GenBreed Publisher

Plant Gene and Trait 2024, Vol.15, No.2, 62-72
http://genbreedpublisher.com/index.php/pgt

Review Article **Open Access**

The Role of Gene Duplication in Sugarcane Evolution and Trait Diversity

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Plant Gene and Trait, 2024, Vol.15, No.2 doi: 10.5376/pgt.2024.15.0008
Received: 11 Feb., 2024
Accepted: 16 Mar., 2024
Published: 25 Mar., 2024

Preferred citation for this article:
Liang K.W., 2024, The role of gene duplication in sugarcane evolution and trait diversity, Plant Gene and Trait, 15(2): 62-72 (doi: 10.5376/pgt.2024.15.0008)

Abstract Gene duplication has played a significant role in the evolution and trait diversity of sugarcane (*Saccharum* spp.). Sugarcane, a highly polyploid and aneuploid crop, has undergone extensive gene duplication events, contributing to its complex genome structure and large genome size (~10 Gb). These duplications have facilitated the development of novel functions and adaptive traits, such as enhanced disease resistance and stress tolerance, which are crucial for the crop's agronomic performance. The retention of duplicated genes, particularly those involved in essential metabolic pathways, has been a driving force in the diversification and adaptation of sugarcane Furthermore, whole-genome duplications (WGDs) have been instrumental in the evolution of sugarcane, promoting genetic diversity and enabling the crop to adapt to various environmental conditions. Understanding the mechanisms and impacts of gene duplication in sugarcane can provide valuable insights for breeding programs aimed at improving yield traits and stress resilience. This study synthesizes current knowledge on gene duplication in sugarcane, highlighting its role in the crop's evolution and trait diversity.

Keywords Gene duplication; Sugarcane evolution; Trait diversity; Polyploidy; Whole-genome duplication

1 Introduction

Sugarcane (*Saccharum* spp.) is a vital crop in global agriculture, contributing significantly to the production of sugar and bioenergy. It accounts for approximately 80% of the world's sugar supply and around 60% of biofuel production, making it a cornerstone of both food and energy industries (Sforça et al., 2019; Yang et al., 2020). The crop's ability to thrive in tropical and subtropical regions further underscores its importance, as it supports the economies of many countries by providing raw materials for sugar, ethanol, and electricity production (Yadav et al., 2020; Mahadevaiah et al., 2021). The increasing demand for sustainable bioenergy sources has also positioned sugarcane as a key player in the transition towards renewable energy (Yadav et al., 2020; Mahadevaiah et al., 2021).

Gene duplication is a fundamental evolutionary process that contributes to genetic diversity and innovation in plants. In sugarcane, which has a highly complex and polyploid genome, gene duplication events have played a crucial role in shaping its genetic architecture and phenotypic traits (Sforça et al., 2019; Zan et al., 2020). The polyploid nature of sugarcane, resulting from hybridization between *Saccharum officinarum* and *Saccharum spontaneum*, has led to a genome with variable ploidy levels and extensive gene duplications (Sforça et al., 2019; Singh et al., 2020). These duplications can result in novel gene functions, increased gene dosage, and the potential for subfunctionalization or neofunctionalization, thereby enhancing the plant's adaptability and trait diversity (Sforça et al., 2019; Singh et al., 2020; Zan et al., 2020).

This study aims to investigate the contribution of gene duplication to the evolution and trait diversity of sugarcane, with a focus on its role in the genetic and phenotypic complexity of the crop. By examining how gene duplication influences key agronomic traits such as yield, disease resistance, and stress tolerance, this research helps to uncover the profound impact of gene duplication on sugarcane breeding programs and variety improvement. Understanding the mechanisms and effects of gene duplication will not only elucidate the evolutionary dynamics of sugarcane but also provide valuable insights for improving breeding strategies and crop enhancement.

2 Gene Duplication

2.1 Fundamentals of gene duplication processes

Gene duplication is a fundamental process in the evolution of genomes, particularly in plants. It involves the creation of one or more copies of a gene within the genome. These duplications can occur through various mechanisms, including whole-genome duplications (WGDs), segmental duplications, tandem duplications, and transposon-mediated duplications (Rensing, 2014; Panchy et al., 2016; Barreto et al., 2019). WGDs, in particular, have been a significant driver of plant evolution, leading to the retention of numerous duplicate genes that contribute to genetic diversity and complexity (Zhang et al., 2022). The fate of duplicated genes can vary; they may be retained and acquire new functions (neofunctionalization), divide the original function (subfunctionalization), or become nonfunctional pseudogenes (Rensing, 2014; Panchy et al., 2016).

2.2 Role of gene duplication in plant evolution and adaptation

Gene duplication has played a crucial role in the evolution and adaptation of plants. Duplicated genes can provide raw material for evolutionary innovation, allowing plants to develop new traits and adapt to changing environments (Rensing, 2014; Panchy et al., 2016). For instance, gene duplications have been linked to the development of novel floral structures, disease resistance, and stress adaptation (Rensing, 2014; Panchy et al., 2016). In sugarcane, a highly polyploid and aneuploid crop, gene duplications have contributed to its complex genome and the evolution of important agronomic traits (Panchy et al., 2016). The retention of duplicated genes in sugarcane has facilitated the development of traits such as increased yield, improved stress tolerance, and enhanced disease resistance (Panchy et al., 2016).

2.3 Methods for identifying gene duplications in sugarcane

Identifying gene duplications in sugarcane involves a combination of genomic, transcriptomic, and genetic mapping approaches. Comparative genomic analyses can reveal conserved gene content and collinearity with related species, such as sorghum and rice, which helps in identifying duplicated regions (Panchy et al., 2016). Techniques such as Bacterial Artificial Chromosome (BAC) sequencing and the construction of physical and linkage maps are also employed to elucidate the genomic architecture and allelic interactions in sugarcane (Panchy et al., 2016). Additionally, genome-wide association studies (GWAS) and the analysis of simple sequence repeat (SSR) markers can be used to detect marker-trait associations and identify candidate genes involved in important traits (Barreto et al., 2019). These methods collectively enhance our understanding of the complex polyploid genome of sugarcane and facilitate the identification of gene duplications that contribute to its trait diversity and evolution.

3 The Role of Gene Duplication in Sugarcane Evolution and Trait Diversity

3.1 Sugarcane genetic diversity and evolution

Sugarcane (*Saccharum* spp.) is a vital crop for sugar and biofuel production, characterized by its complex genetic architecture and significant genetic diversity. The genetic diversity within sugarcane is a crucial factor for breeding programs aimed at improving yield and stress resistance. This diversity is largely attributed to the polyploid nature of sugarcane, which includes contributions from its progenitor species, *Saccharum officinarum* and *Saccharum spontaneum* (Barreto et al., 2016; Singh et al., 2020; Tolera et al., 2023).

3.2 Genetic architecture of sugarcane

The genetic architecture of sugarcane is highly intricate due to its polyploidy and the presence of sub-genomes from its progenitor species. Modern sugarcane varieties are interspecific hybrids that combine the high sugar content of *S. officinarum* with the hardiness and disease resistance of *S. spontaneum* (Figure 1) (Thirugnanasambandam et al., 2018; Zhang et al., 2018). The genome of sugarcane is characterized by a high degree of polymorphism and genetic variability, which is essential for the crop's adaptability and productivity (Singh et al., 2020). Advances in sequencing technologies have facilitated the assembly of sugarcane genomes, providing valuable resources for genetic research and breeding (Thirugnanasambandam et al., 2018; Yang et al., 2020).

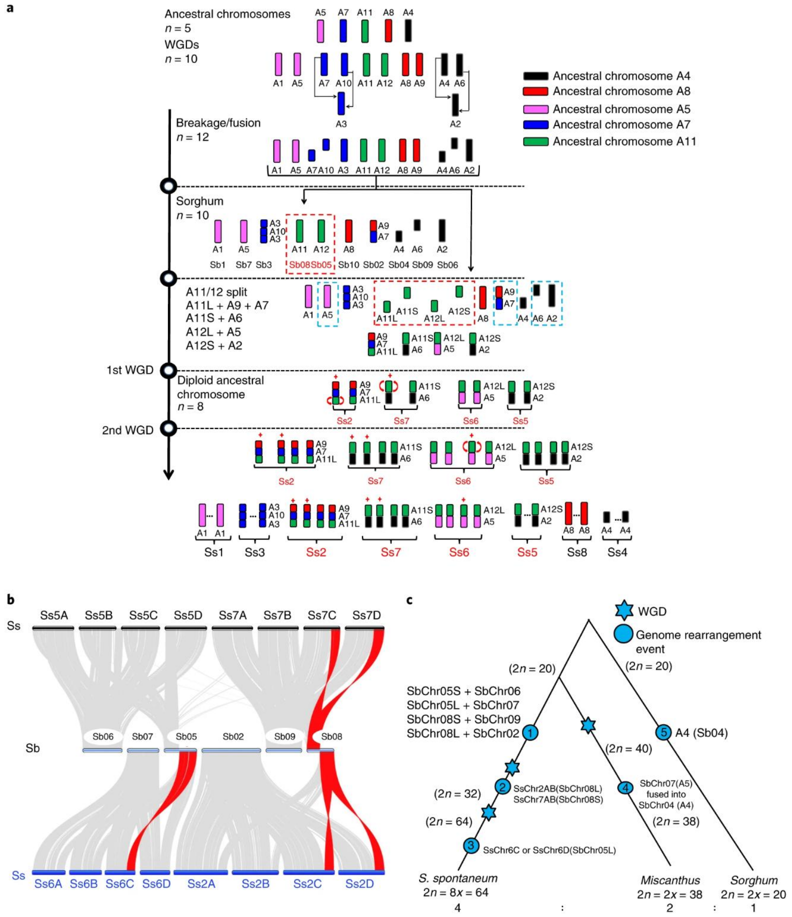

Figure 1 Evolutionary history of *S. spontaneum* chromosomesa (Adopted from Zhang et al., 2018)

Image caption: The image appears to be a complex diagram illustrating the evolutionary history and genome organization of a particular plant species, likely sorghum, and its related species. The diagram is divided into three main sections labeled (a), (b), and (c) (Adopted from Zhang et al., 2018)

3.3 Historical overview of gene duplication events in sugarcane

Gene duplication is a prominent feature in the evolution of plant genomes, including sugarcane. Duplication events have played a significant role in the expansion and functional diversification of gene families in sugarcane. For instance, the CIPK gene family in *Saccharum spontaneum* has undergone multiple duplication events, driven by whole-genome duplications (WGDs) (Su et al., 2020). These duplications have contributed to the genetic complexity and adaptability of sugarcane, allowing it to respond to various environmental stresses (McIntyre et al., 2005; Su et al., 2020). The divergence of duplicated genes, often under strong purifying selection, has led to the development of novel traits and enhanced stress tolerance (Su et al., 2020).

3.4 Case studies, key gene duplications and their phenotypic manifestations

Several key gene duplications in sugarcane have been linked to important phenotypic traits. For example, the duplication of CIPK genes has been associated with responses to abiotic stresses such as salinity and drought (Su et al., 2020). The expression patterns of these duplicated genes under stress conditions suggest their involvement in stress signaling pathways, contributing to the resilience of sugarcane (Su et al., 2020). Another study identified multiple marker-trait associations (MTAs) through genome-wide association studies (GWAS), linking specific genetic loci to yield component traits such as stalk height, stalk number, and cane yield (Barreto et al., 2016; Yang et al., 2020). These findings highlight the role of gene duplication in enhancing the genetic diversity and trait variability in sugarcane, providing valuable targets for breeding programs aimed at improving crop performance (Barreto et al., 2016; Yang et al., 2020; Zan et al., 2020). Gene duplication has been a driving force in the evolution and diversification of sugarcane, contributing to its genetic complexity and adaptability. Understanding the genetic architecture and historical duplication events in sugarcane is essential for leveraging its genetic diversity in breeding programs to develop superior cultivars with enhanced yield and stress tolerance.

4 Advancing Research on Gene Duplication in Sugarcane

4.1 Expanding understanding of gene duplication mechanisms in sugarcane

Gene duplication is a fundamental evolutionary process that has significantly contributed to the genetic diversity and adaptability of many plant species, including sugarcane. The complex polyploid nature of the sugarcane genome, which results from hybridization between *Saccharum officinarum* and *Saccharum spontaneum*, presents unique challenges and opportunities for understanding gene duplication mechanisms (Sforça et al., 2019). Studies have shown that gene duplication can lead to the retention of duplicate genes, which may acquire novel functions or enhance existing ones, thereby contributing to the plant's evolutionary fitness (Panchy et al., 2016; Sforça et al., 2019). In sugarcane, the presence of duplicated genes has been linked to important agronomic traits, such as disease resistance and stress adaptation (Barreto et al., 2019; Rody et al., 2019). Understanding the mechanisms behind gene duplication, including tandem duplications and whole-genome duplications, is crucial for advancing our knowledge of sugarcane genetics and improving breeding programs (Sforça et al., 2019).

4.2 Investigating the impact of gene duplication on stress resistance and climate adaptability

Gene duplication plays a pivotal role in enhancing the stress resistance and climate adaptability of sugarcane. Duplicated genes can undergo neofunctionalization, where one copy acquires a new function, or subfunctionalization, where both copies divide the original function (Kondrashov, 2012; Zimmer et al., 2018). For instance, the duplication and subsequent neofunctionalization of cytochrome P450 genes have been shown to confer insecticide resistance in other plant species, suggesting a similar potential in sugarcane for developing resistance to pests and diseases (Figure 2) (Zimmer et al., 2018). Additionally, recurrent gene duplication has been linked to the adaptation of plant genomes to changing environmental conditions, providing a reservoir of genetic variation that can be selected for under stress conditions (Kondrashov, 2012; Fischer et al., 2014). In sugarcane, the differential expression of resistance gene analogs (RGAs) in response to smut disease highlights the importance of gene duplication in developing disease-resistant cultivars (Rody et al., 2019). These findings underscore the need for further research into the specific duplicated genes that contribute to stress resistance and climate adaptability in sugarcane.

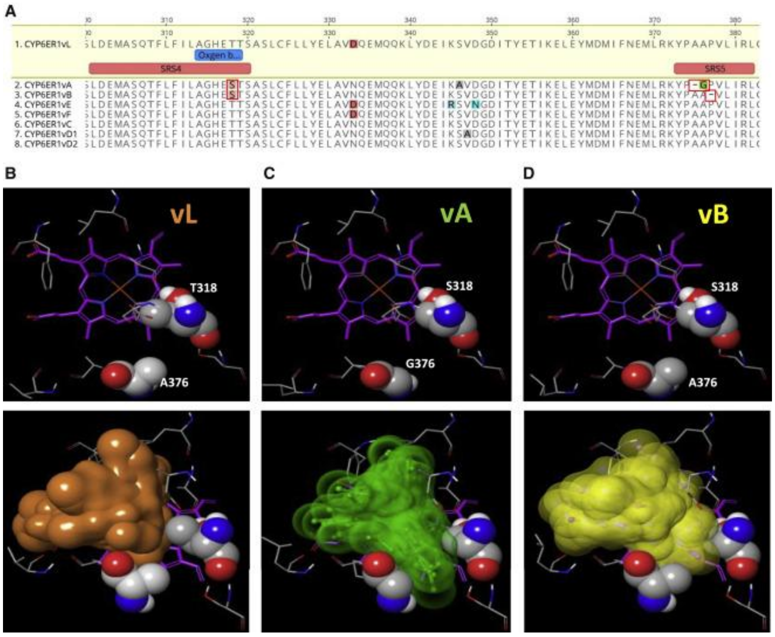

Figure 2 Modeling the active site of CYP6ER1 reveals the impact of amino acid alterations on imidacloprid binding (Adopted from Zimmer et al., 2018)

Image caption: The image consists of two main sections, labeled (A) and (B-D), which appear to describe the sequence and structural analysis of a protein or a set of related proteins (Adopted from Zimmer et al., 2018)

4.3 Exploring the integration of gene duplication studies with functional genomics

Integrating gene duplication studies with functional genomics is essential for a comprehensive understanding of sugarcane biology and for the development of improved cultivars. Functional genomics approaches, such as genome-wide association studies (GWAS) and transcriptome analysis, can identify candidate genes and elucidate their roles in important traits (Barreto et al., 2019). For example, GWAS has been used to identify loci associated with yield component traits in sugarcane, providing valuable insights into the genetic basis of these traits and the potential role of duplicated genes (Barreto et al., 2019). Moreover, the integration of genomic, transcriptomic, and genetic mapping data can reveal the complex interactions between duplicated genes and their regulatory networks (Barreto et al., 2019). This holistic approach can facilitate the identification of key genes involved in sugarcane's response to biotic and abiotic stresses, ultimately aiding in the development of more resilient and high-yielding sugarcane varieties. By leveraging the power of functional genomics, researchers can better understand the evolutionary patterns and functional significance of gene duplication in sugarcane, paving the way for innovative breeding strategies and crop improvement (Sforça et al., 2019).

5 Case Studies

5.1 Detailed analysis of specific duplicated genes in sugarcane

Gene duplication plays a significant role in the evolution and trait diversity of sugarcane. One notable example is the duplication of the HP600 and Centromere Protein C (CENP-C) genes. These genes are found in two different homeologous chromosome groups with ploidies of eight and ten. The first region, orthologous to Sorghum bicolor, showed all haplotypes of HP600 and CENP-C expressed, although HP600 exhibited unbalanced haplotype expression. The second region, a scrambled sugarcane sequence, contained partial duplications of HP600 and CENP-C, resulting in a non-expressed HP600 pseudogene and a recombined fusion version of CENP-C (Figure 3) (Sforça et al., 2019).

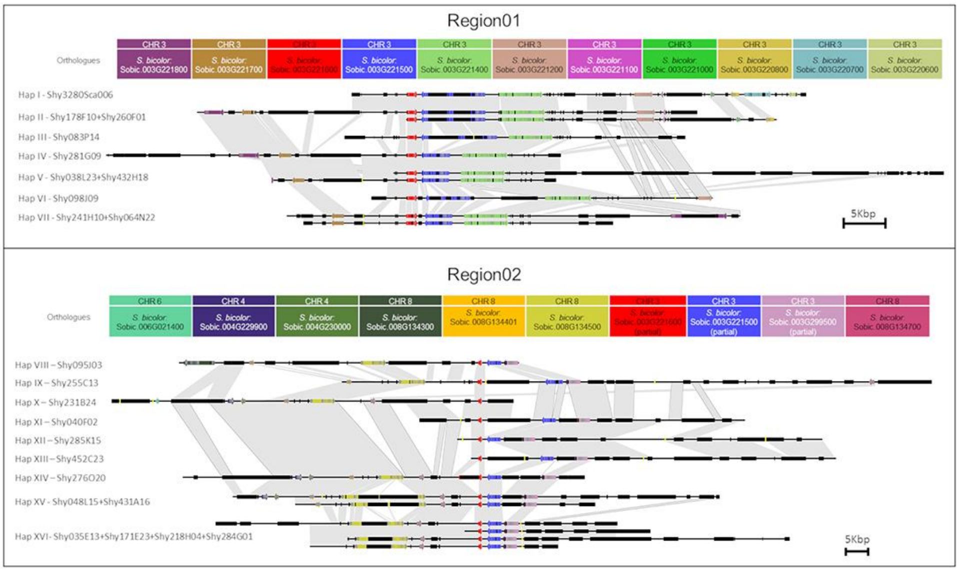

Figure 3 Representation of each sugarcane BAC from Region01 and Region02 (Adopted from Sforça et al., 2019)
Image caption: The image depicts two genomic regions, labeled "Region01" and "Region02" each illustrating the comparative genomics of different haplotypes (Adopted from Sforça et al., 2019)

Another example involves the Calcineurin B-like protein (CBL)-interacting protein kinases (CIPKs) gene family. In *Saccharum spontaneum*, 48 CIPK genes were identified, which likely underwent six gene duplication events. These duplications, driven by whole-genome duplications (WGDs), have been under strong purifying selection pressure, indicating their functional importance (Su et al., 2020).

5.2 Impacts of gene duplications on sugarcane trait development

Gene duplications have profound impacts on sugarcane trait development. For instance, the genome-wide association study (GWAS) identified 23 marker-trait associations (MTAs) for yield component traits such as soluble solid content, stalk height, stalk number, stalk weight, and cane yield (Li et al., 2020). These MTAs can be validated in other populations to support sugarcane breeding programs with the introgression of favorable alleles and marker-assisted selection (Barreto et al., 2019). The study of the CIPK gene family in sugarcane revealed that duplicated genes play various roles in response to different stresses, such as abscisic acid (ABA), polyethylene glycol (PEG), and sodium chloride (NaCl). This indicates that gene duplications contribute to the plant's ability to adapt to environmental stresses, which is crucial for its survival and productivity (Panchy et al., 2016).

5.3 Comparative analysis of sugarcane with other crops

Comparative genomic studies have shown that sugarcane shares a high degree of gene content and collinearity with other crops like sorghum and rice. For example, the analysis of three sugarcane homo/homeologous regions suggested independent polyploidization events of *Saccharum officinarum* and *Saccharum spontaneum*. These regions presented a high degree of conservation of gene content and synteny with sorghum and rice orthologous regions, although they were invaded by transposable elements (Yang et al., 2020). The study of whole genome duplications (WGDs) across various angiosperms, including sugarcane, revealed that WGDs are a major driving force in species diversification. These duplications provide evolutionary potential for generating novel functions and contribute to the complexity and diversity of plant genomes (Ren et al., 2018). Gene duplications in sugarcane have led to significant evolutionary advancements and trait diversifications. These duplications not only enhance the plant's adaptability to environmental stresses but also contribute to its agronomic traits, making sugarcane a vital crop for sugar and biofuel production (Panchy et al., 2016).

6 Technological Advances in Genetic Research

6.1 Next-generation sequencing (NGS) and its impact on gene duplication studies

Next-Generation Sequencing (NGS) has revolutionized the field of genomics, providing unprecedented insights into the complex genome of sugarcane. The large and polyploid nature of the sugarcane genome, which includes sub-genomes from *Saccharum officinarum* and *S. spontaneum*, has historically posed significant challenges for genetic research (Augustine et al., 2015). However, advancements in NGS technologies have facilitated the sequencing and assembly of these complex genomes, enabling more detailed studies of gene duplication events. For instance, the sequencing of 317 euchromatic BACs and the generation of a reference set of 1,400 manually-annotated protein-coding genes have provided a robust framework for understanding gene duplication in sugarcane (Setta et al., 2014). Additionally, long-read sequencing technologies have supported the generation of a more complete set of sugarcane gene transcripts, which is crucial for transcript profiling and understanding the functional implications of gene duplications (Thirugnanasambandam et al., 2018).

6.2 Bioinformatics approaches to analyzing gene duplication

Bioinformatics tools and approaches are essential for analyzing the vast and complex data generated by NGS. In sugarcane, bioinformatics has been pivotal in elucidating the allelic expression and genomic behaviors of duplicated genes. For example, the study of the HP600 and Centromere Protein C (CENP-C) genes revealed the presence of these genes in different homeologous chromosome groups with varying ploidies, highlighting the complexity of gene duplication in sugarcane. Furthermore, bioinformatics analyses have enabled the identification of non-redundant enzyme-encoding genes in key metabolic pathways, such as sucrose and starch metabolism, and the exploration of sequence structural variations and sRNA landscapes associated with duplicated regions (Setta et al., 2014). These approaches are critical for integrating physical and genetic data, thereby enhancing our understanding of gene duplication and its evolutionary significance in sugarcane.

6.3 Emerging technologies and their applications in sugarcane genomics

Emerging technologies continue to push the boundaries of sugarcane genomics, offering new opportunities to study gene duplication and its impact on trait diversity. The development of advanced genome assembly strategies, including the sequencing of BAC clones that cover the gene space of related species like sorghum, has made the sugarcane genome more tractable (Thirugnanasambandam et al., 2018). Additionally, the use of small RNA collections and RNA-seq libraries has provided valuable insights into gene expression patterns and the regulatory roles of duplicated genes (Setta et al., 2014). These technological advancements are not only enhancing our understanding of sugarcane genetics but also contributing to the development of molecular tools for breeding and gene discovery, ultimately supporting the improvement of sugarcane for traditional and novel uses (Thirugnanasambandam et al., 2018). The integration of NGS, bioinformatics, and emerging genomic technologies is transforming our ability to study gene duplication in sugarcane. These advancements are shedding light on the evolutionary processes that shape the sugarcane genome and are driving the development of innovative strategies for crop improvement.

7 Implications for Sugarcane Breeding and Agriculture

7.1 Utilizing gene duplication knowledge in breeding programs

Gene duplication plays a crucial role in the evolution and diversification of plant genomes, including sugarcane. Understanding the mechanisms and impacts of gene duplication can significantly enhance breeding programs. For instance, the study of the HP600 and CENP-C genes in sugarcane revealed complex allelic dynamics and the presence of paralogs, which can be leveraged to improve linkage mapping and integrate physical and genetic data for breeding purposes (Sforça et al., 2019). Additionally, the identification of duplicated genes involved in key metabolic pathways, such as sucrose-6-phosphate phosphohydrolase, provides valuable targets for genetic improvement (Setta et al., 2014). By incorporating knowledge of gene duplication, breeders can better select for desirable traits and enhance the genetic diversity of sugarcane cultivars.

7.2 Challenges and opportunities in developing diverse traits

The development of diverse traits in sugarcane faces several challenges, including the complexity of its polyploid genome and the need for precise phenotyping. However, these challenges also present opportunities. For example, the genetic diversity and population structure analysis using microsatellite markers can help identify promising parents for breeding programs, facilitating the introgression of novel alleles responsible for key agronomic traits (Singh et al., 2020). Moreover, genomic selection schemes can accelerate the breeding process by reducing the breeding cycle length and increasing the accuracy of trait prediction (Panchy et al., 2016; Yang et al., 2017). The integration of environmental covariates and genomic prediction in multi-environment trials can further enhance the prediction of varietal performance across different agro-climatic zones (Panchy et al., 2016).

7.3 Future strategies for exploiting genetic diversity in sugarcane

Future strategies for exploiting genetic diversity in sugarcane should focus on leveraging advanced genomic tools and techniques. Genome-wide association studies (GWAS) and genomic selection can identify and utilize genetic variants associated with yield and quality traits (Mahadevaiah et al., 2021). Additionally, the construction of rapid sucrose yield estimation models based on phenotypic diversity can aid in the selection of high-yielding genotypes (Xu et al., 2023). The evaluation of genetic diversity using both agro-morphological and biochemical traits can provide a comprehensive understanding of the genetic potential of sugarcane genotypes, guiding the development of improved varieties (Rakesh et al., 2023). By combining these approaches, breeders can effectively harness the genetic diversity of sugarcane to develop cultivars with enhanced yield, quality, and stress tolerance.

8 Integrating Genetic Insights into Crop Management

8.1 From laboratory to field: practical applications of genetic research

Genetic research in sugarcane has provided significant insights that can be translated into practical applications in the field. For instance, genomic selection (GS) has been identified as a promising tool to accelerate genetic gains in sugarcane breeding. By reducing the breeding cycle length and increasing the prediction accuracy for clonal performance, GS can significantly enhance the efficiency of breeding programs (Yadav et al., 2020; Mahadevaiah et al., 2021). Additionally, genome-wide association studies (GWAS) have identified numerous markers and candidate genes associated with yield traits, which can be utilized to improve crop performance through marker-assisted selection (Yang et al., 2023). The integration of these genetic tools into breeding programs can lead to the development of sugarcane varieties with improved yield, disease resistance, and stress tolerance, ultimately benefiting farmers and the sugarcane industry.

8.2 Role of gene duplication in sustainable agriculture practices

Gene duplication plays a crucial role in the evolution and diversification of plant genomes, including sugarcane. Duplicated genes can acquire new functions or enhance existing ones, contributing to the adaptability and resilience of crops. In sugarcane, gene duplication has been linked to important agronomic traits such as sucrose metabolism and stress response (Bergès et al., 2014; Sforça et al., 2019; Mahadevaiah et al., 2021). For example, the duplication of the sucrose-6-phosphate phosphohydrolase gene in sugarcane and sorghum, but not in rice and maize, highlights the evolutionary significance of gene duplication in sugarcane's metabolic pathways (Mahadevaiah et al., 2021). Understanding the mechanisms and impacts of gene duplication can inform sustainable agriculture practices by enabling the development of sugarcane varieties that are more productive and resilient to environmental stresses.

8.3 Case examples of management strategies influenced by genetic studies

Several management strategies in sugarcane cultivation have been influenced by genetic studies. For instance, the identification of genetic diversity and population structure using microsatellite markers has provided valuable information for conservation planning and the management of plant genetic resources (Panchy et al., 2016). This knowledge can be used to select promising parents for breeding programs, ensuring the introgression of beneficial alleles into modern cultivars. Additionally, the construction of linkage maps using markers from duplicated and non-duplicated regions has improved the integration of physical and genetic data, facilitating more precise breeding strategies (Sforça et al., 2019). These examples demonstrate how genetic research can directly impact crop management practices, leading to more efficient and effective breeding programs and ultimately enhancing sugarcane production.

9 Concluding Remarks

Gene duplication has played a pivotal role in the evolution and diversification of sugarcane (*Saccharum* spp.), a highly polyploid and aneuploid crop. The complex hybrid genome of modern sugarcane cultivars, derived from *Saccharum officinarum* and *Saccharum spontaneum*, exhibits variable ploidy and a high content of repetitive regions, which complicates genetic analysis and breeding efforts. Whole genome duplications (WGDs) and segmental duplications have contributed significantly to the expansion and functional diversification of gene families in sugarcane, enhancing its adaptability and trait diversity. These duplications have resulted in the retention of multiple gene copies, some of which have evolved new functions or regulatory patterns, thereby contributing to the crop’s robustness and productivity.

This study has provided several key insights into the role of gene duplication in sugarcane evolution and trait diversity. Firstly, the analysis of homeologous and paralogous gene regions has revealed the complex allelic interactions and expression patterns that underpin sugarcane's polyploid genome. Secondly, the identification of significant marker-trait associations through genome-wide association studies (GWAS) has highlighted the genetic basis of important yield traits, offering valuable resources for crop improvement. The study has underscored the importance of purifying selection in maintaining the functionality of duplicated genes, which is crucial for the stability and performance of sugarcane cultivars. These findings have important implications for future research, particularly in the areas of genetic mapping, functional genomics, and breeding strategies aimed at harnessing the genetic potential of sugarcane.

To further explore and exploit the genetic potential of sugarcane, several recommendations can be made. There is a need for more comprehensive and high-resolution genomic and transcriptomic analyses to better understand the dynamics of gene duplication and expression in sugarcane's polyploid genome. The development and application of advanced genomic tools, such as long-read sequencing and CRISPR-based gene editing, will be essential for dissecting complex genetic traits and enhancing breeding programs. Integrating genomic data with phenotypic and environmental information will facilitate the identification of adaptive traits and the development of cultivars with improved performance under diverse conditions. Collaborative efforts among researchers, breeders, and industry stakeholders will be crucial for translating genomic discoveries into practical applications that can drive the sustainable production of sugarcane for sugar, biofuel, and other bioproducts. By continuing to explore the genetic potential of sugarcane through these recommended approaches, we can unlock new opportunities for crop improvement and contribute to the global demand for sustainable agricultural production.

Acknowledgments

The author extends sincere thanks to two anonymous peer reviewers for their feedback on the manuscript.

Conflict of Interest Disclosure

The author affirms 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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