

Genes such as JAGGED (JAG) and NUBBIN (NUB) contribute to anther morphogenesis by promoting microsporangial growth rather than identity specification, indicating the existence of parallel regulatory pathways governing structural development.

Hormonal regulation adds another layer of complexity to stamen development. Jasmonic acid, gibberellins, and auxins act in a coordinated manner to regulate filament elongation, pollen maturation, and anther dehiscence. The crosstalk between these hormones ensures temporal synchronization of developmental events, which is crucial for successful fertilization. Mutant analyses further confirm that disruption in hormonal balance leads to defects in fertility, emphasizing their integrative role (Ishiguro et al., 2001; Cheng et al., 2004; Cecchetti et al., 2008).

These comparative studies indicate that the core molecular mechanisms governing stamen development have been largely conserved during angiosperm evolution. Nevertheless, lineage-specific modifications in gene expression patterns, regulatory interactions, and duplication of MADS-box genes have contributed to the remarkable diversity of floral morphology and reproductive strategies observed among flowering plants. Future comparative genomic and evolutionary developmental (evo-devo) studies will further clarify the origin and diversification of these regulatory networks.

Beyond its fundamental biological significance, understanding the molecular regulation of stamen development has important applications in modern crop improvement and sustainable agriculture. Genes regulating tapetum differentiation and anther development, including *SPL/NZZ*, *EMS1-TPD1*, *BAM1/BAM2*, and *DYT1*, have been widely investigated for the development of stable genetic male-sterility systems used in hybrid seed production (Mariani et al., 1990; Mariani et al., 1991; Denis et al., 1993). Recent advances in CRISPR/Cas-mediated genome editing have further enabled precise manipulation of floral regulatory genes for fertility control, functional validation, and de novo crop domestication. In addition, hormone-regulated pathways involving jasmonic acid, auxin, and gibberellins provide promising targets for improving pollen fertility and reproductive performance under abiotic stresses such as heat and drought. Comparative studies across diverse crop species are expected to accelerate molecular breeding strategies for the development of climate-resilient cultivars with enhanced reproductive efficiency. Furthermore, the integration of multi-omics technologies, including transcriptomics, proteomics, metabolomics, and single-cell sequencing, will facilitate the identification of novel regulatory genes and signaling networks controlling male reproductive development. These advances will not only improve our understanding of the molecular basis of stamen development but also support the development of next-generation crop varieties with enhanced yield, reproductive stability, and resilience under changing climatic conditions. Moreover, integrating artificial intelligence-assisted data analysis with functional genomics and genome editing is expected to accelerate the discovery of novel regulatory genes and improve predictive breeding strategies. Such interdisciplinary approaches will enhance the translation of fundamental knowledge into practical applications for sustainable agriculture and global food security.

4 Conclusion

Stamen development is a complex and tightly regulated process essential for plant reproduction, controlled by the coordinated action of floral identity genes, signaling pathways, and hormonal networks. The ABCDE model provides a robust framework for understanding stamen specification, while studies in *Arabidopsis thaliana* and other species have revealed intricate mechanisms governing anther development, microsporogenesis, and pollen maturation. Key regulators, including receptor-like kinases, transcription factors, and phytohormones, function in an integrated manner to ensure proper tissue differentiation and reproductive success. Advances in molecular genetics and genomics continue to deepen our understanding of these processes, offering potential applications in crop improvement, hybrid seed production, and fertility regulation.

Future research integrating multi-omics approaches, including transcriptomics, proteomics, metabolomics, and single-cell sequencing, together with CRISPR/Cas-mediated genome editing, is expected to further elucidate the molecular mechanisms underlying stamen development. These emerging technologies will facilitate the identification of novel regulatory genes and signaling networks, enabling precision breeding strategies for enhanced pollen fertility, hybrid seed production, and climate-resilient crop development. Continued integration of molecular