Plant Gene and Trait 2024, Vol.15, No.6, 275-284
http://genbreedpublisher.com/index.php/pgt

Review Article **Open Access**

Genetic Diversity in Sweet Potato: A Review of Global Germplasm

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Plant Gene and Trait, 2024, Vol.15, No.6 doi: 10.5376/pgt.2024.15.0027
Received: 11 Oct., 2024
Accepted: 13 Nov., 2024
Published: 21 Nov., 2024

Preferred citation for this article:
Zhang H.Y., and Zhao L., 2024, Genetic diversity in sweet potato: a review of global germplasm, Plant Gene and Trait, 15(6): 275-284 (doi: 10.5376/pgt.2024.15.0027)

Abstract Sweet potato (*Ipomoea batatas* L. Lam) is a globally significant food crop with extensive genetic diversity. This study synthesizes findings from various studies on the genetic diversity of sweet potato germplasm collected worldwide. Chloroplast SSR markers have revealed low genetic diversity among female parents in the National Agrobiodiversity Center's collection, indicating a need for broader germplasm collection. Retrotransposon-based insertion polymorphism (RBIP) markers have demonstrated significant intergroup genetic variation, suggesting limited evolutionary diversification despite geographic speciation. Genome-wide assessments using SNPs have identified three major genetic groups, with a core germplasm set developed for future breeding. Morphological, biochemical, and molecular markers have been used to characterize genetic diversity, highlighting promising genotypes for yield and antioxidant content. AFLP analysis has shown low genetic diversity among Tanzanian accessions, with significant within-region variation. These findings underscore the importance of comprehensive germplasm characterization and conservation to support sweet potato breeding programs.

Keywords Sweet potato; Genetic diversity; Germplasm; Chloroplast SSR markers; Retrotransposon-based insertion polymorphism (RBIP)

1 Introduction

Sweet potato (*Ipomoea batatas* L. Lam) is a vital food crop with significant agricultural and economic contributions worldwide. It ranks as the sixth most important food crop globally, with China leading its production in a market valued at USD 45 trillion (Escobar-Puentes et al., 2022). Sweet potato is not only a staple food in many developing countries but also a crucial source of income and nutrition for poor farming communities (Lamaro et al., 2022). Its rich nutritional profile, including sugars, slow digestible/resistant starch, vitamins, minerals, and bioactive compounds, makes it a valuable crop for both food security and health benefits (Mohanraj and Sivasankar, 2014). Additionally, sweet potato's versatility extends to its use in agroindustry and medicinal applications, further enhancing its economic importance.

The study of genetic diversity and germplasm conservation in sweet potato is essential for several reasons. Firstly, understanding the genetic diversity within sweet potato cultivars can help in the development of improved varieties with higher yields, disease resistance, and better adaptability to different environmental conditions (Lamaro et al., 2022). For instance, genetic diversity studies using various markers such as SSR, AFLP, and RBIP have revealed significant variability among sweet potato accessions, which is crucial for breeding programs (ELameen et al., 2008; Meng et al., 2021). Secondly, conserving sweet potato germplasm ensures the preservation of unique genetic traits that may be lost due to environmental changes or agricultural practices (Roullier et al., 2013; Winnicki et al., 2021). This is particularly important in regions like New Guinea, where traditional landraces have accumulated impressive genetic diversity due to farmers' management practices (Roullier et al., 2016). Lastly, germplasm conservation supports the reinvigoration of cultural heritage and local markets, as seen with the traditional Hawaiian sweet potato varieties (Winnicki et al., 2021).

This study reviews the current status of genetic diversity in global sweet potato germplasm resources, discusses the importance of their conservation, and provides an overview of commonly used diversity assessment markers and methods (such as SSR, AFLP, and RBIP). It analyzes the role of regional germplasm banks (such as the

National Agricultural Biodiversity Center, as well as those in Tanzania and Burkina Faso) in preserving genetic diversity, and proposes measures like on-farm conservation programs and core sample distribution to enhance local adaptability and resilience. Using examples from Hawaii and New Guinea, it explores the economic and cultural impacts of sweet potato genetic diversity, aiming to provide a theoretical basis and practical guidance for the effective conservation and sustainable utilization of global sweet potato germplasm resources.

2 Historical Overview of Sweet Potato Domestication

2.1 The origin and domestication process of sweet potato

The domestication of sweet potato (*Ipomoea batatas*) is a complex process that has intrigued researchers for decades. The origins of this hexaploid species have been debated, with hypotheses suggesting either an autopolyploid origin from the diploid *I. trifida* or an allopolyploid origin involving genomes of *I. trifida* and *I. triloba*. Recent molecular genetic data, however, support an autopolyploid origin of sweet potato from an ancestor shared with *I. trifida*, which might be similar to currently observed tetraploid wild Ipomoea accessions. This suggests that cultivated *I. batatas* evolved from at least two distinct autopolyploidization events in polymorphic wild populations of a single progenitor species (Roullier et al., 2013). Additionally, cytogenetic studies have reinforced the close relationship between *I. trifida* and *I. batatas*, indicating that *I. trifida* might be the progenitor of *I. batatas* (Srisuwan et al., 2006).

2.2 Global distribution of sweet potato germplasm resources

Sweet potato is now cultivated globally, with significant genetic diversity observed across different regions. The germplasm resources of sweet potato are distributed widely, with notable centers of diversity in Central and South America, where the crop is believed to have originated. Molecular marker analysis has revealed high genetic diversity in sweet potato germplasms from these regions, particularly in Central America, which is considered a primary center of origin (Murthy et al., 2021). New Guinea is recognized as a secondary center of diversity, where the introduction of sweet potato from the Northern neotropical genepool and subsequent recombination with local genotypes have led to significant genetic variation (Roullier et al., 2013). Furthermore, studies using chloroplast SSR markers have shown that sweet potato accessions from Korea, Japan, Taiwan, and the USA form distinct clusters, indicating regional differentiation in germplasm resources (Lee et al., 2019).

2.3 Historical development and evolution of sweet potato varieties in different regions

The historical development and evolution of sweet potato varieties have been shaped by both natural and human-mediated processes. In New Guinea, the diversification of sweet potato is primarily attributed to the active management of the crop's reproductive biology by local farmers, who frequently incorporate plants from true seeds, leading to a high number of variants (Roullier et al., 2013). In Polynesia, archaeological evidence suggests that sweet potato was introduced pre-Columbian times, with cultivation practices adapting to local climatic conditions. For instance, in New Zealand, the discovery of ancient storage pits for sweet potato (kūmara) in the cooler southern regions indicates that early Polynesian settlers developed strategies to grow and store the crop despite challenging environmental conditions. This historical adaptation highlights the resilience and versatility of sweet potato as it spread across different regions and climates.

3 Current Status of Sweet Potato Germplasm Collection

3.1 Current state of the collection and preservation of sweet potato germplasm worldwide

The global collection and preservation of sweet potato germplasm have seen significant advancements, with numerous accessions being conserved in various germplasm banks. For instance, the National Agrobiodiversity Center (NAC) has a collection of 558 sweet potato accessions, which have been analyzed for genetic diversity using chloroplast simple sequence repeat (cpSSR) markers. This analysis revealed a relatively low genetic diversity among the female parents of these accessions, indicating a need for further collection efforts to enhance the genetic base (Lee et al., 2019). Similarly, the International Potato Center (CIP) houses one of the largest collections, with nearly 6,000 accessions of cultivated sweet potato and over 1,000 accessions of crop wild relatives. This extensive collection has been genotyped to assess genetic identity, diversity, and population structure, uncovering high levels of redundancy and some genetic identity errors (Anglin et al., 2021).

3.2 The role of major germplasm banks and research institutions

Major germplasm banks and research institutions play a crucial role in the collection, preservation, and characterization of sweet potato germplasm. The CIP, for example, not only maintains a vast collection but also conducts genotyping and phenotyping to ensure the accuracy and utility of the germplasm. Their efforts have identified significant genetic diversity and population structure within their collection, which is essential for breeding and conservation programs (Anglin et al., 2021). The NAC in South Korea also contributes significantly by maintaining a diverse collection and conducting genetic diversity assessments to inform future preservation and breeding strategies (Lee et al., 2019). These institutions provide valuable resources and data that support global sweet potato improvement efforts.

3.3 Advances in germplasm preservation technologies

Recent advances in germplasm preservation technologies have greatly enhanced the ability to maintain and utilize sweet potato genetic resources. Techniques such as retrotransposon-based insertion polymorphism (RBIP) markers have been developed to study genetic diversity and population structure in sweet potato. These markers have proven effective in revealing high levels of polymorphism and genetic variation among sweet potato accessions, which is crucial for identifying and preserving diverse genetic traits (Meng et al., 2021). Additionally, genome-wide assessments using specific length amplified fragment (SLAF) sequencing have provided detailed insights into the genetic relationships and population structure of sweet potato accessions, facilitating the development of core germplasm sets for targeted breeding programs (Su et al., 2017). These technological advancements are instrumental in ensuring the long-term conservation and effective utilization of sweet potato germplasm.

4 Genetic Diversity in Sweet Potato

4.1 Progress in studying sweet potato genetic diversity using molecular markers

The use of molecular markers, particularly simple sequence repeats (SSRs), has significantly advanced the study of genetic diversity in sweet potato. SSR markers are highly polymorphic and reproducible, making them ideal for genetic studies. For instance, a high-density SSR genetic linkage map was developed for sweet potato, which included 5 057 SSR markers covering 13 299.9 cM with a marker density of 2.6 cM in one parent map and 3 009 SSR markers covering 1 122.9 cM with a marker density of 3.7 cM in another parent map. This map is consistent with the autohexaploid nature of sweet potato and provides a robust foundation for quantitative trait locus (QTL) mapping and marker-assisted breeding (Meng et al., 2021). Additionally, SSR markers have been used to assess the genetic diversity of sweet potato germplasms collected worldwide, revealing significant polymorphisms and genetic variability among accessions (Lee et al., 2019).

4.2 Application of genomic analysis in revealing genetic structure and diversity

Genomic analysis using SSR markers has been instrumental in uncovering the genetic structure and diversity of sweet potato. For example, a study using nine chloroplast SSR markers on 558 sweet potato accessions from the National Agrobiodiversity Center (NAC) identified 33 chlorotypes and divided the accessions into four clusters based on their genetic relationships. This analysis highlighted the low genetic diversity of female parents in the NAC collection, suggesting the need for more diverse germplasm collection (Lee et al., 2019). Another study on Brazilian sweet potato landraces using SSR markers found high genetic and intravarietal diversity, with most variability distributed within households rather than between communities. This indicates the influence of outcrossing and anthropic factors such as selection and maintenance of different varieties within small plots and home gardens (Veasey et al., 2008).

4.3 Research on genetic differences and phylogenetic relationships among sweet potato germplasm

Research on genetic differences and phylogenetic relationships among sweet potato germplasm has provided insights into the evolutionary history and breeding potential of this crop. The development of SSR linkage maps has facilitated the identification of homologous groups and the understanding of the genetic architecture of sweet potato (Meng et al., 2021). Furthermore, studies using SSR markers have revealed significant genetic diversity among sweet potato accessions from different geographical regions. For instance, the genetic diversity assessment of sweet potato accessions from Brazil showed a high level of genetic variability, which is crucial for breeding programs aiming to improve sweet potato traits (Ghebreslassie et al., 2016). These findings underscore the importance of molecular approaches in enhancing our understanding of sweet potato genetic diversity and guiding conservation and breeding efforts.

5 Genetic Diversity in Sweet Potato Germplasm from Asia

5.1 Genetic diversity analysis of sweet potato germplasm in Asia

The genetic diversity of sweet potato germplasm in Asia has been extensively studied using various molecular markers. For instance, a genome-wide assessment of 197 sweet potato accessions, primarily from China, utilized 62 363 SNPs to evaluate genetic diversity and population structure. This study identified three distinct genetic groups and highlighted significant genetic variation within the accessions, with a mean genetic distance ranging from 0.290 to 0.311 (Figure 1) (Su et al., 2017). Another study employed retrotransposon-based insertion polymorphism (RBIP) markers to analyze 105 sweet potato germplasm resources from China, Japan, and America. This analysis revealed high polymorphism (91.07%) and significant genetic variation among the accessions, which were divided into three groups (Meng et al., 2021).

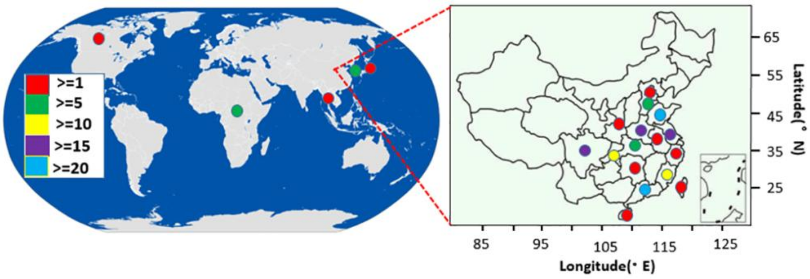

Figure 1 Location of the sweet potato accessions from around the world, highlighting China (Adopted from Su et al., 2017)

5.2 Research background and data sources

The research on sweet potato genetic diversity in Asia has been driven by the need to enhance breeding programs and conserve genetic resources. The studies have utilized germplasm collections from various national and international gene banks. For example, the National Agrobiodiversity Center (NAC) in South Korea has been a significant source of germplasm for genetic diversity studies. One study analyzed 558 sweet potato accessions from the NAC using chloroplast SSR markers, revealing low genetic diversity among the female parents and the need for more diverse collections (Lee et al., 2019). Additionally, the International Potato Center (CIP) has contributed to the understanding of genetic diversity by maintaining a vast collection of sweet potato accessions from around the world, including Asia (Zhang et al., 2000).

5.3 Key findings and their significance for global sweet potato diversity conservation

The key findings from these studies underscore the rich genetic diversity present in Asian sweet potato germplasm. The identification of distinct genetic groups and high levels of polymorphism suggests that Asian germplasm can significantly contribute to global sweet potato breeding programs. The low genetic diversity observed in some collections, such as those from the NAC, highlights the importance of expanding germplasm collections to include more diverse accessions (Figure 2) (Lee et al., 2019; Luo et al., 2023). The development of core germplasm sets, as seen in the study using SNP markers, provides valuable resources for future breeding efforts. Furthermore, the use of advanced molecular markers like RBIP and SSRs has proven effective in characterizing genetic diversity and can be applied to other regions to enhance global conservation strategies (Monteros-Altamirano et al., 2020).

These findings are crucial for the conservation of sweet potato genetic resources, as they provide insights into the genetic structure and diversity of germplasm collections. By identifying areas with low genetic diversity, researchers can prioritize these regions for new germplasm collection efforts. Additionally, the development of core germplasm sets ensures that the most genetically diverse and representative accessions are preserved and utilized in breeding programs, ultimately contributing to the sustainability and improvement of sweet potato crops worldwide.

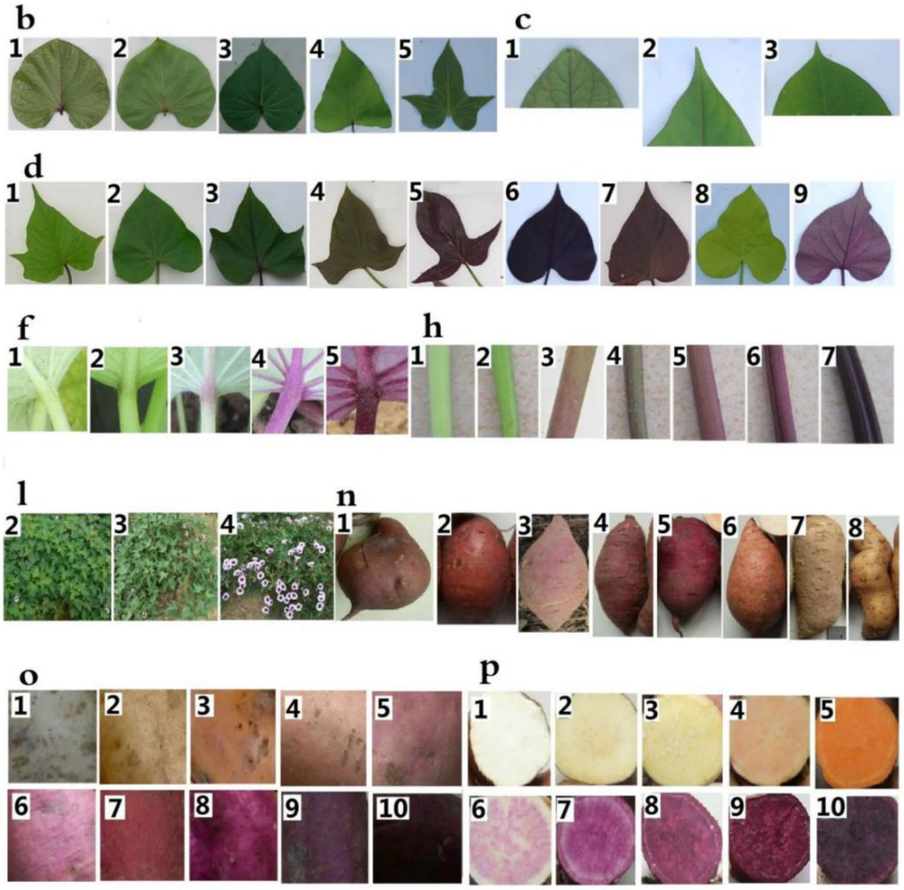

Figure 2 Phenotypic codes and pictures for sweet potato germplasm (Adopted from Luo et al., 2023)

6 Environmental and Agronomic Factors Influencing Genetic Diversity

6.1 Effects of different environmental conditions on sweet potato genetic diversity

Environmental conditions such as climate and soil significantly influence the genetic diversity of sweet potato. For instance, sweet potato genotypes exhibit varying degrees of adaptation to different environmental conditions, which is crucial for breeding programs aimed at improving crop resilience. Studies have shown that sweet potato genotypes can be selected based on their performance across multiple environments, incorporating traits such as yield, quality, and plant architecture (Rosero et al., 2023; Liu and Chen, 2024). Additionally, the genetic diversity of sweet potato is influenced by the specific environmental conditions of the regions where they are cultivated. For example, sweet potato accessions from Korea, Japan, Taiwan, and the USA showed distinct genetic clusters, indicating that regional environmental conditions play a role in shaping genetic diversity (Lee et al., 2019).

6.2 Impact of agronomic management and cultivation practices

Agronomic management and cultivation practices also have a profound impact on the genetic diversity and performance of sweet potato. Practices such as fertilization, crop protection, and rotational designs can influence crop yield and nutritional quality. For example, organic fertilization has been shown to result in higher concentrations of phenolics and other nutritionally desirable phytochemicals in crops, while also reducing the concentrations of toxic metals like cadmium and nickel (Rempelos et al., 2023). Moreover, the selection of sweet potato genotypes based on multi-trait indices and stability analysis helps in identifying superior varieties that perform well under different agronomic conditions (Rosero et al., 2023). This approach ensures that the selected genotypes are not only high-yielding but also stable across various environmental conditions, thereby maintaining genetic diversity.

6.3 Challenges posed by global warming to sweet potato germplasm resources and diversity

Global warming poses significant challenges to the genetic diversity and germplasm resources of sweet potato. Increasing temperatures and extreme weather events can negatively impact the productivity and resilience of sweet potato genotypes. For instance, heat stress is a major concern, and studies have identified specific sweet potato cultivars that exhibit heat tolerance, which is crucial for maintaining crop resilience in the face of climate change (Heider et al., 2020). Additionally, drought stress is another critical factor that affects sweet potato cultivation. Breeding programs are focusing on developing drought-tolerant varieties by studying the physiological and biochemical features of different genotypes (Monteros-Altamirano et al., 2023). These efforts are essential to ensure that sweet potato remains a viable crop under changing climatic conditions, thereby preserving its genetic diversity.

7 Utilization of Sweet Potato Germplasm for Breeding and Improvement

7.1 Breeding strategies to enhance yield, disease resistance, and nutritional value using genetic diversity

Breeding strategies for sweet potato have increasingly focused on leveraging the extensive genetic diversity present within global germplasm collections. The use of morphological, biochemical, and molecular markers has been pivotal in identifying and selecting genotypes with desirable traits. For instance, the study by Paliwal et al. (2020) demonstrated the use of RAPD markers to assess genetic diversity among 21 sweet potato genotypes, identifying promising candidates for yield improvement and disease resistance. Similarly, the analysis of chloroplast SSR markers in 558 sweet potato accessions highlighted the need for broader genetic diversity in breeding programs to enhance traits such as yield and disease resistance (Lee et al., 2019).

Moreover, the integration of advanced genomic tools has revolutionized breeding strategies. Techniques such as marker-assisted selection (MAS) and genomic selection (GS) enable breeders to track and manipulate specific DNA sequences associated with desirable traits, thereby increasing the efficiency of breeding programs (Bethke et al., 2019; Tiwari et al., 2020). These strategies are complemented by traditional breeding methods, which continue to play a significant role in the development of new cultivars with improved nutritional value, such as higher carotene and antioxidant content (Solankey et al., 2015).

7.2 Analysis of successful breeding cases and insights for future breeding

Several successful breeding cases underscore the potential of utilizing genetic diversity for sweet potato improvement. For example, the study by (Vargas et al., 2018) highlighted the significant genetic variability among sweet potato accessions collected from traditional communities, which can be harnessed for breeding programs aimed at enhancing yield and disease resistance. The identification of genotypes with high phenolic and antioxidant content, as reported by (Paliwal et al., 2020), provides a foundation for developing nutritionally superior sweet potato varieties.

Future breeding efforts can benefit from the insights gained through these studies. The use of high-throughput marker systems, such as retrotransposon-based insertion polymorphism (RBIP) markers, has proven effective in assessing genetic diversity and identifying unique genetic resources for breeding (Meng et al., 2021). Additionally, the application of genomic tools, including genome editing and multi-omics platforms, offers new avenues for the precise manipulation of genetic traits, thereby accelerating the development of improved sweet potato cultivars (Tiwari et al., 2022).

7.3 Challenges faced in breeding processes and potential solutions

Despite the advancements in breeding strategies, several challenges persist in the breeding of sweet potato. One major challenge is the limited genetic diversity within certain germplasm collections, which can hinder the development of new varieties with enhanced traits (Lee et al., 2019). To address this, it is crucial to expand germplasm collections by incorporating accessions from diverse geographical regions and traditional farming communities (Vargas et al., 2018).

Another challenge is the complexity of sweet potato genetics, which can complicate the identification and manipulation of desirable traits. The use of advanced genomic tools and high-throughput marker systems can mitigate this issue by providing more precise and efficient methods for trait selection and breeding (Bethke et al., 2019; Meng et al., 2021). Additionally, the integration of phenotypic and genotypic data through association mapping can enhance the understanding of trait inheritance and facilitate the development of superior sweet potato varieties (Gebhardt et al., 2004).

8 Conservation Strategies for Sweet Potato Genetic Resources

8.1 Strategies for maintaining and managing sweet potato genetic diversity

Maintaining and managing the genetic diversity of sweet potato is crucial for ensuring the crop's resilience and adaptability to changing environmental conditions. One effective strategy is the collection and characterization of diverse sweet potato accessions from various geographical regions. For instance, the National Agrobiodiversity Center (NAC) has utilized chloroplast simple sequence repeat (cpSSR) markers to analyze the genetic diversity of 558 sweet potato accessions, revealing the need for more diverse collections to enhance genetic variability (Lee et al., 2019). Similarly, in Puerto Rico, genetic diversity assessments using SSR markers have shown high levels of heterozygosity and genetic diversity among local landraces, underscoring the importance of preserving these genetic resources (Rodríguez-Bonilla et al., 2014).

8.2 Comprehensive applications of in vitro conservation, field gene banks, and community-based germplasm conservation

In vitro conservation, field gene banks, and community-based germplasm conservation are complementary approaches to preserving sweet potato genetic resources. In vitro conservation techniques, such as cryopreservation and tissue culture, allow for the long-term storage of genetic material under controlled conditions, minimizing the risk of genetic erosion (Salgotra and Chauhan, 2023). Field gene banks, on the other hand, maintain living collections of sweet potato accessions, providing a dynamic resource for breeding and research. For example, the Texas A&M University Potato Breeding Program has maintained a collection of advanced clones in vitro over a 40-year period, facilitating the conservation and utilization of genetic diversity (Pandey et al., 2021).

Community-based germplasm conservation involves local farmers and communities in the preservation of sweet potato varieties. This approach not only helps maintain genetic diversity but also ensures the continued use and adaptation of traditional varieties to local conditions. In Ethiopia, local collections of sweet potato have shown significant genetic diversity and better performance compared to improved varieties, highlighting the value of community-based conservation efforts (Mohammed et al., 2015).

8.3 Importance of international cooperation and policy support for the conservation of sweet potato genetic resources

International cooperation and policy support are essential for the effective conservation of sweet potato genetic resources. Collaborative efforts between countries and institutions can facilitate the exchange of germplasm, knowledge, and technologies, enhancing global conservation strategies. For instance, the identification of heat-tolerant sweet potato cultivars through international field experiments underscores the importance of shared research initiatives in addressing climate change challenges (Heider et al., 2020).

Policy support at national and international levels is also critical for the sustainable conservation of genetic resources. Policies that promote the establishment of gene banks, support community-based conservation programs, and facilitate the exchange of genetic material can significantly enhance conservation efforts. The integration of biotechnological tools, such as next-generation sequencing and molecular markers, into conservation policies can further improve the characterization and preservation of sweet potato genetic diversity (Salgotra and Chauhan, 2023).

9 Conclusion

The current status of sweet potato genetic diversity conservation and utilization reveals a complex yet promising landscape. Studies have shown that sweet potato germplasm collections exhibit significant genetic diversity, although there are areas that require further attention. For instance, the genetic diversity of sweet potato accessions conserved at the National Agrobiodiversity Center (NAC) is relatively low, indicating a need for more extensive collection efforts to enhance the genetic base. Retrotransposon-based insertion polymorphism (RBIP) markers have been effectively used to assess genetic diversity, revealing substantial polymorphism and genetic variation among sweet potato germplasms. Additionally, genome-wide assessments using specific length amplified fragment (SLAF) sequencing have provided detailed insights into the population structure and genetic relationships among sweet potato accessions, further highlighting the genetic richness within the species. Despite these advancements, the genetic diversity within sweet potato germplasms is not uniformly distributed, with some studies indicating limited evolutionary diversification and geographic speciation. Overall, while significant progress has been made in understanding and conserving sweet potato genetic diversity, there remains a need for continued efforts to expand and utilize these genetic resources effectively.

Looking forward, several key areas of research and germplasm resource management need to be prioritized to ensure the sustainable conservation and utilization of sweet potato genetic diversity. First, expanding the collection of sweet potato germplasms, particularly from underrepresented regions, is crucial to enhance the genetic base and ensure the availability of diverse genetic material for breeding programs. Advanced molecular techniques, such as RBIP markers and SLAF sequencing, should continue to be employed to provide comprehensive assessments of genetic diversity and population structure, facilitating the identification of core germplasm sets for targeted breeding efforts.

Additionally, integrating ex situ and in situ conservation strategies will be essential to safeguard the genetic diversity of sweet potato and its wild relatives, as demonstrated by successful conservation efforts in Brazil. Collaborative international initiatives, such as those supported by the Global Crop Diversity Trust, can play a pivotal role in coordinating these efforts and ensuring the global exchange of germplasm resources. Furthermore, leveraging the economic benefits of conserved germplasm, as evidenced by the significant contributions of the International Potato Center (CIP) genebank to crop improvement, can provide a strong incentive for continued investment in germplasm conservation and utilization. By addressing these future prospects, researchers and policymakers can ensure the sustainable management of sweet potato genetic resources, ultimately contributing to global food security and agricultural resilience.

Acknowledgments

We would like to thank Prof. Guan for his meticulous reading of the manuscript, providing comprehensive academic suggestions and for editing this article. We're also grateful to the two anonymous peer reviewers for their academic revisions.

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

Anglin N., Robles R., Rossel G., Alagon R., Panta A., Jarret R., Manrique N., and Ellis D., 2021, Genetic identity, diversity, and population structure of CIP's sweetpotato's (*I. batatas*) germplasm collection, Frontiers in Plant Science, 12: 660012.
https://doi.org/10.3389/fpls.2021.660012
PMid:34777403 PMCid:PMC8589021

Bethke P., Halterman D., and Jansky S., 2019, Potato germplasm enhancement enters the genomics era, Agronomy, 9(10): 575.
https://doi.org/10.3390/agronomy9100575

ELameen A., Fjellheim S., Larsen A., Rognli O., Sundheim L., Msolla S., Masumba E., Mtunda K., and Klemsdal S., 2008, Analysis of genetic diversity in a sweet potato (*Ipomoea batatas* L.) germplasm collection from Tanzania as revealed by AFLP, Genetic Resources and Crop Evolution, 55: 397-408.
https://doi.org/10.1007/s10722-007-9247-0

Escobar-Puentes A., Palomo I., Rodríguez L., Fuentes E., Villegas-Ochoa M., González-Aguilar G., Olivas-Aguirre F., and Wall-Medrano A., 2022, Sweet potato (*Ipomoea batatas* L.) phenotypes: from agroindustry to health effects, Foods, 11(7): 1058.
https://doi.org/10.3390/foods11071058
PMid:35407143 PMCid:PMC8997864

Gebhardt C., Ballvora A., Walkemeier B., Oberhagemann P., and Schüler K., 2004, Assessing genetic potential in germplasm collections of crop plants by marker-trait association: a case study for potatoes with quantitative variation of resistance to late blight and maturity type, Molecular Breeding, 13: 93-102.
https://doi.org/10.1023/B:MOLB.0000012878.89855.df

Ghebreslassie B.M., Githiri S.M., Mehari T., Kasili R.W., Ghislain M., and Magembe E., 2016, Genetic diversity assessment of farmers' and improved potato (*Solanum tuberosum*) cultivars from Eritrea using simple sequence repeat (SSR) markers, African Journal of Biotechnology, 15(35): 1883-1891.
https://doi.org/10.5897/AJB2016.15237

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

Lamaro G., Tsehaye Y., and Girma A., 2022, Orange-fleshed sweet potato [*Ipomoea batatas* (L.) Lam] genotype by environment interaction for yield and yield components and SPVD resistance under arid and semi-arid climate of northern Ethiopia, Ethiopian Journal of Science and Technology, 7(3): 255-276.
https://doi.org/10.4314/ejst.v15i3.3

Luo Z., Yao Z., Yang Y., Wang Z., Zou H., Zhang X., Chen J., Fang B., and Huang L., 2023, Genetic fingerprint construction and genetic diversity analysis of sweet potato (Ipomoea batatas) germplasm resources, BMC Plant Biology, 23: 355.
https://doi.org/10.1186/s12870-023-04329-1
PMid:37434130 PMCid:PMC10334575

Liu Y., and Chen Y., 2024, Subsoiling treatment on soil permeability and its impact on the growth of sweet potato (*Ipomoea atatas*), International Journal of Horticulture, 14(1): 1-10.
https://doi.org/10.5376/ijh.2024.14.0001

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

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

Meng Y., Zheng C., Li H., Li A., Zhai H., Wang Q., He S., Zhao N., Zhang H., Gao S., and Liu Q., 2021, Development of a high-density SSR genetic linkage map in sweet potato, Crop Journal, 9(6): 1367-1374.
https://doi.org/10.1016/j.cj.2021.01.003

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

Mohanraj R., and Sivasankar S., 2014, Sweet potato (*Ipomoea batatas* [L.] Lam)-a valuable medicinal food: a study, Journal of Medicinal Food, 17(7): 733-741.
https://doi.org/10.1089/jmf.2013.2818
PMid:24921903

Monteros-Altamirano Á., Paredes D., Buitrón-Bustamante J., Tapia C., and Peña G., 2020, Genetic diversity of sweet potatoes [*Ipomoea batatas* (L) Lam.] in Ecuador, Genetic Resources and Crop Evolution, 68: 307-320.
https://doi.org/10.1007/s10722-020-00987-4

Murthy P., Patel N., Kapadia C., Desai K., and Rao G., 2021, Genetic diversity analysis of sweet potato [*Ipomoea batatas* (L.) Lam.] germplasms through RAPD and ISSR markers, Bangladesh Journal of Botany, 50: 119-129.
https://doi.org/10.3329/bjb.v50i1.52679

Paliwal P., Jain D., Joshi A., Ameta K., Chaudhary R., and Singh A., 2020, Diversity analysis of Sweet Potato (*Ipomoea batatas*[L.] Lam) genotypes using morphological, biochemical and molecular markers, Indian Journal of Experimental Biology, 58: 276-285.
https://doi.org/10.56042/ijeb.v58i04.65463

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

Rempelos L., Barański M., Sufar E., Gilroy J., Shotton P., Leifert H., Średnicka-Tober D., Hasanaliyeva G., Rosa E., Hajšlová J., Schulzova V., Cakmak I., Ozturk L., Brandt K., Seal C., Wang J., Schmidt C., and Leifert C., 2023, Effect of climatic conditions, and agronomic practices used in organic and conventional crop production on yield and nutritional composition parameters in potato, cabbage, lettuce and onion; results from the long-term NFSC-trials, Agronomy, 13(5): 1225.
https://doi.org/10.3390/agronomy13051225

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

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

Roullier C., Duputié A., Wennekes P., Benoit L., Bringas V., Rossel G., Tay D., McKey D., and Lebot V., 2013, Disentangling the origins of cultivated sweet potato (*Ipomoea batatas* (L.) Lam.), PLoS One, 8(10): e62707.
https://doi.org/10.1371/annotation/936fe9b4-41cb-494d-87a3-a6d9a37c6c68
PMid:23723970

Roullier C., Kambouo R., Paofa J., McKey D., and Lebot V., 2013, On the origin of sweet potato (*Ipomoea batatas* (L.) *Lam*.) genetic diversity in New Guinea, a secondary centre of diversity, Heredity, 110: 594-604.
https://doi.org/10.1038/hdy.2013.14
PMid:23531982 PMCid:PMC3656641

Salgotra R., and Chauhan B., 2023, Genetic diversity, conservation, and utilization of plant genetic resources, Genes, 14(1): 174.
https://doi.org/10.3390/genes14010174
PMid:36672915 PMCid:PMC9859222

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

Srisuwan S., Sihachakr D., and Siljak-Yakovlev S., 2006, The origin and evolution of sweet potato (*Ipomoea batatas Lam*.) and its wild relatives through the cytogenetic approaches, Plant Science, 171(3): 424-433.
https://doi.org/10.1016/j.plantsci.2006.05.007
PMid:22980213

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

Tiwari J., Buckseth T., Zinta R., Bhatia N., Dalamu D., Naik S., Poonia A., Kardile H., ChalLam C., Singh R., Luthra S., Kumar V., and Kumar M., 2022, Germplasm, breeding, and genomics in potato improvement of biotic and abiotic stresses tolerance, Frontiers in Plant Science, 13: 805671.
https://doi.org/10.3389/fpls.2022.805671
PMid:35197996 PMCid:PMC8859313

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

Veasey E., Borges A., Rosa M., Queiroz-Silva J., Bressan E., and Peroni N., 2008, Genetic diversity in Brazilian sweet potato (*Ipomoea batatas* (L.) Lam., Solanales, Convolvulaceae) landraces assessed with microsatellite markers, Genetics and Molecular Biology, 31(3): 725-733.
https://doi.org/10.1590/S1415-47572008000400020

Winnicki E., Kagawa-Viviani A., Perez K., Radovich T., and Kantar M., 2021, Characterizing the diversity of Hawai‘i sweet potatoes (*Ipomoea batatas* [L.] Lam.), Economic Botany, 75: 48-62.
https://doi.org/10.1007/s12231-020-09511-2

Zhang D., Cervantes J., Huáman Z., Carey E., and Ghislain M., 2000, Assessing genetic diversity of sweet potato (*Ipomoea batatas* (L.) Lam.) cultivars from tropical America using AFLP, Genetic Resources and Crop Evolution, 47: 659-665.