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Meta Analysis **Open Access**

Leveraging Global Sweet Potato Germplasm to Promote Genetic Diversity in Breeding

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Abstract Sweet potato (*Ipomoea batatas*) is a globally important crop, and its genetic diversity is vital for breeding programs aimed at enhancing disease resistance, yield, and stress tolerance. Genetic diversity studies provide crucial insights for crop improvement, but the vast amount of data across various regions remains underutilized. This study synthesizes findings from global genetic diversity studies on sweet potato, focusing on the geographic distribution of germplasm, genetic markers employed, and regional variability. Our analysis reveals key trends in diversity levels, highlights the impact of breeding practices, and identifies regions where germplasm variability is highest. These findings have important implications for breeding strategies, providing guidance on selecting traits for improvement and integrating diversity data into breeding programs. This study concludes by recommending the incorporation of emerging genomic technologies and bioinformatics tools to enhance the efficiency of sweet potato breeding efforts, and provides a roadmap for future breeding initiatives to maximize the use of genetic diversity for crop improvement.

Keywords Sweet potato; Genetic diversity; Breeding strategies; Meta-analysis; Germplasm

1 Introduction

Sweet potato (*Ipomoea batatas* (Lour.) Burkill) is a vital food crop globally, ranking as the sixth most important food crop worldwide (Lamaro et al., 2022). Originating from the Americas, it has spread across various continents, with China leading its production in a market valued at USD 45 trillion. The crop is known for its rich nutritional profile, including sugars, resistant starch, vitamins, minerals, and bioactive compounds, which contribute to its health benefits and global significance (Escobar-Puentes et al., 2022). The genetic diversity of sweet potato is crucial for its adaptability and resilience, with significant variations observed in different regions, such as the moderate diversity found in New Guinea compared to tropical America (Roullier et al., 2013).

Genetic diversity is a cornerstone for crop improvement, providing the necessary variability for breeding programs to enhance yield, disease resistance, and environmental adaptability (Li, 2024). In sweet potato, genetic diversity studies have revealed significant polymorphisms and diversity indices, which are essential for developing robust breeding strategies(Sun et al., 2022). The genetic diversity within sweet potato germplasms, such as those conserved at the National Agrobiodiversity Center, highlights the need for efficient management and collection of diverse accessions to support breeding efforts (Lee et al., 2019). Furthermore, the role of genetic diversity in suppressing invasive species and improving crop resilience underscores its importance in sustainable agriculture (Shen et al., 2019).

This study, by compiling and analyzing data from multiple research papers, assesses the genetic diversity of sweet potato, including intra- and inter-population genetic variability, explores the impact of this diversity on breeding and crop improvement, and identifies key factors influencing sweet potato genetic diversity, aiming to contribute to the development of more resilient and productive varieties, ultimately supporting global food security and agricultural sustainability.

2 Genetic Diversity in Sweet Potato

2.1 Geographic distribution of sweet potato germplasm

Sweet potato (*Ipomoea batatas* (Lour.) Burkill) is cultivated globally, with significant germplasm collections in various regions. For instance, the National Agrobiodiversity Center (NAC) in South Korea has a substantial collection of sweet potato accessions from Korea, Japan, Taiwan, and the USA, highlighting the broad geographic distribution of this crop (Figure 1) (Lee et al., 2019). Similarly, sweet potato germplasms have been collected from six provinces of China, Japan, and America, indicating a wide geographic spread (Meng et al., 2021). The diversity within these collections is crucial for breeding programs aimed at improving sweet potato varieties.

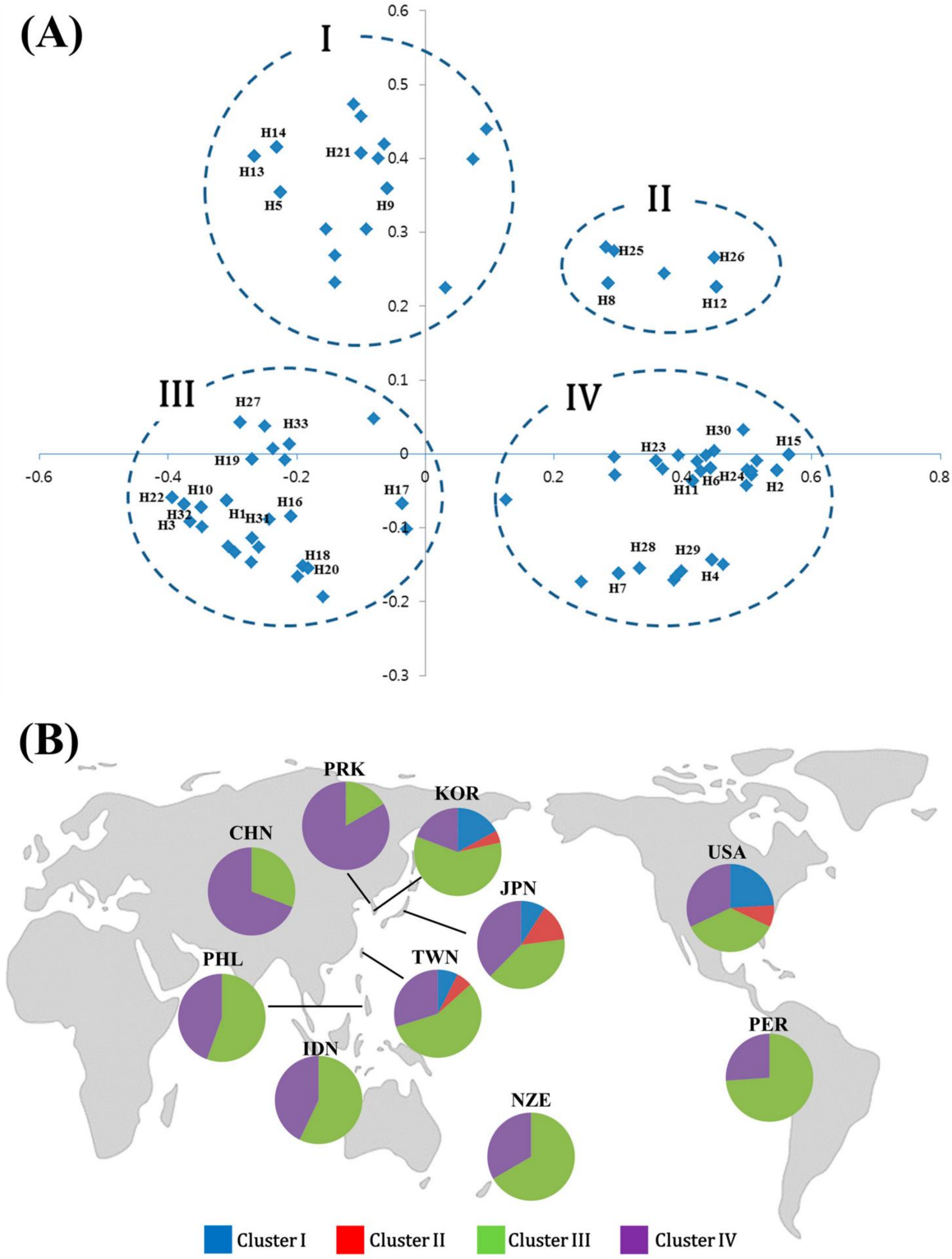

Figure 1 (A) Factorial analysis of the 8 cpSSR haplotypes. H, chloroplast haplotypes based on the median-joining network. (B) Original countries of sweet potato accessions and geographic distributions of the chloroplast haplotypes found. Pie charts on the map represent the chlorotype composition of the accessions and the colors in each chart represent the chlorotype indicated by factorial analysis (Adopted from Lee et al., 2019)

2.2 Genetic markers used in diversity studies

Several genetic markers have been employed to study the genetic diversity of sweet potato. Chloroplast simple sequence repeat (cpSSR) markers have been used to analyze the genetic diversity of sweet potato accessions, revealing polymorphisms and diversity indices that are essential for understanding the genetic makeup of the crop. Retrotransposon-based insertion polymorphism (RBIP) markers have also been utilized, providing high-throughput systems to study genetic diversity and population structure. Additionally, Random Amplified Polymorphic DNA (RAPD) and Inter-Simple Sequence Repeats (ISSR) markers have been used to evaluate genetic relatedness among sweet potato germplasms, offering insights into the genetic variation present within different accessions (Murthy et al., 2021). Specific Length Amplified Fragment (SLAF) sequencing has also been employed for genome-wide assessments, using single nucleotide polymorphisms (SNPs) to evaluate genetic diversity and population structure.

2.3 Key findings from global diversity studies

Global studies on sweet potato genetic diversity have yielded several key findings. The use of cpSSR markers revealed that the genetic diversity of female parents in the NAC collection is low, suggesting the need for more diverse accessions to be collected for effective germplasm management. RBIP markers have shown that sweet potato germplasms are not well evolutionarily diversified, although some geographic speciation has occurred. RAPD and ISSR markers have demonstrated high levels of polymorphism, indicating significant genetic variation among sweet potato germplasms. SLAF sequencing has provided a comprehensive genome-wide assessment, identifying three major genetic groups and highlighting the importance of within-accession diversity (Su et al., 2017). These findings underscore the importance of using diverse genetic markers to capture the full extent of genetic variation in sweet potato, which is essential for breeding and conservation efforts.

3 Meta-Analysis of Genetic Diversity Data

3.1 Statistical synthesis of diversity measures

The genetic diversity of sweet potato has been assessed using various molecular markers, including retrotransposon-based insertion polymorphism (RBIP), chloroplast simple sequence repeats (cpSSR), and single nucleotide polymorphisms (SNPs). For instance, RBIP markers revealed an average polymorphism of 91.07% among 105 sweet potato germplasm resources, indicating significant genetic variability. Similarly, cpSSR markers showed polymorphisms in eight out of nine markers, with diversity indices ranging from 0.148 to 0.626 (Lee et al., 2019). SNP-based studies also demonstrated substantial genetic diversity, with mean polymorphic information content (PIC) values ranging from 0.232 to 0.251.

3.2 Key trends observed in genetic diversity studies

Several key trends have emerged from genetic diversity studies in sweet potato. Firstly, the genetic diversity within sweet potato germplasms is generally high, as evidenced by the high polymorphism rates and diversity indices across different studies. Secondly, the genetic structure analyses consistently divide sweet potato accessions into distinct groups, reflecting underlying genetic differentiation. For example, RBIP and SNP analyses both identified three major groups among the studied germplasms (Su et al., 2017). Thirdly, there is a notable consensus across different analytical methods, such as UPGMA dendrograms, principal component analysis (PCA), and model-based genetic structure analyses, in grouping the germplasms.

3.3 Variability across regions and germplasm collections

Genetic diversity studies have highlighted variability across different regions and germplasm collections. For instance, cpSSR marker analysis of 558 sweet potato accessions from the National Agrobiodiversity Center (NAC) revealed low genetic diversity among female parents, suggesting the need for more diverse collections. Similarly, studies on sweet potato accessions from traditional communities in Vale do Ribeira Paulista showed wide genetic diversity, with no clear grouping according to collection points (Vargas et al., 2018). These findings underscore the importance of regional and germplasm-specific studies to capture the full extent of genetic variability.

3.4 Impact of breeding practices on diversity levels

Breeding practices have a significant impact on the genetic diversity of sweet potato. Long-term self-retention and selective breeding can lead to reduced genetic variability within germplasm collections. For example, the analysis of molecular variance (AMOVA) indicated higher intergroup genetic variation (53%) than intrapopulation variation, suggesting limited evolutionary diversification due to breeding practices (Table 1) (Meng et al., 2021). Conversely, the development of core germplasm sets, as seen in studies using CoreHunter software, helps maintain genetic diversity while minimizing redundancies. These practices are crucial for ensuring the sustainability and improvement of sweet potato breeding programs.

Table 1 AMOVA results of 105 sweet potato germplasms with the $K = 3$ model (Adopted from Meng et al., 2021)

Source	df	Sum of squares	Mean of squares	Estimated variance	Percentage of total variance (%)	AMOVA statistics	Value	P
Among groups	2	225.601	112.800	3.698	53			
Within groups	102	339.371	3.327	3.327	47	PhiPT4	0.526	0.001
Total	104	564.971		7.026	100			

4 Implications for Breeding

4.1 Insights for improving genetic traits

The genetic diversity within sweet potato cultivars offers significant insights for improving various genetic traits. For instance, the identification of heat-tolerant cultivars and breeding lines, as well as traits predictive of heat tolerance such as canopy temperature depression, chlorophyll content, and storage root-flesh color, provides a foundation for breeding programs aimed at enhancing heat resilience (Heider et al., 2020). Additionally, the study of genetic variability and trait interrelationships, such as the positive phenotypic correlation between fresh weight of tubers per plant and the number of tubers per plant, days to maturity, and vine internode length, can guide the selection of genotypes with desirable yield traits (Solankey et al., 2015).

4.2 Role of diversity in disease resistance, yield, and stress tolerance

Genetic diversity plays a crucial role in enhancing disease resistance, yield, and stress tolerance in sweet potato. For example, the presence of natural fungicides and insect repellents like chlorogenic acids and coumarins in the storage root periderm can reduce post-harvest losses and insect damage, thereby improving overall crop resilience (Lebot et al., 2021). Furthermore, the identification of genotypes with high resistance to sweet potato virus disease (SPVD) and other biotic stresses through genotype-by-environment interaction analysis underscores the importance of genetic diversity in breeding for disease resistance (Ngailo et al., 2019). The study of drought tolerance mechanisms and the selection of drought-tolerant genotypes based on physiological and biochemical traits also highlight the role of genetic diversity in stress tolerance (Sapakhova et al., 2023).

4.3 Breeding strategies based on diversity findings

Breeding strategies can be significantly informed by findings on genetic diversity. The use of simple sequence repeat (SSR) markers to determine genetic diversity and resistance responses to various stresses can aid in the selection of parents for breeding and the design of effective crossing schemes (Carputo et al., 2013; Bhardwaj et al., 2023). The integration of metabolite profiling to differentiate chemotypes and assist in the selection of parents with desirable traits, such as high chlorogenic acid content, can enhance the efficiency of breeding program. Additionally, the application of advanced genomic tools, such as genome editing and genomic selection, can leverage the genetic diversity within sweet potato to develop varieties with improved biotic and abiotic stress tolerance (Tiwari et al., 2022).

4.4 Enhancing breeding programs using genetic diversity data

The comprehensive analysis of genetic diversity data can enhance breeding programs by providing a deeper understanding of the genetic makeup of breeding materials. For instance, the molecular characterization of breeding clone banks and the identification of core sets of clones can facilitate the long-term conservation of genetic resources and assist in the selection of parents for breeding (Pandey et al., 2021). The use of morphological, biochemical, and molecular markers to characterize germplasm and identify promising genotypes with high yield and stress tolerance traits can further improve breeding outcomes (Paliwal et al., 2020). By incorporating genetic diversity data into breeding strategies, programs can develop more resilient and productive sweet potato varieties, thereby contributing to global food security and climate change adaptation efforts (Karan and Şanli, 2021; Spanoghe et al., 2022).

5 Case Study

5.1 Overview of the regional sweet potato breeding programs

Regional sweet potato breeding programs have been established to address the specific needs of local farmers and consumers (Winnicki et al., 2021). These programs often focus on improving yield, disease resistance, and nutritional content. For instance, the international potato center (CIP) and its partners have been actively involved in breeding programs aimed at poverty alleviation, nutrition improvement, and gender responsiveness (Ojwang' et al., 2023). Additionally, the national agrobiodiversity center (NAC) has been working on conserving and managing sweet potato germplasm, which is crucial for maintaining genetic diversity and supporting breeding efforts.

5.2 Application of meta-analysis findings to regional breeding strategies

The findings from meta-analyses of genetic diversity studies can significantly enhance regional breeding strategies. For example, understanding the genetic diversity and population structure of sweet potato genotypes can help breeders select parents with desirable traits and avoid genetic bottlenecks. Studies have shown that there is substantial genetic variability in sweet potato genotypes, which can be harnessed for crop improvement (Otoboni et al., 2020). By integrating molecular markers and diversity analysis, breeders can develop more efficient selection indices and improve the genetic gains from breeding programs (Hirsch et al., 2013).

5.3 Successes and challenges in breeding for improved varieties

Breeding programs have achieved notable successes in developing sweet potato varieties with improved traits. For instance, genotypes with high beta-carotene content have been identified, which are crucial for addressing vitamin A deficiency. Additionally, the use of morphological, biochemical, and molecular markers has facilitated the identification of promising genotypes with high yield and disease resistance (Paliwal et al., 2020). However, challenges remain, such as the need for more diverse germplasm collections and the integration of advanced breeding techniques to accelerate the development of new varieties (Solankey et al., 2015).

5.4 Recommendations for future breeding efforts in the region

Future breeding efforts should focus on expanding germplasm collections to include more diverse genetic material, which will enhance the genetic base of breeding programs (Lee et al., 2019). Additionally, the use of advanced molecular techniques, such as genome-wide association studies (GWAS) and marker-assisted selection (MAS), should be prioritized to improve the efficiency and accuracy of breeding efforts. Breeding programs should also be more demand-driven, taking into account the preferences and needs of local farmers and consumers to ensure the adoption of new varieties. Finally, collaborative efforts between regional and international breeding programs can facilitate the exchange of germplasm and knowledge, further strengthening breeding initiatives.

6 Future Perspectives

6.1 Emerging technologies for assessing genetic diversity

Emerging technologies are revolutionizing the assessment of genetic diversity in sweet potato. Techniques such as DNA fingerprinting and retrotransposon-based insertion polymorphism (RBIP) markers have proven to be powerful tools for plant diversity studies, cultivar identification, and germplasm conservation (Bali et al., 2018; Meng et al., 2021). Additionally, the use of specific length amplified fragment (SLAF) sequencing and single nucleotide polymorphism (SNP) markers has enabled genome-wide assessments of genetic diversity, providing detailed insights into the population structure and genetic relationships among sweet potato accessions (Su et al., 2018). These high-throughput genotyping methods facilitate the identification of genetic variability and the development of core germplasm sets, which are crucial for future breeding programs (Pandey et al., 2021).

6.2 Potential impact of genomics and bioinformatics on breeding

The integration of genomics and bioinformatics into sweet potato breeding programs holds significant potential for enhancing crop improvement. Advances in sequencing technologies, such as the development of pan-genomics and multi-omics platforms, have enabled comprehensive molecular characterization of sweet potato germplasm (Tiwari et al., 2022). These technologies allow for the identification of genetic markers associated with desirable traits, such as disease resistance and stress tolerance, which can be used in marker-assisted selection and genomic selection. Furthermore, bioinformatics tools facilitate the analysis of large-scale genomic data, enabling the identification of genetic diversity trends and the development of strategies to broaden the genetic base of breeding programs (Deperi et al., 2018; Chen, 2024). The application of genome editing technologies, such as CRISPR/Cas9, also offers the potential to introduce targeted genetic modifications, accelerating the development of improved sweet potato varieties.

6.3 Global collaboration for preserving and utilizing genetic diversity

Global collaboration is essential for preserving and utilizing the genetic diversity of sweet potato. The establishment of germplasm banks and the characterization of genetic resources collected from diverse geographical regions are critical for maintaining a broad genetic base (Vargas et al., 2018). Collaborative efforts among international research institutions can facilitate the exchange of germplasm and the sharing of knowledge and technologies, enhancing the overall efficiency of breeding programs (Lee et al., 2019). Additionally, the development of core germplasm sets and the implementation of efficient management plans for genetic resources can ensure the long-term conservation and sustainable use of sweet potato diversity (Anderson et al., 2021). By fostering global partnerships, researchers can address the challenges of food security and climate change, ultimately contributing to the development of resilient and high-yielding sweet potato varieties (Spanoghe et al., 2022).

7 Conclusion

The meta-analysis of genetic diversity studies in sweet potato (*Ipomoea batatas*) reveals significant insights into the genetic variability and interrelationships among various genotypes. Studies have consistently shown a wide range of genetic variation for economically important traits such as tuber yield, carotene content, and starch content. Molecular markers, including RAPD, SSR, and RBIP, have been effectively used to assess genetic diversity, revealing substantial polymorphism and genetic differentiation among sweet potato accessions. Additionally, cluster analyses have consistently grouped genotypes into distinct clusters, indicating clear genetic relationships and diversity patterns.

The findings from these genetic diversity studies have several practical applications for sweet potato breeding programs. The identification of genotypes with desirable traits such as high tuber yield, carotene content, and disease resistance can guide the selection of parent plants for breeding. The use of molecular markers like SSR and RBIP can facilitate marker-assisted selection, enabling breeders to efficiently track and select for these traits in breeding populations. Additionally, the establishment of core collections that capture the genetic diversity of larger populations can help in the conservation and management of sweet potato germplasm, ensuring the availability of diverse genetic resources for future breeding efforts.

Future research should focus on expanding the genetic base of sweet potato by incorporating wild relatives and underutilized genotypes into breeding programs. This can enhance the genetic diversity available for breeding and potentially introduce novel traits. Advances in genomic tools and technologies, such as high-density SNP genotyping and genome-wide association studies (GWAS), should be leveraged to identify and map quantitative trait loci (QTLs) associated with key agronomic traits. Furthermore, integrating phenomic approaches, such as RGB imaging and colorimetry, can improve the precision and efficiency of phenotypic characterizations, aiding in the identification of polymorphisms and target traits for breeding. Overall, a multidisciplinary approach combining traditional breeding methods with modern genomic and phenomic tools will be crucial for the continued improvement and sustainability of sweet potato breeding programs.

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Conflict of Interest Disclosure

The authors affirm that this research was conducted without any commercial or financial relationships that could be construed as a potential conflict of interest.

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