-407	-	FJ3019	FJ3048	PT48	PT145	QX3032	TP93	XX3018
14	Zhe 6025	BX3028	CH610	CJ3019	CJ3048	-	-	FJ3020	FJ3049	PT49	PT399	QX3036	TP94	XX3019
15	Zheshu 255	BX3029	CH613	CJ3020	CJ3049	-	-	FJ3021	FJ3050	PT61	PT502	QX3037	TP99	XX3020
16	Zhezishu No.4	-	CH616	CJ3021	CJ3051	-	-	FJ3022	FJ3051	PT63	PT503	QX3038	TP112	XX3021
17	Jishu 26	-	CH617-1	CJ3023	CJ3052	-	-	FJ3023	FJ3052	-	-	QX3039	TP118	XX3022
18	Shangshu 19	-	CH626	CJ3024	CJ3053	-	-	FJ3024	FJ3054	-	-	QX3042	TP122	-
19	-	-	CH635	CJ3025	CJ3054	-	-	FJ3025	FJ3055	-	-	QX3044	TP127	-
20	-	-	CH637	CJ3026	CJ3055	-	-	FJ3026	FJ3057	-	-	QX3047	-	-
21	-	-	CH638	CJ3028	CJ3056	-	-	FJ3028	FJ3058	-	-	QX3055	-	-
22	-	-	CH646	CJ3030	CJ3057	-	-	FJ3029	FJ3059	-	-	QX3056	-	-
23	-	-	-	CJ3031	CJ3059	-	-	FJ3030	FJ3060	-	-	QX3059	-	-
24	-	-	-	CJ3032	CJ3060	-	-	FJ3031	FJ3062	-	-	QX3060	-	-
25	-	-	-	-	-	-	-	FJ3032	FJ3063	-	-	QX3061	-	-
26	-	-	-	-	-	-	-	FJ3033	FJ3065	-	-	-	-	-

Figure 2 Sweet potato resources

Table 2 Statistics of disease-infected plants in sweet potato resources

Name of sweet potato resource	Average infection rate
CH60	3.2
CH637	1.6
CP37	3.8
CP142	4.9
CP158	2.9
CJ3038	2.4
CJ3056	2.6
PT77	11.2
PT92	8.1
PT122	22.9
FJ3042	14.1
FJ3044	8.9
BX3001	10.2
BX3001	3.1
QX3009	1.6

5.3 Case study: enhancing nutritional quality in African varieties

Enhancing the nutritional quality of sweet potato varieties, particularly in Africa, is crucial for addressing malnutrition and improving food security. Breeding programs have increasingly focused on developing varieties that are rich in essential nutrients such as vitamin A. The International Potato Center (CIP) and its partners have been responsive to development indicators like poverty, malnutrition, and gender, aiming to create varieties that can alleviate these issues (Ojwang et al., 2023). By targeting market segments with high rates of stunting among children and anemia among women, these programs aim to maximize the nutritional impact of new sweet potato varieties.

5.4 Insights from case studies

These sweet potato breeding case studies highlight the significant role of targeted breeding programs in addressing specific agricultural challenges. In Wenzhou, the establishment of a resistance identification nursery effectively tackled the region's sweet potato basal rot issue, identifying superior varieties such as CH60 and QX3009. This approach underscores the importance of localized breeding efforts, which address regional disease problems and significantly enhance crop sustainability and productivity. Similarly, efforts to breed resistance to sweet potato

virus disease (SPVD) demonstrate that combining traditional methods with advanced techniques such as marker-assisted selection and genetic engineering can effectively overcome the limitations of conventional breeding (Ngailo et al., 2013).

Beyond disease resistance, improving the nutritional quality of sweet potato varieties, especially in Africa, also showcases the potential of breeding programs to address societal challenges. Work led by the International Potato Center (CIP) focuses on developing varieties rich in essential nutrients like vitamin A. Targeted breeding programs addressing nutritional deficiencies can significantly impact public health, particularly in regions with high rates of malnutrition (Ojwang et al., 2023). These initiatives maximize the social and economic benefits of agricultural innovation, together demonstrate the effectiveness of breeding programs in balancing agricultural, nutritional, and societal goals.

6 Yield and Performance Analysis of Improved Varieties

6.1 Yield trials and comparative studies

Yield trials and comparative studies are essential for evaluating the performance of different sweet potato genotypes under various environmental conditions. For instance, a study conducted in Odisha, India, evaluated fifteen sweet potato genotypes and found significant variability in traits such as vine length, number of branches per plant, and root yield per plant, which are crucial for yield improvement (Kar et al., 2022). Similarly, in Indonesia, yield stability analysis using AMMI and GGE biplot models identified stable genotypes like F1-038 and F1-069, which showed higher yields across different agroecosystems (Karuniawan et al., 2021). In Ethiopia, genetic variability studies on twenty sweet potato varieties revealed significant differences in tuber yield and other agronomic traits, indicating the potential for selecting superior varieties for breeding programs (Tessema et al., 2022).

6.2 Factors influencing yield performance

Several factors influence the yield performance of sweet potato varieties. Genetic diversity plays a crucial role, as seen in the study from Odisha, where traits like root girth and β-carotene content were positively correlated with total root yield per hectare (Kar et al., 2022). Environmental conditions also significantly impact yield, as demonstrated in the Indonesian study, where location-specific genotypes were identified based on their performance in different agroecosystems (Karuniawan et al., 2021). Additionally, the physiological status of seed tubers and environmental factors like frost can affect yield, as observed in the Andean potato study, where genotypic differences were evident under simulated frost scenarios (Condori et al., 2010).

6.3 Statistical analysis of yield data

Statistical analysis is vital for interpreting yield data and making informed decisions in breeding programs. In the Odisha study, analysis of variance (ANOVA) and D2 statistics were used to assess genetic variability and divergence among genotypes (Kar et al., 2022). The Indonesian study employed combined variance analysis, AMMI, and GGE biplot models to evaluate yield stability and identify superior genotypes (Karuniawan et al., 2021). In Ethiopia, broad-sense heritability and genetic advance were calculated to determine the potential for genetic improvement in sweet potato varieties (Tessema et al., 2022). These statistical methods provide a robust framework for understanding the genetic and environmental factors influencing yield and for selecting high-performing genotypes for crop improvement.

7 Environmental Adaptation of Sweet Potato Varieties

7.1 Adaptation to diverse climatic conditions

Sweet potato varieties exhibit significant genetic diversity, which is crucial for their adaptation to diverse climatic conditions. Studies have shown that sweet potato production is at risk from extreme heat events, but certain tolerant cultivars can thrive and potentially provide climate resilience (Figure 3) (Heider et al., 2020; Pironon and Gomez, 2020). In West Africa, the genetic diversity of sweet potato is structured along a climatic gradient, with specific genetic groups adapted to particular climatic areas, such as tropical humid or Sahelian climates (Glato et al., 2017). This diversity is essential for developing strategies to adapt agriculture to ongoing climate variations.
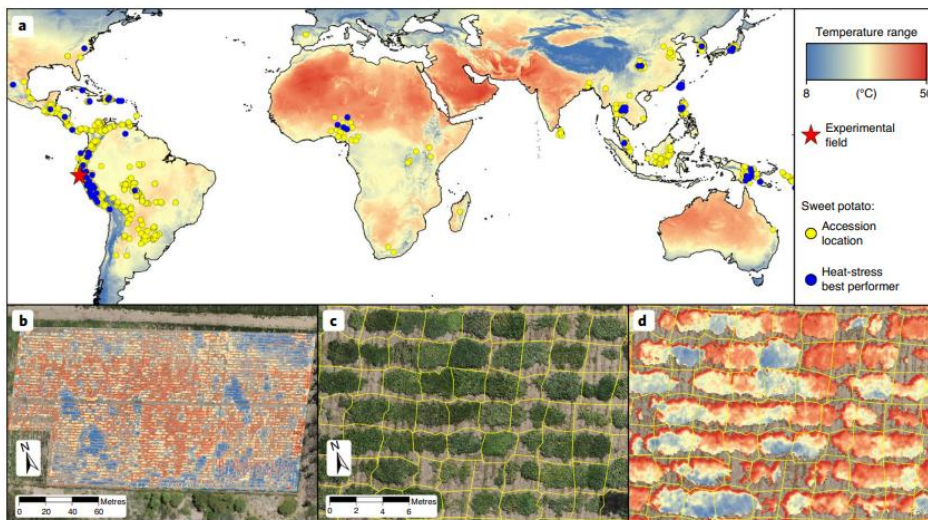
Figure 3 World map of the 1 973 sweet potato cultivars and breeding lines tested in the intentional exposure and control trial for HS tolerance (Adopted from Heider et al., 2020)

Image caption: a, Originlocation of each cultivar and breeding line overlaid with the Worldclim maximum temperature of the warmest month. Blue dots indicate heat-tolerantcultivars under future climate scenario RCP 8.5 (tolerance to heat stress >1). The experimental field site for sweet potato heatscreening is marked with a red star. b, Visual drone-based mapping of the 4 040 test plots at the experimental field site in Piura, Peru. c, Close-ups on thedemarcation of sweet potato cultivar plots in the visual map. d, Corresponding high-precision thermographic image of plant canopy temperatures under HS conditions. Temperatures represent means of the warmest month in a and snapshot of surface canopy temperatures in b and d (Adopted from Heider et al., 2020)

7.2 Agronomic practices to enhance adaptation

Agronomic practices play a vital role in enhancing the adaptation of sweet potato varieties to different environmental conditions. Multi-trait selection indexes, such as those used in the CropInd tool, help breeders identify genotypes with superior agronomic performance across multiple environments (Rosero et al., 2023). These practices include selecting for traits like total and commercial fresh root yield, survival percentage, and stability. Additionally, understanding the physiological and biochemical features of drought-tolerant varieties can inform crop management strategies for drought mitigation (Sapakhova et al., 2023). By employing these practices, breeders can develop varieties that are better suited to withstand environmental stresses.

7.3 Long-term sustainability and climate resilience

For long-term sustainability and climate resilience, it is crucial to exploit the intraspecific diversity of sweet potato. This diversity serves as a reservoir for traits that confer tolerance to abiotic stresses, such as extreme heat and drought (Dwivedi et al., 2017; Heider et al., 2020). The identification of heat-tolerant cultivars and breeding lines, along with traits predictive of heat tolerance, underscores the importance of maintaining genetic diversity for future crop resilience (Heider et al., 2020). Moreover, integrating traditional and molecular breeding methods, along with biotechnological approaches, can enhance the drought tolerance and overall resilience of sweet potato varieties (Sapakhova et al., 2023). These strategies ensure that sweet potato remains a viable crop in the face of climate change, contributing to food security and sustainable agriculture.

8 Challenges in Exploiting Genetic Diversity for Crop Improvement

8.1 Limited genetic resources and bottlenecks

One of the primary challenges in exploiting genetic diversity for crop improvement is the limited availability of genetic resources. Genetic bottlenecks, often resulting from domestication and selective breeding, have reduced the genetic variability within cultivated species. For instance, the genetic diversity of sweet potato accessions shows significant variability, but the number of cultivars available on the market remains low, limiting the potential for genetic gains (Vargas et al., 2020). Similarly, the genetic diversity of potato has been maintained over centuries, but the introduction of new genetic groups is still necessary to enhance the crop's resilience and productivity (Pandey et al., 2021; Spanoghe et al., 2022).

8.2 Breeding and agronomic challenges

Breeding programs face several agronomic challenges, including the complexity of polyploidy in crops like sweet potato and potato, which complicates genetic analysis and breeding efforts. The hexaploid nature of sweet potato presents difficulties in developing high-quality integrated genetic maps, which are essential for effective molecular breeding (Swanckaert et al., 2021). Additionally, the autotetraploid nature of potato poses challenges for traditional breeding due to inbreeding depression and the need for extensive time to introgress desirable traits from wild relatives (Martínez-Prada et al., 2021). The development of new breeding technologies, such as CRISPR/Cas9, offers potential solutions but also introduces new challenges related to regulatory and consumer acceptance (Hameed et al., 2018; Nahirñak et al., 2022).

8.3 Adoption and market challenges

The adoption of new crop varieties is often hindered by market preferences and consumer acceptance. For example, despite the introduction of high-yield and pest-resistant sweet potato varieties, consumer preferences for specific color, texture, and taste can lead to low adoption rates. Market challenges also include the need for improved marketing strategies to promote the health benefits of new varieties, as seen with the orange-fleshed sweet potato in Sub-Saharan Africa (Swanckaert et al., 2021). Additionally, the commercialization of genetically modified crops faces significant hurdles due to regulatory restrictions and public concerns about the safety and ethics of genetic engineering (Martínez-Prada et al., 2021; Nahirñak et al., 2022).

9 Future Directions in Sweet Potato Breeding

9.1 Innovations in breeding technologies

The future of sweet potato breeding lies in the adoption and integration of advanced breeding technologies. Techniques such as CRISPR/Cas9 and TALENs have shown promise in other crops like potatoes, enabling precise and efficient genetic modifications without introducing foreign DNA, which can help in overcoming regulatory and consumer acceptance hurdles (Hameed et al., 2018; Nahirñak et al., 2022). These technologies can be employed to enhance nutritional content, improve resistance to biotic and abiotic stresses, and increase overall yield. Additionally, the use of molecular marker-assisted selection can accelerate the introgression of desirable traits from wild species into cultivated varieties, thereby enhancing the genetic base of sweet potatoes (Martínez-Prada et al., 2021).

9.2 Expanding the genetic resource pool

Expanding the genetic resource pool is crucial for the continued improvement of sweet potato varieties. The genetic diversity within sweet potato accessions offers significant opportunities for breeding programs. Studies have shown that there is high genetic variability in sweet potato populations, which can be harnessed to achieve substantial genetic gains (Vargas et al., 2020). Utilizing both wild and cultivated species can introduce new traits and enhance existing ones, thereby improving the crop's adaptability to various environmental conditions. Moreover, the development of core collections that retain the genetic diversity of larger populations can facilitate long-term conservation and efficient utilization of genetic resources (Pandey et al., 2021).

9.3 Potential impact of genetic diversity on global agriculture

The exploitation of genetic diversity in sweet potato breeding has the potential to significantly impact global agriculture. Sweet potato is a key crop for food security, especially in developing countries where it can thrive under suboptimal conditions and provide essential nutrients. By developing varieties that are more resilient to climate change, such as drought-tolerant genotypes, breeding programs can help mitigate the adverse effects of global environmental changes on agriculture (Sapakhova et al., 2023). Furthermore, breeding programs that focus on market segment needs, including poverty alleviation, nutrition, and gender responsiveness, can ensure that the benefits of improved sweet potato varieties reach the most vulnerable populations (Ojwang et al., 2023). This approach not only enhances food security but also promotes sustainable agricultural practices and socio-economic development.

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

Condori B., Hijmans R., Quiroz R., and Ledent J., 2010, Quantifying the expression of potato genetic diversity in the high Andes through growth analysis and modeling, Field Crops Research, 119: 135-144.
https://doi.org/10.1016/j.fcr.2010.07.003

Dwivedi S., Scheben A., Edwards D., Spillane C., and Ortiz R., 2017, Assessing and exploiting functional diversity in germplasm pools to enhance abiotic stress adaptation and yield in cereals and food legumes, Frontiers in Plant Science, 8: 1461.
https://doi.org/10.3389/fpls.2017.01461
PMid:28900432 PMCid:PMC5581882

Fan W., Zhang M., Zhang H., and Zhang P., 2012, Improved tolerance to various abiotic stresses in transgenic sweet potato (*Ipomoea batatas*) expressing spinach betaine aldehyde dehydrogenase, PLoS One, 7(5): e37344.
https://doi.org/10.1371/journal.pone.0037344
PMid:22615986 PMCid:PMC3353933

Glato K., Aidam A., Kane N., Bassirou D., Couderc M., Zekraoui L., Scarcelli N., Barnaud A., and Vigouroux Y., 2017, Structure of sweet potato (*Ipomoea batatas*) diversity in west Africa covaries with a climatic gradient, PLoS One, 12(5): e0177697.
https://doi.org/10.1371/journal.pone.0177697
PMid:28552989 PMCid:PMC5446114

Hameed A., Zaidi S., Shakir S., and Mansoor S., 2018, Applications of new breeding technologies for potato improvement, Frontiers in Plant Science, 9: 925.
https://doi.org/10.3389/fpls.2018.00925
PMid:30008733 PMCid:PMC6034203

Hardigan M., Laimbeer F., Newton L., Crisovan E., Hamilton J., Vaillancourt B., Wiegert-Rininger K., Wood J., Douches D., Farré E., Veilleux R., and Buell C., 2017, Genome diversity of tuber-bearing *Solanum* uncovers complex evolutionary history and targets of domestication in the cultivated potato, Proceedings of the National Academy of Sciences of the United States of America, 114(46): E9999-E10008.
https://doi.org/10.1073/pnas.1714380114
PMid:29087343 PMCid:PMC5699086

Heider B., Struelens Q., Faye É., Flores C., Palacios J., Eyzaguirre R., Haan S., and Dangles O., 2020, Intraspecific diversity as a reservoir for heat-stress tolerance in sweet potato, Nature Climate Change, 11: 64-69.
https://doi.org/10.1038/s41558-020-00924-4

Huang W.Z., and Hong Z.M., 2024, Impact of climate change on cassava cultivation: genetic adaptations and breeding strategies, Field Crop, 7(1): 27-36.

Imbo M., Budambula N., Mweu C., Muli J., and Anami S., 2016, Genetic transformation of sweet potato for improved tolerance to stress: a review, Advances in Life Science and Technology, 49: 67-76.

Kapazoglou A., Gerakari M., Lazaridi E., Kleftogianni K., Sarri E., Tani E., and Bebeli P., 2023, Crop wild relatives: a valuable source of tolerance to various abiotic stresses, Plants, 12(2): 328.
https://doi.org/10.3390/plants12020328
PMid:36679041 PMCid:PMC9861506

Kar D., Panda C., Sahu G., Tripathy P., Das A., Sahu S., and Mohanty A., 2022, Assessment of growth and yield of sweet potato genotypes, International Journal of Environment and Climate Change, 12(11): 3650-3656.
https://doi.org/10.9734/ijecc/2022/v12i111414

Karuniawan A., Maulana H., Ustari D., Dewayani S., Solihin E., Solihin M., Amien S., and Arifin M., 2021, Yield stability analysis of orange-fleshed sweet potato in Indonesia using AMMI and GGE biplot, Heliyon, 7(4): e06881.
https://doi.org/10.1016/j.heliyon.2021.e06881

Lee K., Lee G., Lee J., Sebastin R., Shin M., Cho G., and Hyun D., 2019, Genetic diversity of sweet potato (*Ipomoea batatas* L. Lam) germplasms collected worldwide using chloroplast SSR markers, Agronomy, 9(11): 752.

https://doi.org/10.3390/agronomy9110752

Martínez-Prada M., Curtin S., and Gutierrez-Gonzalez J., 2021, Potato improvement through genetic engineering, GM Crops & Food, 12: 479-496.

https://doi.org/10.1080/21645698.2021.1993688

PMid:34991415 PMCid:PMC9208627

Medina-Lozano I., and Díaz A., 2022, Applications of genomic tools in plant breeding: crop biofortification, International Journal of Molecular Sciences, 23(6): 3086.

https://doi.org/10.3390/ijms23063086

PMid:35328507 PMCid:PMC8950180

Meng Y., Su W., Ma Y., Liu L., Gu X., Wu D., Shu X., Lai Q., Tang Y., Wu L., and Wang Y., 2021, Assessment of genetic diversity and variety identification based on developed retrotransposon-based insertion polymorphism (RBIP) markers in sweet potato (*Ipomoea batatas* (L.) Lam.), Scientific Reports, 11: 17116.

https://doi.org/10.1038/s41598-021-95876-w

PMid:34429441 PMCid:PMC8385064

Merrick L., Herr A., Sandhu K., Lozada D., and Carter A., 2022, Optimizing plant breeding programs for genomic selection, Agronomy, 12: 714.

https://doi.org/10.20944/preprints202202.0048.v1

Mohammed W., Ali S., Shimelis B., and Burga S., 2015, Genetic diversity of local and introduced sweet potato [*Ipomoea batatas* (L.) Lam.] collections for agro-morphology and physicochemical attributes in Ethiopia, Science, Technology and Arts Research Journal, 4: 9-19.

https://doi.org/10.4314/STAR.V4I1.2

Nahirñak V., Almasia N., González M., Massa G., Oneto C., Feingold S., Hopp H., and Rovere C., 2022, State of the art of genetic engineering in potato: from the first report to its future potential, Frontiers in Plant Science, 12: 768233.

https://doi.org/10.3389/fpls.2021.768233

PMid:35082806 PMCid:PMC8784693

Ngailo S., Shimelis H., Sibiya J., and Mtunda K., 2013, Sweet potato breeding for resistance to sweet potato virus disease and improved yield: progress and challenges, African Journal of Agricultural Research, 8: 3202-3215.

https://doi.org/10.5897/AJAR12.1991

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

PMid:37008496 PMCid:PMC10050369

Pandey J., Scheuring D., Koym J., Coombs J., Novy R., Thompson A., Holm D., Douches D., Miller J., and Vales M., 2021, Genetic diversity and population structure of advanced clones selected over forty years by a potato breeding program in the USA, Scientific Reports, 11: 8344.

https://doi.org/10.1038/s41598-021-87284-x

PMid:33863959 PMCid:PMC8052460

Pironon S., and Gomez M., 2020, Plant agrodiversity to the rescue, Nature Climate Change, 11: 6-8.

https://doi.org/10.1038/s41558-020-00925-3

Rodríguez-Bonilla L., Cuevas H., Montero-Rojas M., Bird-Picó F., Luciano-Rosario D., and Siritunga D., 2014, Assessment of genetic diversity of sweet potato in Puerto Rico, PLoS One, 9(12): e116184.

https://doi.org/10.1371/journal.pone.0116184

PMid:25551388 PMCid:PMC4281141

Rosero A., Burgos-Paz W., Araujo H., Pastrana-Vargas I., Martínez R., Pérez J., and Espitia L., 2023, Sweet potato varietal selection using combined methods of multi-trait index, genetic gain and stability from multi-environmental evaluations, Horticulturae, 9(9): 974.

https://doi.org/10.3390/horticulturae9090974

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

PMid:36015442 PMCid:PMC9412483

Sapakhova Z., Raissova N., Daurov D., Zhapar K., Daurova A., Zhigailov A., Zhambakin K., and Shamekova M., 2023, Sweet potato as a key crop for food security under the conditions of global climate change: a review, Plants, 12(13): 2516.

https://doi.org/10.3390/plants12132516

PMid:37447081 PMCid:PMC10346279

Solankey S., Singh P., and Singh R., 2015, Genetic diversity and interrelationship of qualitative and quantitative traits in sweet potato, International Journal of Vegetable Science, 21: 236-248.

https://doi.org/10.1080/19315260.2013.867295

Spanoghe M., Marique T., Nirsha A., Esnault F., and Lanterbecq D., 2022, Genetic diversity trends in the cultivated potato: a spatiotemporal overview, Biology, 11(4): 604.

https://doi.org/10.3390/biology11040604

PMid:35453803 PMCid:PMC9026384

Springer N., and Schmitz R., 2017, Exploiting induced and natural epigenetic variation for crop improvement, Nature Reviews Genetics, 18: 563-575.

https://doi.org/10.1038/nrg.2017.45

PMid:28669983

Su W., Wang L., Lei J., Chai S., Liu Y., Yang Y., Yang X., and Jiao C., 2017, Genome-wide assessment of population structure and genetic diversity and development of a core germplasm set for sweet potato based on specific length amplified fragment (SLAF) sequencing, PLoS One, 12(2): e0172066.

https://doi.org/10.1371/journal.pone.0172066

PMid:28187178 PMCid:PMC5302839

Swanckaert J., Gemenet D., Anglin N., and Grüneberg W., 2021, Sweet potato (*Ipomoea batatas* (L.) Lam.) breeding, In: Al-Khayri J.M., Jain S.M., and Johnson D.V. (eds.), Advances in plant breeding strategies: vegetable crops, Springer, Cham, Switzerland, pp.513-546.

https://doi.org/10.1007/978-3-030-66965-2_12

Tessema G., Mohammed A., and Abebe D., 2022, Genetic variability studies for tuber yield and yield attributes in Ethiopian released potato (*Solanum tuberosum* L.) varieties, PeerJ, 10: e12860.

https://doi.org/10.7717/peerj.12860

PMid:35186467 PMCid:PMC8841037

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: 321-350.

https://doi.org/10.1080/07352689.2022.2130361

Vargas P., Engelking E., Almeida L., Ferreira E., and Charlo H., 2018, Genetic diversity among sweet potato crops cultivated by traditional farmers, Revista Caatinga, 31(3): 779-790.

https://doi.org/10.1590/1983-21252018V31N329RC

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

Varshney R., Roorkiwal M., and Sorrells M., 2017, Genomic selection for crop improvement: an introduction, In: Varshney R., Roorkiwal M., and Sorrells M. (eds.), Genomic selection for crop improvement, Springer, Cham, Switzerland, pp.1-6.

https://doi.org/10.1007/978-3-319-63170-7_1

PMCid:PMC5467034

Zhou X.X., and Chen S.Y., 2024, Phylogenetic relationships and genetic diversity among domesticated legumes, Legume Genomics and Genetics, 15(4): 187-198.

https://doi.org/10.5376/lgg.2024.15.0019