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Progress in Breeding of *Vitis vinifera* for Fruit Quality Improvement

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Abstract This study summarizes the latest progress in grape fruit quality improvement breeding, compares the advantages and disadvantages of traditional breeding and molecular breeding, and introduces the application of QTL mapping, genome-wide association study (GWAS), genomic selection (GS), and gene editing in the research and improvement of quality traits. It also discusses the relationship among yield, quality, and stress resistance. And it was proposed that in the future, molecular design strategies should be combined with multi-omics integration, climate-adaptive breeding and consumer demand-driven approaches. This research aims to provide theoretical references and technical support for the precise improvement of grape quality and the sustainable development of the industry.

Keywords Grapevine breeding; Fruit quality; Molecular breeding; Multi-omics; Sustainability

1 Introduction

The grape (*Vitis vinifera*) is one of the most important fruit trees in the world, with an annual output of approximately 75 to 85 million tons. It is widely used to produce table grapes, wine, fruit juice and dried fruits, and has a significant impact on global agriculture and the economy (Bigard et al., 2020; Butiuc-Keul and Coste, 2023). The quality of the fruit directly determines the market value of both table and wine grapes (Lan, 2025). Fresh table grapes usually require large berries, good taste, balanced sugar and acid, and unique flavor. Wine grapes, on the other hand, pay more attention to sugar, acidity, polyphenols and aromatic substances to ensure the flavor and aging potential of the wine (Gascuel et al., 2017; Bigard et al., 2018). Therefore, improving the quality of grapes not only meets the diverse demands of consumers but also serves as a key driving force for the sustainable development of the grape industry.

The genetic basis of the quality traits of grapes is very complex, involving multi-gene regulation and strongly influenced by genotype and environmental interaction (Bigard et al., 2018). Traditional breeding is limited by the high heterozygosity, long life cycle and complex trait inheritance of grapes, resulting in the difficulty of aggregation and stable inheritance of superior traits (Butiuc-Keul and Coste, 2023; García-Abadillo et al., 2024). The high temperature and drought stress brought about by climate change can also lead to a decline in quality, such as an imbalance in the sugar-acid ratio and a reduction in flavor substances, which makes breeding more difficult (Gascuel et al., 2017; Bigard et al., 2020). Meanwhile, consumers' demands for health, flavor and sustainable production are increasing. This requires breeding not only to ensure yield and stress resistance, but also to take into account nutrition and sensory quality (Sosa-Zuniga et al., 2022; Butiuc-Keul and Coste, 2023).

This study summarizes the latest progress in grape fruit quality improvement breeding, introduces the application and achievements of genetic diversity, molecular markers, genomic selection and biotechnology in quality improvement, analyzes the current main challenges, and looks forward to future breeding strategies in the context of climate change and consumption upgrade. This research aims to provide theoretical basis and practical reference for the precise improvement of grape quality and the sustainable development of the industry.

2 Fruit Quality Traits in *Vitis vinifera*

2.1 Primary metabolites: sugars, acids, and organic compounds influencing flavor balance

The sugar and organic acids in grape fruits are the key substances that determine the flavor balance. Sugars are mainly glucose and fructose, while organic acids include tartaric acid, malic acid and citric acid. When the fruit ripens, sugar gradually accumulates while organic acids decrease, which directly affects the sweetness, acidity and overall flavor of the fruit (Wang et al., 2022a). Proteins, soluble solids and vitamin C, etc. also play important roles in the nutrition and flavor of fruits (Filimon et al., 2017; Deng et al., 2025). Meanwhile, environmental conditions such as temperature, precipitation and soil nutrients can also significantly affect the accumulation of these substances (Biasi et al., 2019; Li et al., 2024).

2.2 Secondary metabolites: anthocyanins, tannins, and aroma-related compounds

Secondary metabolites are also very important in grape quality. Anthocyanins, tannins and polyphenols not only determine the color and taste of fruits, but are also related to antioxidant activity and health functions (Gascuel et al., 2017; Wang et al., 2022a). Anthocyanins are the main source of fruit peel color, while tannins bring astringency and a sense of structure. Aroma-related substances, such as terpenoids, alcohols and esters, determine the unique flavors of grapes and wines (Laucou et al., 2018; Wang et al., 2022a). The accumulation of these substances is influenced by multiple aspects such as genetics, light, temperature and cultivation management (Wang et al., 2022a; Ganugi et al., 2023).

2.3 Texture, firmness, seedlessness, and consumer-preferred traits

The texture and hardness of the fruit will affect its storage and transportation performance as well as its eating taste. Fruit size, peel thickness, pulp firmness and seedlessness are important goals in table grape breeding (Ban et al., 2016; Kui et al., 2020; García-Abadillo et al., 2024). Among them, seedlessness is particularly popular in the market. Currently, related QTL and candidate genes have been identified (Laucou et al., 2018). In addition, traits such as fruit appearance (such as color and shape), crack resistance and disease resistance are also often included in the indicators for quality improvement (Vafaee et al., 2017; García-Abadillo et al., 2024).

3 Traditional Breeding Approaches

3.1 Germplasm collection and phenotypic selection

The diversity of germplasm resources is the foundation for improving the quality of grapes. By collecting and preserving wild relatives, local varieties and traditional strains of grapes, breeders can obtain rich genetic variations. These variations provide a gene pool for the improvement of traits such as fruit flavor, nutritional components and stress resistance. Phenotypic selection relies on systematic evaluation of traits such as fruit appearance, flavor, sugar-acid ratio and disease resistance, from which individuals with outstanding performance are selected as breeding materials. Although long-term domestication and selection have reduced genetic diversity, there are still obvious differences in fruit traits among the existing germplasms. Through systematic phenotypic identification and genetic analysis, these differences can be utilized to provide a genetic basis for responding to climate change and market demand (Gascuel et al., 2017; Bigard et al., 2018; Bigard et al., 2020).

3.2 Hybridization for seedlessness, disease resistance, and quality

Hybrid breeding is the core means for improving the quality of grapes. Through sexual hybridization, breeders combine superior fruit qualities (such as large size, good flavor, and balanced sugar and acid) with target traits like seedlessness and disease resistance. For instance, grape breeding has developed new varieties such as ‘Shine Muscat’ through diploid and tetraploid hybridization. These varieties are both large and seedless, and have disease resistance (Yamada and Sato, 2016). In addition, by using intraspecular hybridization and repeated backcrossing of grapes, traits such as cold resistance and disease resistance can be gradually introduced while maintaining high-quality fruits, avoiding the problem of fruit quality decline after hybridization of wild varieties (Wang et al., 2021; Wang et al., 2022b; Wang et al., 2024). Hybrid breeding is also widely used in the cultivation of seedless grapes, often combined with techniques such as embryo rescue to increase the yield of seedless offspring.

3.3 Clonal selection for stabilizing desirable fruit quality traits

Clonal selection is an important method for maintaining and stabilizing excellent fruit traits. Grapes are mostly propagated asexually. Excellent individual plants can be cloned and expanded through methods such as cuttings and grafting to ensure the stable inheritance of fruit quality, flavor and yield. Clonal selection not only maintains the superior traits of varieties but also discovers new quality variations by screening natural mutants (such as bud mutations). Many improved or local varieties of high-quality grape varieties are obtained through clonal selection and bud mutation screening (Gascuel et al., 2017; Butiuc-Keul and Coste, 2023). Meanwhile, clonal selection also provides a stable genetic background for molecular breeding and precise improvement.

4 Molecular and Genomic Insights

4.1 Quantitative trait loci (QTL) mapping for fruit quality traits

QTL (Quantitative trait loci) mapping is an important method for studying the genetic basis of complex fruit quality traits in grapes. In recent years, QTL mapping based on high-density genetic maps has achieved many results in traits such as fruit flavor, firmness, shape and sugar-acid content. For instance, by using high-throughput molecular marker techniques such as SLAF-seq, researchers constructed high-density genetic maps on 19 linkage groups and identified multiple stable QTLS related to musk flavor, fruit firmness and fruit shape. On LG8, new QTLs closely related to fruit firmness and fruit shape were discovered for the first time, and candidate genes were screened out, such as VIT_08s0007g00440 (Jiang et al., 2020; Wang et al., 2020). Furthermore, the QTLs of traits such as fruit firmness and fruit shape showed high stability in different populations and years, providing a theoretical basis for molecular marker-assisted selection (MAS) and precision breeding (Jiang et al., 2020; Wu et al., 2022).

4.2 Genome-wide association studies (GWAS) and genomic resources in grape

GWAS conducts correlation analysis using genotype and phenotypic data from large-scale natural populations, significantly enhancing the analytical ability for fruit quality traits. The latest research, based on three years of multi-trait data from 588 grape samples, discovered new QTLS related to fruit diameter, fruit weight and post-ripening qualities (such as rot and weight loss), and identified some key candidate genes, such as Vitvi11g000454, which is involved in jasmonic acid signaling regulation (Guo et al., 2019; García-Abadillo et al., 2024; Liu et al., 2024). The establishment of the Grapepan pan-genome (Grapepan v.1.0) integrates structural variations (SV) and short variations, improving the accuracy of QTL mapping and the estimation of trait heritability. This provides a solid foundation for multi-trait genomic selection and precision breeding (Liu et al., 2024). The results of GWAS and traditional QTL mapping were highly consistent, and new loci could also be discovered, promoting the molecular breeding research of grape quality traits (Guo et al., 2019; García-Abadillo et al., 2024).

4.3 Functional genomics: candidate gene discovery and expression analysis

Functional genomics, combined with QTL/GWAS mapping and transcriptome and expression analysis, has accelerated the identification and functional verification of candidate genes. For example, in the study of fruit firmness, GWAS and expression analysis jointly identified key genes such as CesA and VvCslD5 involved in cellulose synthesis, and their functions were verified through transgenic and subcellular localization experiments (Jiang et al., 2020; Hu et al., 2025). In the study of fruit shape, by combining QTL mapping and RNA-seq, researchers screened out candidate genes related to DNA replication, cell wall modification and hormone synthesis, and found that the contents of auxin (IAA) and zeaxanthin (tZ) were significantly different among different fruit shape types (Wu et al., 2022). Furthermore, by using expression analysis methods such as qRT-PCR, the expression differences of candidate genes within the QTL interval (such as VIT_18s0041g02410, VIT_18s0089g00210) in different varieties and developmental stages were further verified. It indicates that they play an important role in the formation of fruit quality (Jiang et al., 2020).

5 Molecular Breeding Strategies

5.1 Marker-assisted selection (MAS) for sugar content, berry size, and anthocyanins

Marker-assisted selection (MAS) utilizes molecular markers closely linked to the target trait to efficiently screen complex traits. In grapes, quality traits such as sugar content, grape size and anthocyanin accumulation are mostly quantitative traits and are regulated by multiple genes. Through QTL mapping and association analysis, researchers have identified candidate genes and molecular markers related to grape width, grape weight, glycolic acid metabolism and anthocyanin synthesis, laying a foundation for the application of MAS in the improvement of grape quality. For instance, GWAS studies have found that the *Vitvi11g000454* gene is closely related to fruit width and can be used for the development of molecular markers for fruit size (García-Abadillo et al., 2024). In addition, transcription factors such as *VvbHLH137* have been confirmed to positively regulate anthocyanin synthesis, providing molecular targets for the improvement of fruit peel color (Figure 1) (Niu et al., 2025). MAS has shown obvious advantages in the early selection of disease resistance, stress resistance and fruit quality traits of grapes (Gascuel et al., 2017; Butiuc-Keul and Coste, 2023; García-Abadillo et al., 2024).

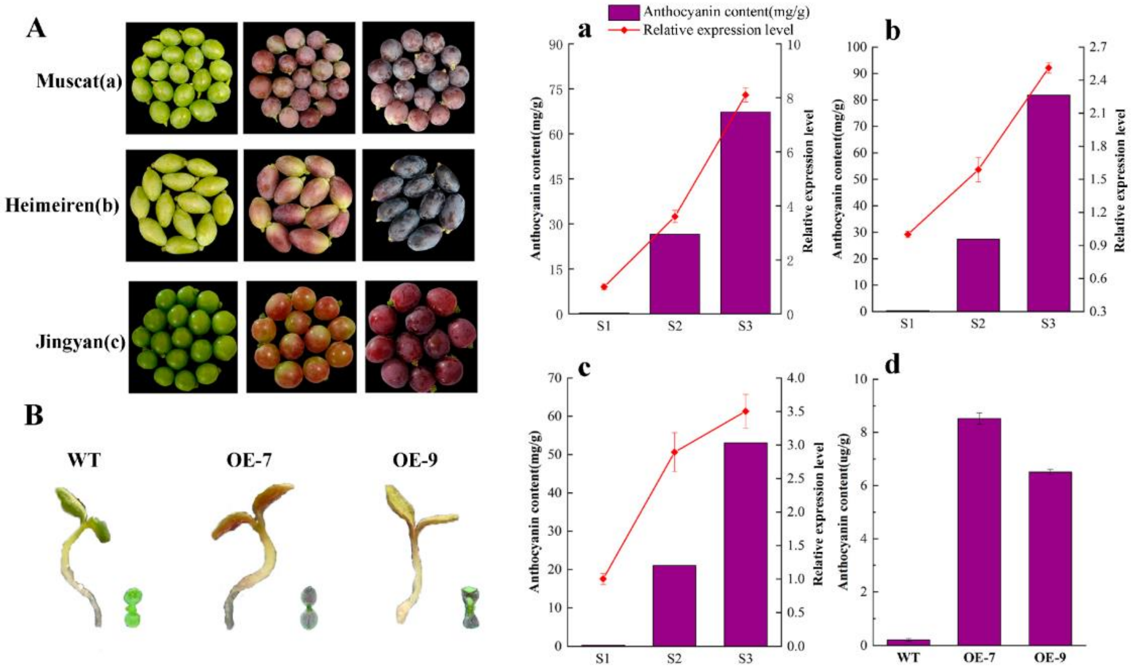

Figure 1 *VvbHLH137* expression and genetic function (Adopted from Niu et al., 2025)

Image caption: (A) Variations in fruit appearance, *VvbHLH137* expression, and corresponding anthocyanin content in grape peels during developmental stages (S1 to S3) for three grape varieties. Data are means ± SDs of 3 replicates. (B) Over-expression of *VvbHLH13*7 in Arabidopsis increased anthocyanin content compared to wild-type (WT) plants. (a) The change of anthocyanin content and *VvbHLH137* expression in Muscat; (b) The change of anthocyanin content and *VvbHLH137* expression in Heimeiren; (c) The change of anthocyanin content and *VvbHLH137* expression in Jingyan. (d) The comparison of anthocyanin content in transgenic lines and WT (Adopted from Niu et al., 2025)

5.2 Genomic selection for multi-trait improvement

Genomic selection (GS) establishes predictive models through high-density genotyping and phenotypic data of the entire genome, which can achieve overall selection of complex quantitative traits. Compared with traditional QTL analysis, GS can capture genetic variations related to fruit quality (such as sugar content, fruit size, stress resistance, etc.) more comprehensively and improve the efficiency of simultaneous improvement of multiple traits (Viana et al., 2016). In grape breeding, GS has been proven to accelerate the breeding process of superior varieties, especially suitable for fruit trees with long cycles and complex traits (Viana et al., 2016; Gascuel et al., 2017). The introduction of GS helps to break through the limitations of MAS in the improvement of complex traits of multiple genes.

5.3 Genome editing for precise modification of quality-related genes

Genome editing technology, especially the CRISPR/Cas system, provides a new approach for the precise improvement of grape quality traits. By targeting and knocking out or modifying specific genes, key pathways such as sugar metabolism, anthocyanin synthesis and fruit development can be directionally regulated. In recent years, CRISPR/Cas has been used to study and improve genes related to disease resistance, stress resistance and fruit quality in grapes, showing advantages such as short cycle, high efficiency and no residue of exogenous genes (Butiuc-Keul and Coste, 2023). In addition, the combination of genome editing with high-throughput omics and phenotypic analysis is expected to achieve precise improvements in the quality of grape fruits in multiple aspects.

6 Case Study: Breeding Progress for Fruit Quality in *Vitis vinifera*

6.1 Breeding objectives: aroma, anthocyanin accumulation, and seedlessness

The improvement of grape fruit quality mainly focuses on aroma, anthocyanin content and seedlessness. Aroma substances (such as monoterpenoids and other volatile compounds) directly determine the flavor of grapes and wine and are also the factors that consumers care about the most. Anthocyanins are the main pigments in fruits. They not only affect the color of fruits and wine but also have antioxidant and health-promoting effects. Seedlessness is an important trait of table grapes and some wine grapes, as it meets the market's demand for convenience in consumption. In recent years, climate change has affected the sugar-acid ratio and balance of fruits, and the breeding goals have gradually expanded to acidity regulation and stress resistance to ensure fruit quality (Yamada and Sato, 2016; Gascuel et al., 2017; Bigard et al., 2018; Bigard et al., 2020; García-Abadillo et al., 2024).

6.2 Methods: integration of classical hybridization with molecular tools

Traditional hybrid breeding has made progress in quality improvement through sexual hybridization and phenotypic selection of superior varieties. However, due to the long life cycle and complex genetic traits of grapes, relying solely on traditional methods is not very efficient. In recent years, tools such as molecular marker-assisted selection (MAS), genome-wide association study (GWAS), QTL mapping and gene editing (such as CRISPR/Cas9) have been widely applied. These technologies can accelerate the localization and utilization of genes related to target traits and improve the efficiency of selection and breeding. For instance, the early screening of traits such as seedlessness, fruit size and anthocyanin synthesis by using molecular markers has significantly shortened the breeding cycle. Meanwhile, genomic sequencing and high-throughput phenotypic analysis also provide support for genetic analysis and precise improvement of complex traits (Figure 2) (Tello et al., 2019; Butiuc-Keul and Coste, 2023; Rao, 2023; García-Abadillo et al., 2024; Rahman et al., 2024; Xie et al., 2025).

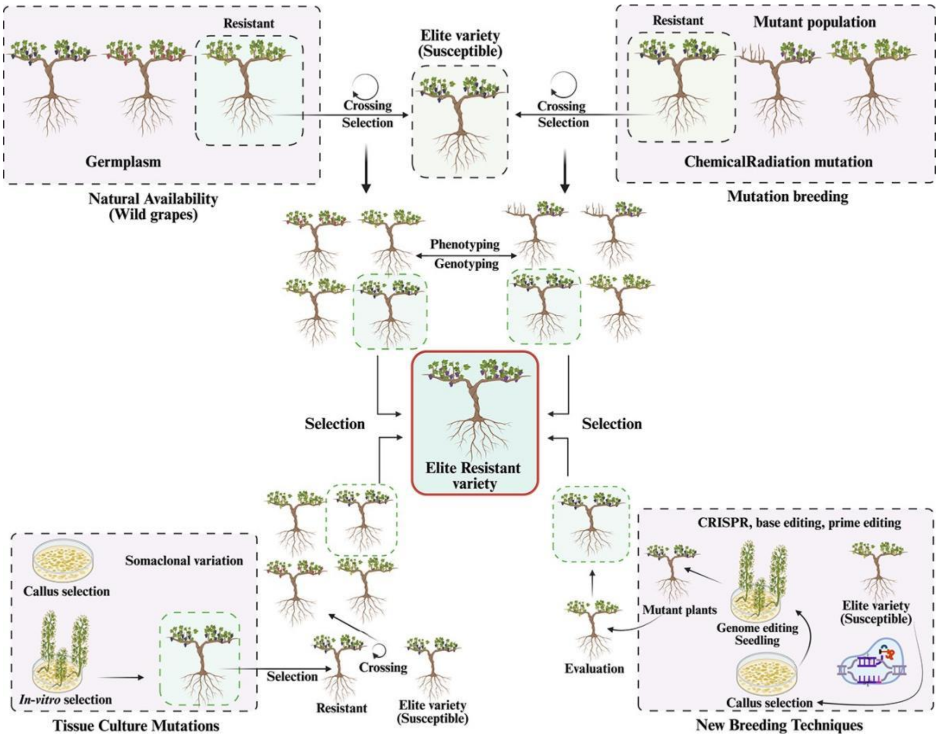

Figure 2 Progression of agricultural breeding methods (Adopted from Rahman et al., 2024)

Image caption: The process of crossbreeding takes a significant amount of time, often 8-10 years, to improve desirable characteristics or features in a particular species, such as disease tolerance or resistance. Mutation breeding uses chemical or physical irradiation to develop unique genetic variants in the genome over 6-7 years. Tissue culture improves crop attributes in 4-6 years by exogenously transforming genes into commercially relevant elite cultivars. Genome editing: precisely updating the target gene or regulatory sequence or modifying elite kinds' DNA and/or RNA bases in 2-3 years to improve a specified characteristic (Adopted from Rahman et al., 2024)

6.3 Outcomes: improved cultivars and implications for viticulture and winemaking

Through these methods, many high-quality new varieties have been cultivated and applied to production. For example, varieties such as ‘Ecolly’ have both high quality and strong stress resistance through compound selection and multi-gene accumulation, and have good adaptability, promoting the sustainable development of the industry (Wang et al., 2021; Wang et al., 2022b; Wang et al., 2024). ‘Shine Muscat’ is obtained through multi-generation hybridization and molecular-assisted selection. It has the characteristics of large grains, seedless, crisp flesh and excellent aroma, and has strong market competitiveness (Yamada and Sato, 2016). Molecular breeding has also promoted the precise improvement of complex traits such as anthocyanin content and sugar-acid ratio, helping to address climate change and meet the diverse market demands. Improved varieties not only enhance the flavor of fruits and wines, but also strengthen disease resistance and stress resistance, reduce production costs, and promote the high-quality development of viticulture and winemaking (Bigard et al., 2018; Tello et al., 2019; Bigard et al., 2020; García-Abadillo et al., 2024; Gómez et al., 2024).

7 Challenges and Limitations

7.1 Long generation cycles and heterozygosity in grape breeding

Grapes are perennial fruit trees with a long generation cycle and a high degree of heterozygosity. This makes the breeding speed of new varieties very slow. Due to the long juvenile period, each round of hybridization and trait screening takes several years, significantly reducing the breeding efficiency. High heterozygosity also makes the stable inheritance of superior traits complex. Many target traits are controlled by multiple genes, and there are complex interactions among genes, which makes directed improvement more difficult (Butiuc-Keul and Coste, 2023; Kumar et al., 2023; Wang et al., 2024). These factors together lead to a long cycle and slow progress in the improvement of grape quality.

7.2 Trade-offs between yield, quality, and stress tolerance

In grape breeding, there is often a trade-off between yield, quality (such as flavor and nutrition) and stress resistance (such as disease resistance, cold resistance and salt-alkali resistance). For instance, when introducing disease-resistant or cold-resistant genes, it often brings about some undesirable fruit traits of wild species or American species, making it difficult for hybrid offspring to simultaneously achieve high quality and high resistance (Yamada and Sato, 2016; Wang et al., 2021; Wang et al., 2024). In addition, there is a negative correlation between some quality traits (such as sugar-acid ratio and fruit size) and stress resistance, which makes simultaneous improvement of multiple traits more difficult (Gascuel et al., 2017; Bigard et al., 2018; Bigard et al., 2020). Therefore, how to strike a balance among high yield, high quality and high stress resistance is the core challenge in current grape breeding.

7.3 Limited adoption of molecular tools in traditional breeding programs

Although molecular breeding techniques such as molecular marker-assisted selection and genome editing have made progress both theoretically and experimentally, they are still not widely applied in traditional breeding projects. There are several main reasons: First, the genetic background of grapes is complex, with many traits regulated by multiple genes, making the development and application of molecular markers difficult. Second, some molecular tools have not yet achieved high throughput and low cost, making them difficult to commercialize. Thirdly, some breeders have a low acceptance of new technologies and limited operational capabilities (Gascuel et al., 2017; Zhang et al., 2021; Butiuc-Keul and Coste, 2023; Kumar et al., 2023). Furthermore, the application of molecular breeding in complex traits such as fruit flavor and nutrition is still in the exploratory stage, and a complete technical system has not yet been formed (García-Abadillo et al., 2024).

8 Future Perspectives

8.1 Application of multi-omics and systems biology for trait dissection

Multi-omics techniques (such as genomics, transcriptomics, metabolomics, etc.) combined with systems biology are becoming important tools for studying the complex quality traits of grape fruits. By integrating transcriptome and metabolome data, the gene-metabolite networks that affect flavor, nutrition and stress resistance can be revealed. These achievements provide theoretical support for the development of molecular markers and precision breeding. At present, there is an increasing amount of data related to grape fruit quality. Integrated analysis platforms (such as TransMetaDb) have been initially established, which helps to explore the connections between key genes and metabolites and provides resources for functional validation and molecular design breeding (Gascuel et al., 2017; Savoi et al., 2022; Butiuc-Keul and Coste, 2023; García-Abadillo et al., 2024). In addition, the research on new genomic regulatory elements such as G-tetrahedral also provides new targets for grape stress resistance and quality improvement (Xie et al., 2025).

8.2 Integration of molecular breeding with climate-resilient viticulture

Climate change has brought significant challenges to the quality and yield of grape fruits, especially the pressure of high temperatures, droughts and diseases. Combining molecular breeding techniques (such as genome selection, QTL mapping, gene editing, etc.) with traditional methods can accelerate the cultivation of new materials that are both of high quality and stress resistance. For instance, through genome-wide association study (GWAS) and high-density genetic mapping, multiple genes and QTLs related to fruit size, acidity and disease resistance have been identified, laying the foundation for aggregated stress resistance and superior traits (Tello et al., 2019; Bigard et al., 2020; Wang et al., 2021; Wang et al., 2022; García-Abadillo et al., 2024; Wang et al., 2024). Meanwhile, by using natural germplasm diversity and molecular marker-assisted selection, varieties with stronger adaptability can be bred for different climatic conditions, promoting sustainable cultivation (Bigard et al., 2018; Bigard et al., 2020; Sosa-Zuniga et al., 2022; Gómez et al., 2024).

8.3 Consumer-driven breeding for diversified quality traits

With the upgrading of consumption, the market's demand for grapes is becoming increasingly diverse. It not only requires high yield and resistance, but also pursues flavor, texture and nutrition. Modern breeding is gradually shifting towards consumer-oriented traits. The use of high-throughput phenomics, molecular markers and bioinformatics tools can better analyze and aggregate these complex quality traits (Yamada and Sato, 2016; Gascuel et al., 2017; García-Abadillo et al., 2024). Meanwhile, the utilization of traditional varieties and wild germplasm provides rich resources for the diversity of flavors and nutrients. In the future, the "reverse breeding" model involving consumers and precise molecular design breeding will drive the development of grape quality towards diversification and personalization (Yamada and Sato, 2016; Gascuel et al., 2017; Bigard et al., 2018).

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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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