

## 7.2 Insufficient understanding of molecular mechanisms

Although considerable progress has been made in QTL mapping, GWAS, and candidate gene identification for traits related to berry size, shape, and cluster structure, research on the genetic mechanisms underlying the composite trait of berry uniformity remains limited. Most existing studies focus on mean values of traits such as berry weight, length, diameter, cluster compactness, or berry number, whereas relatively few directly use intra-cluster variability (e.g., CV) or spatial uniformity as core phenotypic traits for genetic mapping (García-Abadillo et al., 2024; Thorat et al., 2024).

Previous studies have shown that berry size and cluster structure are controlled by multiple genes, with candidate genes involved in processes such as cell division, cell expansion, hormone signaling, cell wall modification, and stress responses (De Sousa Moreira et al., 2024; Meneses et al., 2025). Pangenome studies further indicate that complex traits in grapevine are influenced not only by single nucleotide polymorphisms (SNPs) but also by structural variations, and that integrating SNP and structural variation analyses can improve the explanation of heritability (Liu et al., 2024). However, how these genetic variations regulate developmental synchrony, intra-cluster resource allocation, and spatial distribution of uniformity remains largely unclear.

Future research should treat berry uniformity as an independent core phenotype and integrate multi-stage developmental phenotypes with transcriptomic, metabolomic, hormonal, and genomic data to elucidate the regulatory networks underlying synchronous and asynchronous berry development. At the same time, functional validation of key candidate genes should be strengthened to facilitate the transition from empirical selection to molecular design breeding for uniformity improvement.

## 7.3 Insufficient integration of multi-source data

With the advancement of high-throughput phenotyping, genomics, and intelligent agriculture technologies, grape uniformity research is entering a data-driven era. However, the integration of phenotypic, genomic, environmental, and management data remains insufficient. Most existing studies focus on a single data type, such as phenotypic measurement, QTL mapping, or GWAS, while integrated modeling of genotype  $\times$  environment  $\times$  management interactions is still limited. This restricts the comprehensive understanding of the stability of berry uniformity across years, regions, and management conditions (Herzog et al., 2025; Zhang et al., 2025).

The integration of high-density genotyping with high-throughput phenotyping has already demonstrated significant value in the study of complex traits such as berry morphology, quality, and stress resistance (Liu et al., 2024; Zhang et al., 2025). Meanwhile, genomic selection and multi-trait selection indices are becoming important approaches to improve breeding efficiency in grapevine (Bharati et al., 2023; Brault et al., 2024). However, in practical production, management variables such as thinning intensity, GA<sub>3</sub> application, water status, microclimate, and vine load are often not recorded and modeled alongside genetic and phenotypic data, limiting the development of predictive models and precision regulation strategies for berry uniformity.

In the future, it will be necessary to establish a multi-source data platform specifically for berry uniformity, standardize data collection protocols, and integrate phenotypic, genotypic, environmental, and management information. By leveraging machine learning, genomic prediction, and digital twin technologies, dynamic predictive models can be developed. On this basis, uniformity-related traits can be incorporated into ideotype design and multi-trait selection indices, enabling the coordinated improvement of high uniformity, high yield, superior quality, and strong adaptability.

## 8 Concluding Remarks

Berry size, shape, and cluster structure are core components of grape quality, directly influencing consumer acceptance, suitability for fresh consumption or processing, and ultimately economic returns. With the advancement of high-throughput image analysis and machine vision technologies, researchers are now able to quantify berry and cluster traits at large scales and to elucidate the relationships between berry size, compactness, structural variation, and yield and quality attributes. Genomic and association studies have demonstrated that most berry-related traits, including size, weight, texture, and shape, are controlled by multiple genes. Nevertheless,