

identified, providing new technical support for breeding cucumber cultivars with high yield, multiple stress resistance, and adaptability to complex environmental conditions (Dey et al., 2023).

3 Genetic Variation of Cucumber Yield Traits

3.1 Variation in natural germplasm resources

Cucumber germplasm resources contain abundant genetic variation and constitute an important genetic foundation for breeding programs targeting high yield, superior quality, and stress resistance. Owing to long-term natural evolution, ecological adaptation, and geographical differentiation, cucumber materials from different regions and ecotypes have developed significant differences in plant architecture, flowering habits, fruit morphology, fruiting ability, and environmental adaptability. Extensive germplasm evaluations have demonstrated broad natural phenotypic diversity in yield-related traits such as fruit length, fruit diameter, fruit number per plant, single fruit weight, and yield per plant in cucumber (Tadkal et al., 2024). This rich natural variation not only reflects the long-term ecological adaptation and cultivation history of cucumber but also provides abundant allelic resources for the genetic improvement of high-yield traits.

Landraces are important sources of natural variation in cucumber and represent core germplasm types for maintaining genetic diversity. Previous studies have shown that different landraces exhibit high coefficients of variation and broad-sense heritability for traits such as yield per plant, fruit number per plant, single fruit weight, and vine-related characteristics, indicating strong selection potential and substantial genetic control over these traits (Tadkal et al., 2024). Compared with modern commercial cultivars, traditional landraces may possess certain limitations in terms of fruit uniformity and adaptability to protected cultivation systems; however, they still exhibit important breeding value in stress adaptability, continuous fruiting ability, and yield stability. Therefore, landrace germplasm resources are not only important components of cucumber genetic diversity but also valuable materials for mining superior yield-related genes.

With the establishment of global germplasm repositories and genomic databases, the population genetic structure of natural variation in cucumber has gradually been elucidated (Figure 1). The 1 234 cucumber accessions conserved in the U.S. National Plant Germplasm System can be classified into three major genetic subpopulations, which differ significantly in geographical origin and horticultural type. Further genome-wide SNP analyses and core germplasm construction have revealed abundant and structured genetic diversity within cucumber germplasm resources, particularly among East Asian materials, which exhibit distinct characteristics in fruit length and fruit shape index (Lin et al., 2024). The extensive genetic variation present in natural germplasm resources provides important genetic sources for breeding new cucumber cultivars with high yield, superior quality, and stress resistance and also establishes a material foundation for elucidating the genetic basis of complex quantitative traits.

3.2 Variation formed through artificial selection

Artificial selection has been an important driving force promoting the continuous optimization of cucumber yield traits and the differentiation of cultivation types. During long-term domestication, cultivation, and modern breeding processes, breeders have continuously selected materials with high yield, early maturity, high female flower ratio, strong continuous fruiting ability, and adaptability to protected cultivation, resulting in significant changes in plant architecture, flowering habits, fruit morphology, and yield components. Modern greenhouse cucumbers generally exhibit characteristics such as shorter internodes, higher degrees of femaleness, stable fruit set, and strong continuous fruiting ability, all of which are the result of long-term directional selection and genetic fixation. Artificial selection has not only altered the phenotypic range of yield-related traits in cucumber but also significantly affected the frequency distribution of related alleles and overall genome structure.

QTL mapping studies based on wild and cultivated cucumber populations have shown that multiple important loci associated with flowering time, fruit size, fruit number, and fruit weight per plant have undergone continuous selection during domestication. Some QTL regions exhibit clear signatures of domestication and breeding selection. Notably, certain alleles derived from wild or semi-wild materials still exert positive transgressive effects on fruit size and fruiting ability, indicating that wild germplasm resources retain abundant superior genetic