

described as “single-spike large-flower” versus “multi-spike multifloral” commercial types. Inflorescence length and flower number per spike show considerable variation and are key quantitative indicators for distinguishing market types. In addition, flower arrangement patterns, including density and curvature, significantly influence the overall visual presentation.

Whole-plant architecture results from the integration of inflorescence traits and vegetative growth, reflecting plant height, leaf number, and spike distribution. Compact plant types are well suited for home gardening, whereas taller or spreading forms are preferred for landscape and public space applications. Studies have shown that vegetative traits such as biomass and leaf number can predict subsequent flowering performance, indicating that plant architecture reflects cumulative growth status. Notably, structural and metabolic traits may be co-regulated; for example, genes involved in anthocyanin metabolism can also influence branching and floral organ development (Lou et al., 2023). Furthermore, cultivation practices such as paclobutrazol application can modify plant architecture by reducing spike length and improving compactness (Lu et al., 2024b). Therefore, inflorescence and plant architecture are not only outcomes of genetic selection but also important targets for cultivation management.

### 3 Mechanisms Underlying Trait Variation in *Phalaenopsis*

#### 3.1 Genetic factors

The variation in flower color and morphological traits in *Phalaenopsis* is fundamentally rooted in its genetic background. Significant genetic differentiation exists among species, wild germplasm, and hybrid cultivars in pigment metabolism, floral organ development, and inflorescence formation, collectively determining the diversity of flower color types, floral structures, and plant architecture. Studies based on hybrid populations derived from *Phalaenopsis aphrodite* and *P. equestris* have revealed extensive segregation in traits such as flower color and size. Genome-wide association analyses have identified multiple quantitative trait loci (QTLs) and 35 candidate genes associated with these traits, many of which are involved in anthocyanin biosynthesis (Hsu et al., 2022). These findings indicate that ornamental traits in *Phalaenopsis* are complex quantitative traits controlled by multiple genes and their interactions.

At the molecular level, pigment metabolic networks constitute the core genetic mechanism underlying flower color formation. The accumulation intensity and spatial distribution of anthocyanins, flavonoids, and carotenoids form the basis of monochromatic, bicolored, and patterned phenotypes. Comparative studies of purple and white *P. amabilis* have shown that purple petals accumulate high levels of anthocyanins (mainly cyanidin derivatives), accompanied by upregulation of key structural genes, whereas white petals exhibit restricted metabolic flux and altered flavonoid composition, resulting in pigment deficiency. In *P. pulcherrima*, the transcription factors PpMYB1 and PpbHLH1 form a regulatory complex that activates key genes such as F3H, DFR, and ANS, thereby significantly promoting anthocyanin accumulation (Wen et al., 2025). These results demonstrate that differences in expression intensity and spatial regulation within pigment biosynthesis pathways are the direct genetic basis of flower color diversity.

The formation of complex color patterns is also governed by specific regulatory networks. Members of the R2R3-MYB transcription factor family play differentiated roles in various pigmentation patterns, with distinct genes regulating background coloration, spot formation, and venation. Their differential expression ratios determine the regional distribution of pigments across floral organs. In addition, structural genes such as CHS and F3'5'H not only affect color intensity but also influence branching and floral organ number (Lou et al., 2023), suggesting coordinated regulation between metabolic pathways and morphological development. Therefore, flower color, floral form, and plant architecture are not independent traits but may be interconnected through shared regulatory networks. In breeding practice, hybridization remains the primary approach for expanding trait diversity; however, due to polygenic control and complex genetic backgrounds, progeny often exhibit significant phenotypic segregation and low stability of desirable trait combinations (Hsu et al., 2022). Furthermore, distant hybridization may produce triploid or aneuploid individuals, which can negatively affect fertility and subsequent utilization (Sevilleno et al., 2023).