

FlowerBase: An integrated multi-omics database for ornamental flowering plants

Dear Editor,

Flowering plants are cornerstones of global horticulture and floriculture, and the burgeoning field of “flower omics” is becoming indispensable for advancing both basic plant science and industrial breeding. These plants hold immense economic significance. In 2019, U.S. floriculture sales alone reached approximately \$13.8 billion (Rayamajhi, 2024). However, genomic and multi-omics resources for ornamental flowers remain critically fragmented or restricted to individual species. Such data isolation severely hampers comparative studies and systematic investigations of key agronomic traits, such as flower color, scent, and flowering time. For instance, ornamental species such as *Prunus mume* (Mei) have been cultivated for millennia and possess rich phenotypic diversity (Fan et al., 2024). A unified platform for exploring the genetic underpinnings of these traits has been conspicuously absent. While comprehensive public archives provide valuable repositories for raw genomic and transcriptomic data, a major bottleneck remains in the functional integration of this information within analytical workflows tailored for floral biology. Researchers often face the challenge of navigating vast, general-purpose databases to manually collate information across disparate ornamental taxa. Critically, these archives typically lack integrated analytical tools capable of performing advanced analyses—such as comparative genomics and gene co-expression network investigation—directly on curated datasets. This fragmented environment necessitates substantial bioinformatic expertise and manual data handling, hindering efficient discovery. To overcome this long-standing challenge, we developed FlowerBase (<https://bioinformatics.hainanu.edu.cn/flowerbase>), the first dedicated database platform designed to unify ornamental flower genomics and empower modern breeding. FlowerBase provides a centralized, user-friendly portal that seamlessly integrates disparate multi-omics datasets with a powerful suite of analytical tools previously unavailable to the floral research community.

FlowerBase DATA CONTENT AND ANALYTICAL TOOLS

FlowerBase establishes an unprecedented foundation for floral research. It currently houses 62 high-quality genome assemblies from 58 ornamental species, 44 curated transcriptome datasets, 2 581 336 annotated gene models, and 8754 identified metabolites. The platform spans a broad taxonomic range, covering globally important ornamentals such as *Lilium*, *Orchidaceae*, *Paeonia*, *Prunus*, *Rhododendron*, *Rosa*, *Bougainvillea*, *Chrysanthemum*, *Dianthus caryophyllus*, *Jasminum sambac*, *Nelumbo*, *Nymphaea*, and *Osmanthus*. Notably, the inclusion of multiple genomes within key genera such as *Prunus*

provides an invaluable resource for dissecting intraspecific variation and cultivar-specific traits. By also incorporating reference genomes for the model plants *Arabidopsis thaliana* and *Oryza sativa*, FlowerBase creates a powerful framework for comparative and evolutionary studies of conserved floral traits—a feature absent in single-species databases. The platform’s architecture is designed to seamlessly connect these extensive data layers—from phenomics to genomics, transcriptomics, and metabolomics—with a sophisticated suite of analytical tools designed for biological discovery and accelerated breeding (Figure 1).

Advanced analytical workflows are built directly into the FlowerBase portal, allowing researchers to translate complex data into biological insights. The platform’s functionalities are organized around four key areas of flower biology (Figure 1A): flower structure, colors, scents, and flowering time. To facilitate the genetic improvement of these traits, FlowerBase offers a dedicated breeding toolbox (Figure 1B), featuring modules for simple sequence repeat identification, primer design (Primer3), and a “GuideRNA” tool to streamline genome editing. The power behind these applications lies in the platform’s core: a multi-omics integration engine (Figure 1C) that connects disparate data layers. This engine supports holistic data mining using algorithms such as MICE, KNN, and iCluster, and integrates phenomic research through its “FlowerCV” and “FlowerAI” tools for flower recognition and quantitative image analysis.

This central engine provides access to multi-layered omics data through several specialized modules. The genomics module (Figure 1D) allows users to explore genomic landscapes via a JBrowse-powered genome browser, complemented by tools for sequence analysis (BLAST), functional annotation (GO/KEGG enrichment), and biosynthetic gene cluster identification. The transcriptomics module (Figure 1E) offers dynamic visualization of gene expression patterns across tissues and conditions through interactive uniform manifold approximations and projections (UMAPs) and heatmaps derived from both bulk and single-cell RNA sequencing data. For population-level inquiries, the variomics module (Figure 1F) provides robust analyses, including principal component analysis, to elucidate the genetic architecture and relationships among germplasms. At the forefront of translational research, an advanced genomic selection breeding module (Figure 1G) integrates multiple statistical models (e.g., BMTME, Bayesian LASSO, and GBLUP) to predict breeding values and substantially accelerate breeding cycles. Together, these sequentially organized functionalities establish FlowerBase as a one-stop, high-performance platform for the global flower-omics community.

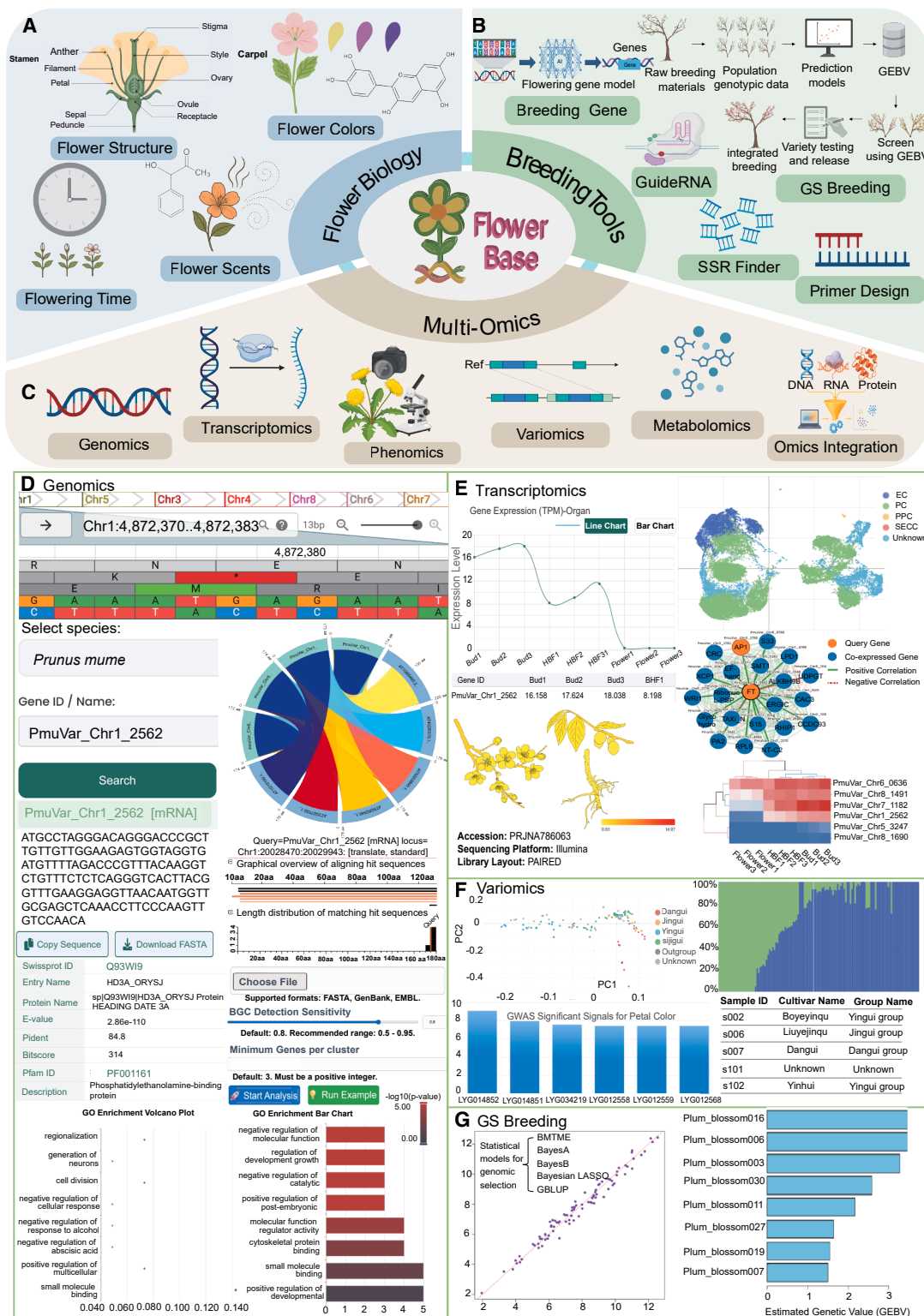


Figure 1. Architecture and main functionalities of the FlowerBase platform.

(A) The platform focuses on four key areas of flower biology: floral structure, flower colors, flowering time, and flower scents.

(B) A suite of breeding tools supports the identification and application of breeding-related genes, including genomic selection (GS) breeding, simple sequence repeat (SSR) identification, and primer design.

(C) The core of FlowerBase features a multi-omics integration engine that connects diverse data types, including genomics, transcriptomics, phenomics, variomics, and metabolomics.

(legend continued on next page)

CASE STUDY: EXPLORING A FLOWERING-TIME GENE IN *P. MUME*

To demonstrate the discovery power of FlowerBase, we used the platform to investigate FLOWERING LOCUS T (FT), a central integrator of flowering signals in *P. mume* (Li et al., 2022). Using the gene search tool, we rapidly retrieved the annotated FT gene, its sequence, and its functional annotations (GO: “regulation of flower development”). The integrated JBrowse viewer instantly displayed its genomic context. We then used the “expression analysis” tool, which confirmed significantly higher FT transcript levels in leaf tissue compared with buds, consistent with its known role.

To elucidate its regulatory network, we employed the “co-expression network” tool. This network revealed potential partners of FT, including an AP1 homolog (another flowering regulator), suggesting the presence of a conserved regulatory module. The expression profile of this novel candidate strongly correlates with FT, indicating a potential role in the flowering regulatory cascade of *Prunus*. Finally, the genomic selection breeding module was used to evaluate the breeding potential of these candidate genes for Mei. This entire analytical workflow, from gene identification to network discovery, was efficiently executed within the integrated environment of FlowerBase, pinpointing a novel, high-priority candidate for functional validation and demonstrating the platform’s ability to accelerate our understanding of flowering-time control and inform breeding strategies for desired bloom phenotypes (Naik et al., 2025).

FlowerBase marks a milestone in the systematization of flower omics, transforming a scattered data landscape into a unified, high-value discovery engine. Its originality lies in its focus on the ornamental flower niche with unmatched depth and breadth. Looking forward, our team is dedicated to continuous expansion, with plans to incorporate additional species and new omics layers, including epigenomics and metabolomic flux data. We are also developing new modules for enhanced regulatory network visualization and AI-driven trait prediction. To ensure sustainability and relevance, we have established a dedicated maintenance plan. Our multidisciplinary team—comprising experts in bioinformatics, genomics, and molecular breeding—will oversee the database’s operation and updates. Major data releases are scheduled at least twice a year to incorporate new genome assemblies and transcriptome datasets. Furthermore, we have implemented a user-feedback mechanism through the “contact us” portal on our website, encouraging community input to ensure that the platform evolves to meet researchers’ needs. By continually expanding its data coverage and refining its analytical capabilities, FlowerBase is poised to become the core international platform for floral genomics and breeding design. Its

comprehensive, expert-curated resources will enable researchers to address complex, long-standing questions in flower biology—from the molecular basis of color and scent to the genetic regulation of flowering time—ultimately advancing both fundamental plant science and the global flower industry (Xia et al., 2006).

DATA AND CODE AVAILABILITY

All data supporting the findings of this study are openly available in FlowerBase at <https://bioinformatics.hainanu.edu.cn/flowerbase>.

FUNDING

This work was supported by the National Natural Science Foundation of China (32172614) and the Youth Innovation Promotion Association, Chinese Academy of Sciences (Y2021094).

ACKNOWLEDGMENTS

We thank the editor and anonymous reviewers for their insightful comments and constructive suggestions. We sincerely acknowledge the support of the FAN system provided by the Precision Design and Intelligent Manufacturing Platform of Yazhouwan National Laboratory, which greatly facilitated this work. The authors declare no known financial or personal conflicts of interest that could have influenced the work presented in this paper.

AUTHOR CONTRIBUTIONS

F.C. and M.L. conceived and designed the research. C.W. and Zhidong Li performed the analyses and drafted the manuscript. Ji Zhang, Yufan Liang, H.Z., S.W., X.F., X.Z., Jiahao Zhang, Z.Z., Yunqing Luo, W.D., Z. L., W.W., and G.B. contributed to data collection, manuscript reviewing, and drafting revision. All authors read and approved the final manuscript.

Received: August 15, 2025

Revised: September 22, 2025

Accepted: October 13, 2025

Published: October 15, 2025

Chong Wang^{1,2,4}, Zhidong Li^{1,2,4},
Jiahao Zhang^{1,2}, Ji Zhang^{1,2}, Yufan Liang^{1,2},
Hongbin Zhang^{1,2}, Shenghao Wang^{1,2},
Xinmei Feng^{1,2}, Xiaolong Zhang^{1,2},
Zihao Zhang^{1,2}, Yunqing Luo^{1,2},
Wenbao Dai^{1,2}, Zhiheng Lin^{1,2},
Wenquan Wang^{1,2}, Genxiang Bai³,
Ming Luo^{3,*} and Fei Chen^{1,2,*}

¹State Key Laboratory of Tropical Crop Breeding, College of Breeding and Multiplication (Sanya Institute of Breeding and Multiplication), Hainan University, Sanya 572025, China

²College of Tropical Agriculture and Forestry, Hainan University, Danzhou 571737, China

³State Key Laboratory of Plant Diversity and Specialty Crops, South China Botanical Garden, Chinese Academy of Sciences, Guangzhou, China

⁴These authors contributed equally to this article.

(D) Genomics module: features a JBrowse-powered genome browser, BLAST search, tools for biosynthetic gene cluster (BGC) analysis, and GO/KEGG enrichment analysis.

(E) Transcriptomics module: provides gene expression analysis across organs and conditions, along with co-expression network analysis and heatmap visualization.

(F) Variomics module: offers population genetics analyses, such as principal component analysis (PCA), to illustrate genetic relationships among germplasms.

(G) Breeding module: includes advanced tools such as GS breeding for predicting and evaluating breeding values.

*Correspondence: Ming Luo (luoming@scbg.ac.cn), Fei Chen (feichen@hainanu.edu.cn)
<https://doi.org/10.1016/j.xplc.2025.101565>

REFERENCES

- Fan, D., Miao, R., Lv, W., et al. (2024). Prunus mume genome research: current status and prospects. *Ornam. Plant Res* **4**:e006.
- Li, P., Zhang, Q., Shi, B., Liu, L., Zhang, X., Wang, J., and Yi, H. (2022). Integration of genome and transcriptome reveal molecular regulation mechanism of early flowering trait in Prunus genus (Prunus mume and Prunus persica). *Front. Plant Sci.* **13**:1036221.
- Naik, Y.D., Bahuguna, R.N., Garcia-Caparrós, P., Zwart, R.S., Reddy, M.S.S., Mir, R.R., Jha, U.C., Fakrudin, B., Pandey, M.K., Challabathula, D., et al. (2025). Exploring the multifaceted dynamics of flowering time regulation in field crops: Insight and intervention approaches. *Plant Genome* **18**:e70017.
- Rayamajhi, A. (2024). Precision Sprayer Technologies for Enhanced Ornamental Crop Management (University of Georgia).
- Xia, Y., Deng, X., Zhou, P., Shima, K., and Teixeira da Silva, J.A. (2006). The world floriculture industry: Dynamics of production and markets. *Floriculture, ornamental and plant biotechnology* **4**:336–347.