

given to materials with higher mean values of berry weight, length, width, and volume, combined with lower CV values. Previous studies have shown that grape germplasm resources and breeding populations exhibit wide variation in berry weight, length, diameter, seed number, and cluster structural traits, providing a genetic basis for selecting genotypes with uniform berries and coordinated cluster architecture (Güler and Karadeniz, 2023; Gharate et al., 2025).

At the cluster level, an ideal cluster should maintain a balance between compactness and openness. Overly loose clusters may exhibit large gaps and uneven berry distribution, whereas excessively compact clusters are prone to berry compression, deformation, and uneven development. Therefore, selection for uniformity should comprehensively consider cluster length, width, berry number, berry density, compactness, and overall cluster regularity (Thorat et al., 2024; Sharma et al., 2025). Genome-wide association studies (GWAS) and QTL analyses have shown that berry size and cluster structure traits are controlled by multiple genes but generally exhibit moderate to high heritability, enabling gradual improvement through continuous selection and the utilization of stable genetic loci (De Oliveira et al., 2026).

5.2 Breeding strategies

From a genetic improvement perspective, enhancing grape berry uniformity requires an integrated strategy combining high-quality germplasm evaluation, hybridization design, and marker-assisted selection. It is essential to systematically identify superior genetic resources from existing cultivars, local germplasm, and breeding materials that exhibit high berry uniformity, stable cluster structure, and consistent fruit set performance, and to use these as parental lines in hybrid breeding. Germplasm studies indicate that grape berry size, cluster density, berry number, and seed traits show substantial variation, providing a foundation for targeted selection of uniformity-related traits (Güler and Karadeniz, 2023; Gharate et al., 2025).

Because berry uniformity is a complex quantitative trait, relying solely on phenotypic selection is often time-consuming and susceptible to environmental interference. In recent years, technologies such as QTL mapping, GWAS, RNA-Seq, and high-density SNP genotyping have provided powerful tools for dissecting the genetic basis of uniformity-related traits. Multiple studies have identified QTLs associated with berry weight, length, diameter, seed traits, and cluster structure, with some loci showing stable expression across years and populations (García-Abadillo et al., 2024). For example, QTLs associated with berry weight have been located on chromosomes 11, 17, and 18, while major loci for berry length and width have been identified on chromosomes 14 and 3-5 (Figure 3) (Thorat et al., 2024; De Oliveira et al., 2026).

Marker-assisted selection (MAS) enables the early identification of progeny carrying favorable alleles, thereby improving breeding efficiency for uniformity-related traits. Studies based on RNA-Seq and GWAS have identified multiple SNP and InDel markers associated with berry size, some of which co-localize with candidate genes involved in cell number, cell wall modification, and hormone signaling pathways. In practice, a strategy integrating “phenotypic pre-screening + marker-assisted selection + multi-year stability validation” can be adopted: first selecting materials with low CV, large average berry size, and coordinated cluster structure, then enriching favorable alleles through MAS or genomic prediction, and finally validating the stability of uniformity across multiple environments.

5.3 Cultivation regulation

At the production level, cultivation practices represent the most direct and rapidly effective approach for improving berry uniformity. Even when cultivars possess favorable genetic potential, inappropriate cluster load, thinning intensity, growth regulator application, or water and nutrient management may still result in uneven berry size, excessive compactness, or localized developmental imbalance. Therefore, uniformity optimization should be based on cultivar-specific genetic characteristics and achieved through coordinated regulation of cluster shaping, quantitative thinning, and appropriate application of plant growth regulators to ensure balanced and stable berry development.