

such as fruit texture, flavor balance, aroma compound accumulation, storability, and postharvest softening, studies on key allelic variations, regulatory networks, and functional validation remain insufficient.

Simple Scene



Multi-objective Stacking Scene



Figure 3 Prediction performance of the regression model (Adopted from Zheng et al., 2025)

Image caption: A simple scenario and a complex scenario with multiple stacked fruits. The predicted maturity percentage is shown above each fruit. Each color represents a distinct instance mask (Adopted from Zheng et al., 2025)

Existing studies mainly focus on a limited number of quality indicators, including sugars, acidity, anthocyanins, and flavonoids, whereas research on terpene metabolism, cell wall metabolism, antioxidant systems, hormone signaling, and volatile aroma formation is still inadequate (Yang et al., 2025). Transcriptomic studies during fruit ripening have shown that anthocyanin biosynthesis-related genes are generally upregulated during fruit maturation, and significant changes also occur in sugar-acid metabolism and energy metabolism pathways. However, many candidate genes remain at the stage of correlation analysis, lacking further validation through gene editing, transient expression, genetic transformation, or population genetics approaches (Sun et al., 2024).

In addition, Chinese bayberry fruit quality formation is the result of interactions among genetic factors, environmental conditions, developmental stages, and cultivation practices, yet most current studies still focus on single factors or a few cultivars. For example, studies on light exposure and fruit bagging have demonstrated that weak light conditions reduce the accumulation of sugars, organic acids, vitamin C, flavonoids, and anthocyanins, and identified HY5 and LDOX as possible regulators involved in light-induced coloration (Yang et al., 2025). However, the interactions among light signaling, hormone signaling, transcription factor networks, and metabolic pathways remain unclear. Furthermore, most studies are concentrated on a few major cultivars such as ‘Biqi’ and ‘Dongkui’, while investigations involving large germplasm populations, multiple ecological regions, and different cultivation systems are still relatively limited (Zhang et al., 2024). Therefore, current quality regulation in Chinese bayberry production still relies heavily on empirical cultivation practices rather than precise regulation based on mechanistic understanding.