

variation that has not yet been fully utilized. Therefore, the genetic complementarity between wild germplasm and modern cultivated varieties provides new directions for high-yield cucumber breeding.

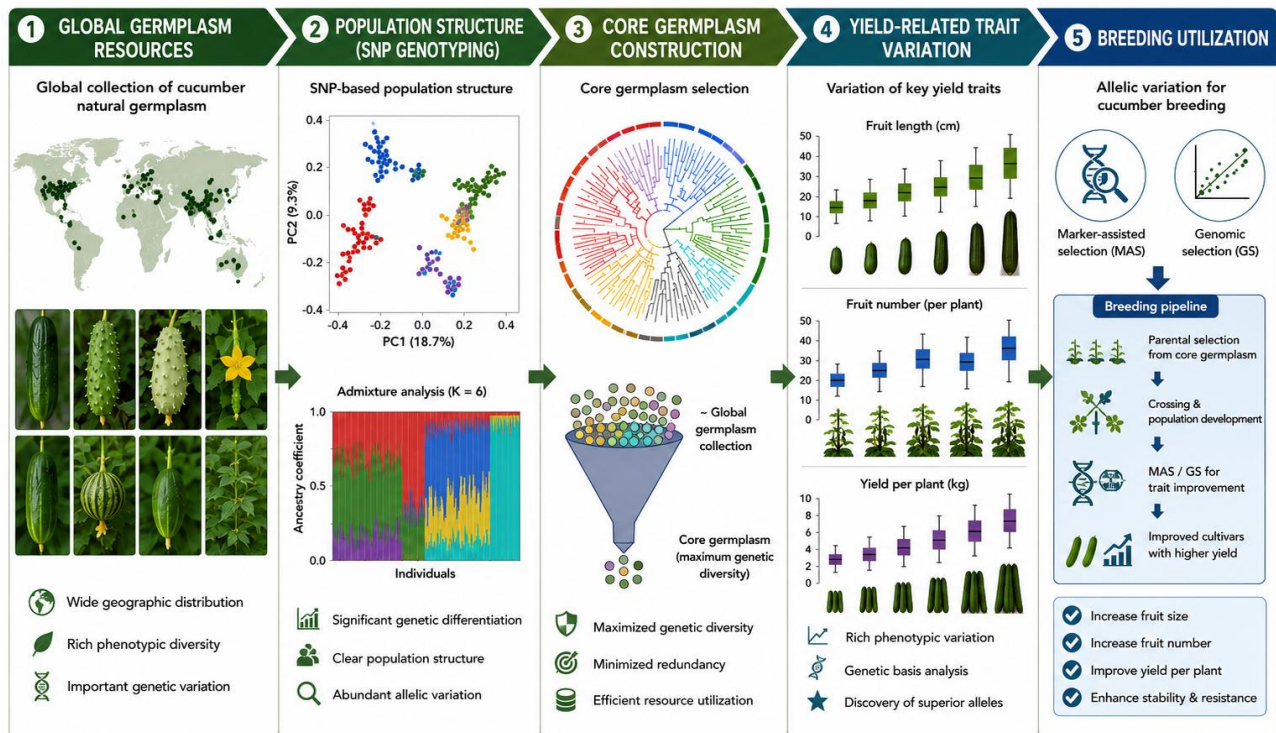


Figure 1 Genetic diversity and yield-related trait variation in cucumber natural germplasm resources

Clear signatures of artificial selection are also evident in modern breeding populations. Genome analyses of elite inbred lines from different breeding backgrounds have revealed significant differentiation in several important QTL regions associated with earliness, fruit size, and productivity, reflecting continuous reinforcement selection for high-yield-related traits during breeding processes. In addition, multi-environment evaluations and hybrid combination analyses have demonstrated substantial genetic variation among breeding materials, with some hybrid combinations exhibiting significantly higher total yield and fruit number than ordinary materials and even outperforming commercial control cultivars (El-Remaly and Shehata, 2023; Serhienko et al., 2025). In recent years, the utilization of heterosis, marker-assisted selection, and pyramiding of complex traits have further improved the efficiency of cucumber yield improvement (Shukla et al., 2025). Artificial selection has not only shaped the genetic variation patterns of modern cucumber yield traits but has also driven the continuous evolution of cucumber from traditional landraces to protected-cultivation-adapted and high-yield, high-quality cultivars.

3.3 Molecular-level genetic variation

With the development of genomics and high-throughput sequencing technologies, studies on cucumber yield traits have gradually progressed from traditional phenotypic and quantitative genetic analyses to the molecular level. Molecular variations such as single nucleotide polymorphisms (SNPs), insertions/deletions (InDels), copy number variations, and structural variations constitute important genetic bases underlying differences among cucumber materials in fruit size, flowering time, female flower ratio, fruiting ability, and stress resistance. Numerous studies have demonstrated that cucumber yield traits are typical complex quantitative traits generally regulated by multiple loci with small or moderate effects and jointly influenced by environmental factors and gene interactions.

Based on genome-wide SNP data and high-density genetic maps, researchers have identified important QTLs and significant SNP loci associated with fruit length, fruit diameter, fruit shape, and fruit weight in multiple populations. Genome-wide association studies (GWAS) have shown that many significant loci related to fruit size and fruit shape are clustered within known QTL regions, suggesting that cucumber yield-related traits possess relatively stable genetic foundations (Lin et al., 2024). Meanwhile, high-density SNP genetic maps constructed