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Feature Review **Open Access**

Selection of Grapevine Varieties for Wine Production: Advances in Genomic Approaches

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Abstract Grapevines (*Vitis vinifera*) are among the most economically significant perennial fruit crops globally, primarily used in wine production. Traditional breeding methods, such as phenotypic selection and hybridization, have achieved success in developing regionally adapted grapevine varieties but often require decades and fail to address rapidly changing environmental challenges. This study focuses on the latest advancements in genomic technologies for selecting grapevine varieties suitable for wine production, including genomic selection, marker-assisted selection, and CRISPR/Cas9 gene-editing techniques. The results demonstrate that these approaches enable precise identification of key trait-associated genes and enhance selection efficiency, significantly accelerating the development of disease-resistant, stress-tolerant, and high-quality grapevine varieties. Furthermore, the integration of multi-omics data (e.g., transcriptomics and metabolomics) has improved the understanding of grapevine genomic functions, offering novel solutions to challenges posed by climate change and market demands. This study summarizes the current applications and challenges of genomic technologies and proposes strengthening interdisciplinary collaboration to advance precision agriculture and sustainable viticulture.

Keywords Grapevine genomics; Wine grape varieties; Marker-assisted selection; Genomic selection; Gene editing; Precision agriculture

1 Introduction

Grapevines (*Vitis vinifera*) are among the most economically significant perennial fruit crops globally, primarily due to their role in wine production. The cultivation of grapevines has evolved significantly over the years, driven by changing environmental conditions and market demands, which necessitate the development of new and improved varieties to ensure sustainability (Zhang et al., 2021; Butiuc-Keul and Coste, 2023). The wine industry, in particular, benefits from grapevine biotechnology, which aims to establish stress-tolerant and disease-resistant varieties that enhance productivity, efficiency, and environmental sustainability (Vivier and Pretorius, 2002).

However, selecting optimal grapevine varieties for wine production presents several challenges. Climate change, pests, and diseases pose significant threats to grapevine yield and fruit quality, leading to financial losses (Bharati et al., 2023). Traditional *Vitis vinifera* varieties are often susceptible to these biotic and abiotic stresses, necessitating the development of genotypes that can adapt to changing climates and resist pathogens (Gómez et al., 2024). Moreover, the genetic diversity within grapevine varieties, influenced by somatic mutations and clonal propagation, adds complexity to the selection process (Calderón et al., 2021; Villano et al., 2023).

This study aims to identify genotypes with desirable traits by integrating genomic selection with multi-omics data, thereby accelerating the development of novel and improved grapevine varieties. The primary objective is to demonstrate how modern genomic technologies can address the challenges in grapevine breeding, ultimately enhancing the sustainability and quality of wine production.

2 Traditional Methods of Grapevine Selection

2.1 Historical practices in grapevine breeding and selection

Historically, grapevine breeding and selection have relied heavily on traditional methods such as cross-breeding and selection based on phenotypic traits. These methods have been used for centuries to develop grapevine varieties that are well-suited to specific climates and soil conditions. The process typically involves selecting parent plants with desirable traits and cross-breeding them to produce offspring that inherit these traits. This approach has been instrumental in developing many of the grapevine varieties that are popular today, such as *Vitis vinifera*, which is widely cultivated for wine production (Costa et al., 2019; Wang et al., 2021). However, the traditional breeding process is time-consuming, often taking decades to produce a new variety due to the long generation intervals and the need for extensive field testing to evaluate the performance of new cultivars (Gaspero and Cattonaro, 2010; Brault et al., 2024).

2.2 Limitations of traditional selection methods

Despite their historical success, traditional methods of grapevine selection have several limitations. One major drawback is the lengthy time required to develop new varieties, which can be a significant barrier in responding to rapidly changing environmental conditions and market demands. Additionally, traditional breeding methods often involve a degree of uncertainty, as the inheritance of traits can be complex and influenced by multiple genetic and environmental factors (Bharati et al., 2023; Magon et al., 2023). This complexity can make it difficult to predict the outcome of breeding efforts, leading to a trial-and-error approach that is both time-consuming and resource-intensive. Furthermore, traditional methods may not effectively address the challenges posed by climate change, such as increased susceptibility to pests and diseases, which require the development of more resilient grapevine varieties (Wang et al., 2021; Gómez et al., 2024).

2.3 Examples of regionally adapted grapevine varieties

Regionally adapted grapevine varieties have been developed through traditional breeding methods to thrive in specific environmental conditions. For instance, the variety "Ecolly" was bred using intraspecific recurrent selection and minor-polygenes substitution and accumulation (MPSA) to enhance its resistance to cold, drought, and diseases, making it suitable for cultivation in areas with harsh winter conditions without the need for protective measures like soil burial (Wang et al., 2021). Similarly, other varieties have been developed to withstand the unique challenges of their growing regions, such as resistance to local pests or adaptation to specific soil types. These regionally adapted varieties are crucial for maintaining the sustainability and productivity of vineyards in diverse climates and are a testament to the effectiveness of traditional breeding methods in addressing local agricultural needs (Wang et al., 2021; Bharati et al., 2023).

3 Advances in Genomic Technologies

3.1 Overview of genomic tools in grapevine research

Recent advancements in genomic technologies have significantly enhanced grapevine research, providing new insights into the genetic basis of important traits. Precision breeding, which involves the use of genomic resources to improve elite cultivars, has become more feasible with the advent of various "omics" databases. These databases allow researchers to identify genetic elements and genes associated with key agronomic and enological traits, although the complexity of these traits often involves multiple genes and regulatory networks (Gray et al., 2014). The development of molecular marker-based methods has also been crucial for proper cultivar identification, enabling more accurate genotyping and trait mapping (Butiuc-Keul and Coste, 2023). Furthermore, the manipulation of the grapevine genome through biotechnologies has been refined over the years, with genome editing technologies offering precise modifications without altering the phenotype of existing cultivars (Costa et al., 2019).

3.2 Application of next-generation sequencing (NGS)

Next-generation sequencing (NGS) has revolutionized grapevine genomics by providing high-throughput capabilities for genotyping and trait mapping. NGS technologies have facilitated the development of genomic selection methods, allowing breeders to select plants based on DNA sequences rather than phenotypic traits, which can be influenced by environmental factors (Gaspero and Cattonaro, 2010). This approach enhances the efficiency of breeding programs by enabling the selection of elite genotypes with desirable traits, such as disease resistance and improved fruit quality (Butiuc-Keul and Coste, 2023). The integration of NGS with other genomic tools has also allowed for the saturation of loci with targeted genetic markers, providing unprecedented possibilities for grapevine improvement (Gaspero and Cattonaro, 2010). Additionally, the use of NGS in conjunction with CRISPR/Cas genome editing has accelerated the genetic improvement of grapevine by enabling precise modifications of specific genes (Ren et al., 2024).

3.3 Integration of transcriptomics, proteomics, and metabolomics

The integration of transcriptomics, proteomics, and metabolomics has provided a comprehensive understanding of grapevine biology, linking gene expression to phenotypic traits. Transcriptomics allows for the analysis of gene expression patterns, while proteomics and metabolomics provide insights into protein functions and metabolic pathways, respectively (Berger et al., 2022). This multi-omics approach is essential for functional genomics, as it helps to elucidate the regulatory networks governing important traits such as stress tolerance and fruit quality (Vidal et al., 2010). The ability to extract high-quality DNA and RNA from grapevine tissues has further facilitated the application of these technologies, enabling the analysis of "omics" data from a single plant sample (Berger et al., 2022). By combining these approaches, researchers can gain a holistic view of grapevine physiology and adaptation, ultimately leading to the development of improved grapevine varieties (Gray et al., 2014; Zhang et al., 2021).

4 Identification of Key Traits in Grapevine Varieties

4.1 Traits affecting wine quality

Grapevine varieties are selected for wine production based on several key traits that significantly influence wine quality, including flavor, aroma, and phenolic content. The metabolomic profiling of novel grapevine genotypes has shown that these traits can be enhanced through breeding cycles aimed at improving climate adaptation and berry characteristics. For instance, wines from these genotypes exhibited increased polyphenol content, such as anthocyanins, which are crucial for color and mouthfeel attributes like astringency and body (Gómez et al., 2024). Additionally, the identification of stable quantitative trait loci (QTLs) for traits like Muscat flavor and berry firmness further underscores the genetic basis for these quality attributes, allowing for more targeted breeding strategies (Wang et al., 2020). The integration of genomic selection with polyploidization techniques also offers a promising avenue for developing grapevine varieties with superior wine quality traits by combining desirable genetic combinations (Bharati et al., 2023).

4.2 Resistance to biotic stresses

Resistance to biotic stresses, such as pests and diseases, is a critical trait for grapevine varieties used in wine production. Traditional *Vitis vinifera* varieties are often susceptible to these stresses, necessitating the development of resistant varieties through inter-specific hybridization and breeding programs. These efforts have led to the creation of grapevine varieties that can withstand pests and diseases without compromising organoleptic qualities (Teissèdre, 2018). Moreover, genomic studies have identified gene clusters associated with disease resistance, providing a genetic framework for breeding programs to enhance biotic stress resistance in grapevines (Figure 1) (Shi et al., 2023). The use of genomic prediction methods has further facilitated the identification of resistant individuals, accelerating the breeding process and improving the efficiency of developing biotic stress-resistant grapevine varieties (Brault et al., 2024).

4.3 Adaptation to abiotic stresses

Adaptation to abiotic stresses, such as drought and temperature changes, is increasingly important for grapevine varieties due to the impacts of climate change. Breeding programs have focused on developing genotypes that can thrive in warm climates, as demonstrated by the successful adaptation of novel grapevine genotypes with improved climate resilience (Gómez et al., 2024). The identification of genes linked to fruit set-related traits, which are influenced by environmental conditions, highlights the complex genetic architecture underlying abiotic stress adaptation (Zinelabidine et al., 2021). Additionally, the integration of genomic selection with omics data allows for the prediction and selection of genotypes with enhanced abiotic stress tolerance, thereby supporting the development of grapevine varieties that can maintain high yields and quality under challenging environmental conditions (Bharati et al., 2023). The comprehensive understanding of these genetic mechanisms is crucial for optimizing grapevine production in the face of climate variability.

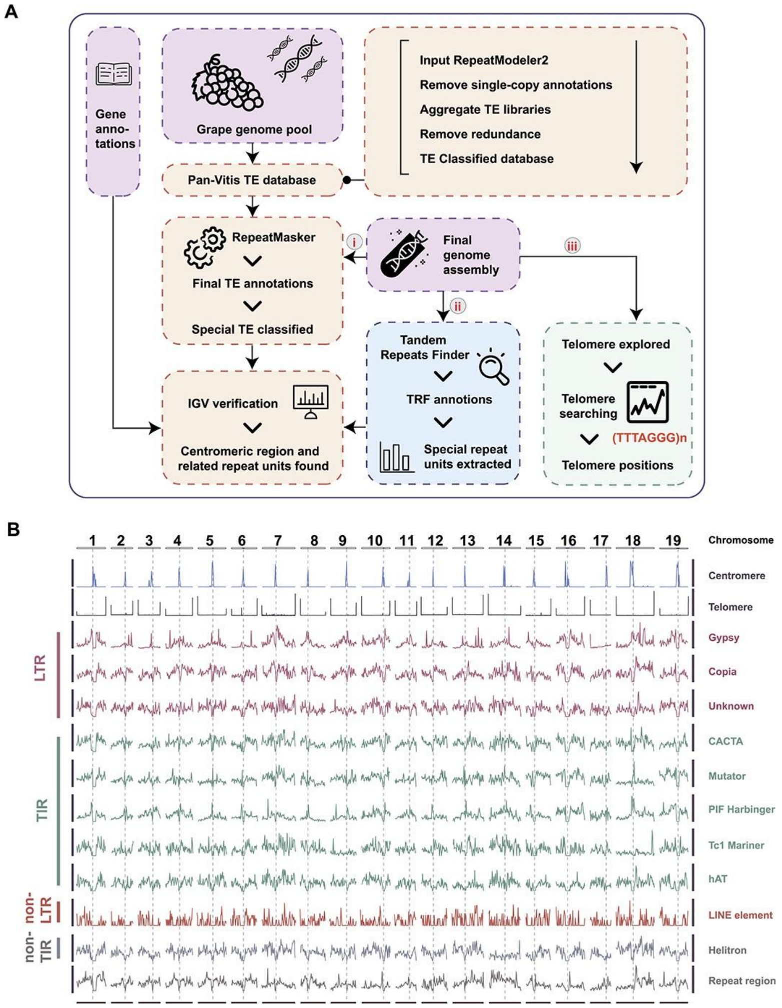

Figure 1 Repeat annotation in PN_T2T reference genome. (A) Dataflow of centromere and telomere predictions. (B) Chromosomal distribution of telomeres, centromeres, and different types of TE. Dashed vertical lines indicate the center locations of predicted centromeres (Adopted from Shi et al., 2023)

5 Genomic Approaches in Grapevine Breeding

The advancement of genomic technologies has significantly transformed grapevine breeding, offering new methods to enhance the selection and development of grapevine varieties. These genomic approaches include marker-assisted selection (MAS), genomic selection (GS), and gene-editing techniques such as CRISPR/Cas9, each providing unique advantages in the breeding process.

5.1 Marker-assisted selection (MAS)

Marker-assisted selection (MAS) is a technique that utilizes molecular markers to select plants with desirable traits, thereby accelerating the breeding process. In grapevine breeding, MAS has been particularly useful for traits governed by a few major genes, such as disease resistance and specific phenotypic characteristics (Costa et al., 2019; Magon et al., 2023). The availability of a complete reference genome for grapevine has enhanced the efficiency of MAS by providing a comprehensive map of genetic markers associated with important agronomic traits (Shi et al., 2023). This approach allows breeders to select plants based on their genetic makeup rather than solely on phenotypic traits, which can be influenced by environmental factors (Gaspero and Cattonaro, 2010).

Despite its advantages, MAS has limitations when dealing with complex traits controlled by multiple genes, such as yield and fruit quality. These traits often require a more comprehensive approach, as MAS may not capture the full genetic architecture involved. Nonetheless, MAS remains a valuable tool in grapevine breeding, particularly when integrated with other genomic approaches to improve the selection process (Gray et al., 2014; Butiuc-Keul and Coste, 2023).

5.2 Genomic selection (GS)

Genomic selection (GS) is an advanced breeding method that uses genome-wide markers to predict the genetic value of individuals, allowing for the selection of superior genotypes even before phenotypic traits are expressed. This approach is particularly beneficial for complex traits with low heritability, where traditional selection methods are less effective (Brault et al., 2021; Bharati et al., 2023). GS has shown promise in grapevine breeding by improving the predictive ability for traits such as yield, berry composition, and disease resistance (Brault et al., 2021).

The integration of GS with polyploidization and omics data further enhances its potential, enabling the prediction of genotypes with desirable traits among diverse grapevine populations (Bharati et al., 2023). This method not only accelerates the breeding process but also increases the genetic gain per breeding cycle, making it a powerful tool for developing new grapevine varieties that can withstand environmental challenges and meet market demands (Gaspero and Cattonaro, 2010; Magon et al., 2023).

5.3 Gene-editing techniques

Gene-editing techniques, particularly CRISPR/Cas9, have revolutionized grapevine breeding by allowing precise modifications of the genome. These techniques enable the targeted alteration of specific genes to enhance desirable traits or eliminate undesirable ones, offering a level of precision that traditional breeding methods cannot achieve (Gray et al., 2014). CRISPR/Cas9 has been used to improve traits such as disease resistance and fruit quality in grapevines, providing a rapid and efficient means of developing new cultivars (Figure 2) (Costa et al., 2019; Capriotti et al., 2020).

The application of gene-editing in grapevine breeding is still in its early stages, but it holds great potential for the future. By enabling the fine-tuning of genetic traits, gene-editing can complement other genomic approaches, such as MAS and GS, to create grapevine varieties that are better suited to changing environmental conditions and consumer preferences (Butiuc-Keul and Coste, 2023; Magon et al., 2023). As the technology continues to advance, it is expected to play a crucial role in the sustainable development of the grapevine industry.

6 Case Studies

6.1 Application of genomics in breeding disease-resistant grapevine varieties

The application of genomics in breeding disease-resistant grapevine varieties has revolutionized viticulture by enabling more precise and efficient selection processes. Genomic tools, such as marker-assisted selection, have been instrumental in identifying and utilizing quantitative trait loci (QTL) associated with resistance to common grapevine diseases like downy and powdery mildew. For instance, research has identified major QTLs on chromosomes 15 and 18 that are linked to resistance against these diseases, providing a genetic basis for developing resistant cultivars (Zyprian et al., 2016; Ricciardi et al., 2024). This genomic approach allows breeders to select for disease resistance at the genetic level, bypassing the limitations of traditional phenotypic selection, which can be less efficient due to the complex nature of these traits (Gaspero and Cattonaro, 2010; Zyprian et al., 2016).

Moreover, the integration of genome-wide association studies (GWAS) has further enhanced the identification of novel loci associated with disease resistance. Recent studies have discovered new loci, such as Rpv36 and Rpv37 for downy mildew resistance, and Ren14 and Ren15 for powdery mildew resistance, which are rich in genes related to biotic stress response (Ricciardi et al., 2024). These advancements not only facilitate the breeding of disease-resistant varieties but also contribute to sustainable viticulture by reducing the reliance on chemical fungicides.

6.2 Developing climate-resilient grapevine cultivars

The development of climate-resilient grapevine cultivars is becoming increasingly critical as climate change poses new challenges to viticulture. Genomic approaches are at the forefront of this effort, offering tools to accelerate the breeding of cultivars that can withstand extreme weather conditions (Figure 3). For example, genomic prediction methods, such as Genomic Best Linear Unbiased Predictor (GBLUP) and Least Absolute Shrinkage

Selection Operator (LASSO), have been employed to predict genotypic values for traits related to climate resilience, such as drought and heat tolerance (Brault et al., 2024). These methods allow for the selection of superior individuals that are better adapted to changing climates, thereby enhancing the efficiency of breeding programs.

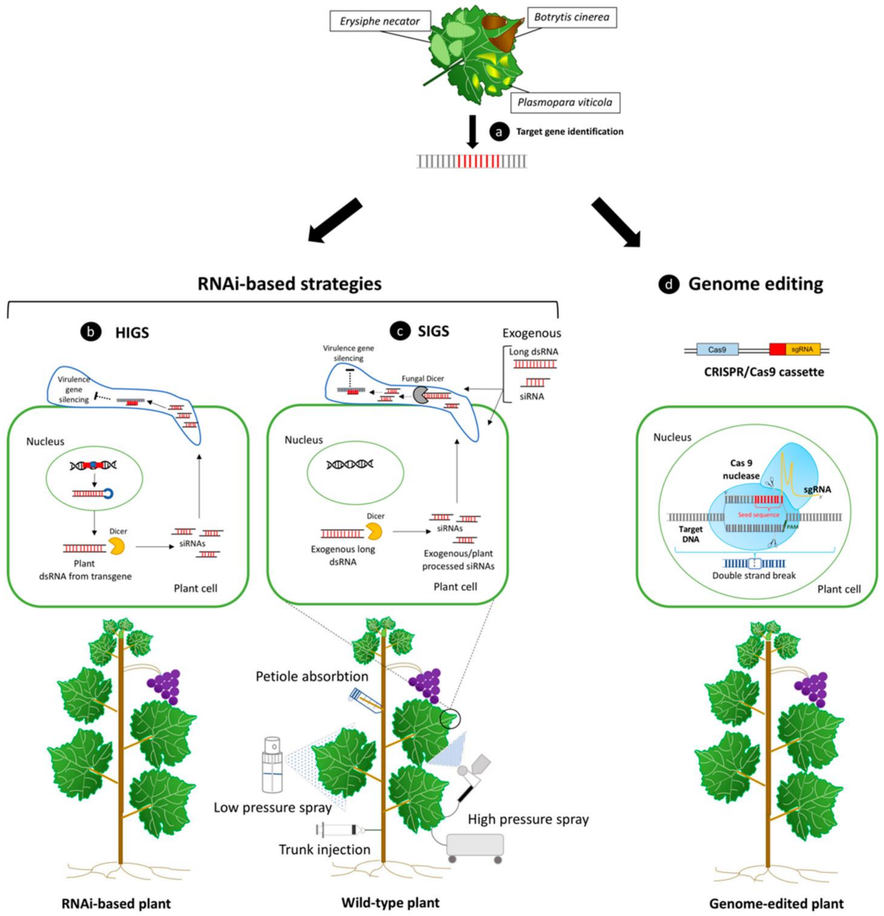

Figure 2 In addition to trans/cisgenesis methods, the expression of RNAi gene constructs in the plant, the exogenous applications of double strand RNA (dsRNA) molecules targeting host/pathogen genes, or plant genome editing, represent valid alternatives to enhance plant immunity during pathogenesis (Adopted from Capriotti et al., 2020)

Image caption: (a) Candidate genes capable of limiting pathogen aggression or improve plant defense responses can be identified during the infection processes caused by the fungal and oomycetes causal agents of the most impactful diseases for grapevine production. RNAi-based strategies can be exploited to improve plant defense by providing dsRNAs to the plant cell through the expression of an introgressed hairpin-based gene construct in the plant genome, or through their delivery by exogenous application. (b) In host-induced gene silencing (HIGS), as a result of transcription of an RNAi sequence, a long dsRNA molecule is formed. When this molecule is recognized by Dicer-like protein, it is cleaved into siRNAs, which can knockdown related target gene expression (Wang et al., 2016). (c) A transgenic-free procedure in which dsRNAs are directly sprayed on the surface of plants and pathogens is known as spray-induced gene silencing (SIGS). These molecules can be absorbed by both types of cells, and, depending on the delivery method used, dsRNAs can be processed by either the fungal/oomycetes and host RNAi machinery, leading to virulence gene knockdown and reduction in pathogen detrimental effects. Low-pressure spray, high-pressure spray, petiole adsorption, and trunk injection of dsRNAs represent some of the different available exogenous dsRNA delivery methods to confer plant protection against different plant pathogens, included fungi (Dalakouras et al., 2020). d) CRISPR/Cas9 system can be used for inducing targeted genome editing in plants, including the inactivation of specific plant susceptibility genes expression, which can help to regulate plant–pathogen interaction processes and disease resistance enhancement. Cas 9 protein complex is guided by artificially designed single guide RNA molecule (sgRNA) and leads to double-strand breaks (DSBs) of targeted DNA. SgRNA contains a seed sequence (around 8-12 bp, shown in red) complementary to target DNA that guides the binding of the Cas 9 protein to the target genomic sequence. The site of cleavage takes place three nucleotides upstream to the protospacer adjacent motif (PAM, shown in green) (Limera et al., 2017) (Adopted from Capriotti et al., 2020)

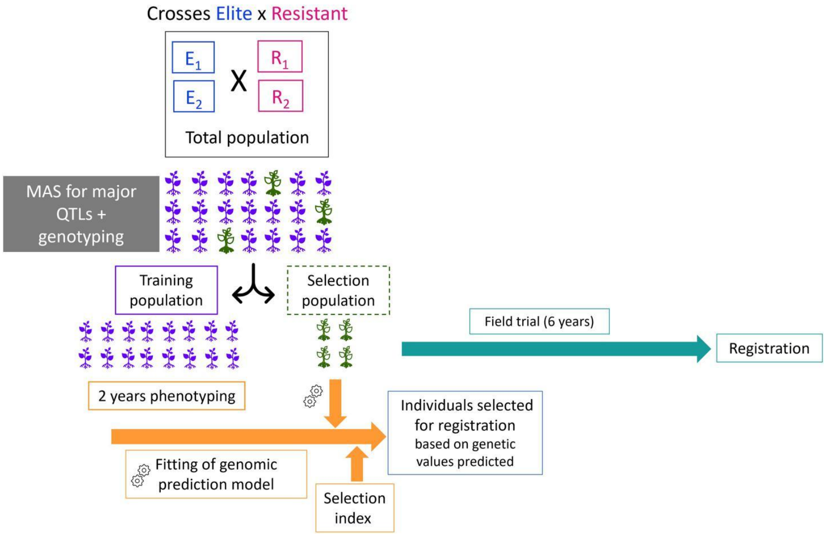

Figure 3 Design of experiment for EDGARR and Martell breeding programs. Green (empty) seedlings carry 2 resistance genes for both powdery and downy mildews; purple seedling are missing resistance genes (Adopted from Brault et al., 2024)

Additionally, the use of genetic resources from diverse germplasm collections has been pivotal in introducing alleles that confer climate resilience. Techniques like genome editing and marker-assisted breeding are being used to incorporate these alleles into new cultivars, thus creating grapevines that are not only resilient to climate change but also maintain high fruit quality (Delrot et al., 2020; Magon et al., 2023). This approach is crucial for ensuring the long-term sustainability of viticulture in the face of global climate shifts (Magon et al., 2023).

6.3 Examples of genomic approaches enhancing specific wine traits

Genomic approaches have also been applied to enhance specific wine traits, such as flavor, aroma, and color, which are critical for wine quality and consumer preference. By leveraging genomic prediction and selection indices, breeders can target traits that contribute to the sensory profile of wines. For instance, studies have shown that novel grapevine genotypes developed through genomic breeding cycles exhibit increased polyphenol content, which is associated with improved wine color and flavor (Gómez et al., 2024). These genotypes have been shown to produce wines with distinct sensory attributes, such as enhanced astringency and body, which are desirable in certain wine markets. Furthermore, metabolomic profiling has been used to identify biomarkers associated with specific wine traits, allowing for the selection of genotypes that produce wines with unique characteristics (Gómez et al., 2024). This approach not only aids in the development of high-quality wines but also supports the diversification of wine products, catering to varying consumer tastes and preferences. By integrating genomic and metabolomic data, breeders can more effectively tailor grapevine breeding programs to enhance specific wine traits, ultimately contributing to the production of premium wines.

7 Challenges and Limitations

7.1 Technical and financial constraints

The integration of genomic approaches in grapevine breeding faces significant technical and financial challenges. Traditional breeding methods are time-consuming, often taking decades to produce new cultivars, which is a major bottleneck in responding to urgent climate change impacts (Magon et al., 2023; Brault et al., 2024). Although genomic selection and marker-assisted breeding offer promising alternatives, their application is limited by the complexity of traits controlled by multiple genes and the high costs associated with genomic technologies (Gaspero and Cattonaro, 2010; Magon et al., 2023). The financial burden of implementing these advanced techniques is substantial, as it involves not only the initial investment in technology but also ongoing costs for data analysis and interpretation (Butiuc-Keul and Coste, 2023). Additionally, the technical expertise required to effectively utilize these genomic tools is a barrier for many breeding programs, which may lack the necessary resources and skilled personnel (Costa et al., 2019; Butiuc-Keul and Coste, 2023).

7.2 Ethical and regulatory considerations in genomic editing

The use of genome editing technologies, such as CRISPR/Cas9, in grapevine breeding raises ethical and regulatory concerns. While these technologies offer precise modifications without altering the overall genetic makeup of the plant, they still face scrutiny similar to that of genetically modified organisms (GMOs) (Costa et al., 2019; Gambino et al., 2024). The wine industry and consumers may have reservations about the acceptance of genome-edited grapevines, despite their potential benefits in improving disease resistance and climate adaptability (Costa et al., 2019). Regulatory frameworks vary significantly across regions, with some countries imposing strict regulations that can hinder the adoption of these technologies (Gambino et al., 2024). The challenge lies in balancing the potential benefits of genomic editing with public perception and regulatory compliance, which requires transparent communication and engagement with stakeholders (Costa et al., 2019; Gambino et al., 2024).

7.3 Knowledge gaps in trait-gene associations

A significant limitation in the application of genomic approaches to grapevine breeding is the incomplete understanding of trait-gene associations. While substantial progress has been made in identifying genetic markers linked to specific traits, many important agronomic and enological traits are controlled by complex interactions among multiple genes (Gaspero and Cattonaro, 2010; Gray et al., 2014). This complexity is compounded by the presence of numerous vestigial genes and sequences with unknown functions, making it difficult to predict the phenotypic outcomes of genetic modifications (Gray et al., 2014). The lack of comprehensive knowledge about these associations limits the effectiveness of genomic selection and precision breeding, as breeders may not fully understand the genetic basis of the traits they aim to improve (Gaspero and Cattonaro, 2010; Gray et al., 2014). Addressing these knowledge gaps requires extensive research and collaboration across disciplines to map the genetic architecture of key traits and develop more accurate predictive models.

8 Future Directions and Opportunities

8.1 Integration of AI and big data in genomic research

The integration of artificial intelligence (AI) and big data analytics into genomic research presents a transformative opportunity for the field of viticulture. AI can enhance the analysis of complex genomic datasets, enabling more precise identification of genetic markers associated with desirable traits in grapevines. This is particularly relevant given the vast amount of data generated by high-throughput sequencing technologies, which require sophisticated computational tools for effective analysis (Gomès et al., 2021; Butiuc-Keul and Coste, 2023). The use of AI in genomic selection can streamline the breeding process by predicting phenotypic outcomes based on genotypic data, thus accelerating the development of new grapevine varieties with improved traits (Brault et al., 2021). Furthermore, AI-driven models can integrate diverse datasets, including transcriptomic, metabolomic, and phenotypic data, to provide a holistic understanding of grapevine biology and its response to environmental stresses (Wong and Matus, 2017).

Big data analytics also offers the potential to enhance precision viticulture by integrating genomic data with environmental and management data. This integration can lead to the development of predictive models that optimize vineyard management practices, improving yield and quality while reducing resource inputs (Massonnet et al., 2019). The ability to process and analyze large datasets in real-time can facilitate adaptive management strategies that respond to changing climatic conditions, thereby supporting sustainable viticulture practices (Keller, 2010).

8.2 Prospects for sustainable and precision viticulture

The prospects for sustainable and precision viticulture are closely linked to advancements in genomic technologies and their application in breeding programs. Precision breeding techniques, such as genomic selection and genome editing, allow for the development of grapevine varieties that are better adapted to specific environmental conditions and resistant to biotic and abiotic stresses (Gray et al., 2014; Berger et al., 2023). These technologies enable the selection of traits that enhance sustainability, such as improved water use efficiency and resistance to pests and diseases, which are critical in the context of climate change (Adam-Blondon et al., 2016; Gomès et al., 2021).

Moreover, the integration of genomic data with precision agriculture technologies, such as remote sensing and automated vineyard management systems, can further enhance sustainability. These technologies can provide detailed insights into vineyard conditions, allowing for targeted interventions that minimize environmental impact while maximizing productivity (Keller, 2010). The use of molecular markers and genomic tools in precision viticulture can also facilitate the development of management practices that are tailored to the specific genetic makeup of grapevine varieties, thereby optimizing fruit quality and yield (Massonnet et al., 2019).

8.3 Collaborative efforts in global grapevine genomics

Collaborative efforts in global grapevine genomics are essential for advancing the field and addressing the challenges posed by climate change and global market demands. International collaborations can facilitate the sharing of genomic data and resources, enabling researchers to build comprehensive databases that support the development of new grapevine varieties. The establishment of open information systems, such as the GrapeIS, can enhance data accessibility and interoperability, fostering a collaborative research environment that accelerates scientific discovery (Adam-Blondon et al., 2016).

These collaborative networks can also support the standardization of genomic tools and methodologies, ensuring that research findings are comparable and reproducible across different studies (Adam-Blondon et al., 2016). By pooling resources and expertise, global collaborations can drive innovation in grapevine genomics, leading to the development of varieties that meet the diverse needs of growers and consumers worldwide (Brault et al., 2021). Such efforts are crucial for ensuring the sustainability and competitiveness of the global grape and wine industries in the face of evolving environmental and economic challenges (Keller, 2010).

9 Concluding Remarks

Advancements in genomic technologies have transformed the selection and breeding of grapevine varieties for wine production. The availability of a complete reference genome has fundamentally changed grape breeding by facilitating marker-assisted selection (MAS), which enables breeders to select plants based on genetic markers linked to desirable traits rather than relying solely on phenotypic characteristics. This genomic-driven approach has significantly improved the efficiency of breeding programs, particularly for traits with low heritability or those that are challenging to phenotype. Furthermore, combining genomic selection (GS) with polyploidization has emerged as a promising strategy to develop grapevine genotypes with enhanced attributes, such as superior fruit quality and increased stress tolerance. Precision breeding techniques, incorporating advanced gene insertion and genomic analyses, have also accelerated the development of elite grapevine cultivars with improved agronomic and enological characteristics. Collectively, these genomic advancements provide a foundation for the creation of innovative grapevine varieties that are better adapted to dynamic environmental conditions and evolving market demands.

To fully capitalize on these advancements, future research must address several critical areas. First, a thorough exploration and characterization of grapevine germplasm are essential to identify and leverage the genetic diversity within the Vitis genus. This will enable the development of new varieties capable of thriving in diverse environmental conditions. Second, integrating genomic selection with other omics data, such as transcriptomics and metabolomics, will enhance the predictive accuracy of breeding models, accelerating the identification of desirable traits and the breeding process itself. Third, refining genome editing techniques, such as CRISPR/Cas9, is imperative to achieve precise modifications of genes associated with key traits, thereby increasing the efficiency and effectiveness of breeding programs. Finally, challenges related to grapevine regeneration and transformation must be addressed to improve the success rates of genetic modifications. By advancing these research priorities, the field of grapevine breeding can further contribute to sustainable viticulture and the production of high-quality wine, ensuring resilience in the face of climate change and market shifts.

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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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