Plant Gene and Trait 2025, Vol.16, No.5, 194-205
http://genbreedpublisher.com/index.php/pgt

Research Insight **Open Access**

Light and Temperature Regulation of Flowering in *Rosa chinensis* under Controlled Cultivation

Zhen Liu [1], Dandan Huang [2], Wenfang Wang [1]
1 Institute of Life Sciences, Jiyang College of Zhejiang A&F University, Zhuji, 311800, Zhejiang, China
2 Hainan Institute of Biotechnology, Haikou, 570206, Hainan, China
Corresponding email: wenfang.wang@jicat.org

Plant Gene and Trait, 2025, Vol.16, No.5 doi: 10.5376/pgt.2025.16.0021
Received: 09 Aug., 2025
Accepted: 15 Sep., 2025
Published: 23 Sep., 2025

Preferred citation for this article:
Liu Z., Huang D.D., and Wang W.F., 2025, Light and temperature regulation of flowering in *Rosa chinensis* under controlled cultivation, Plant Gene and Trait, 16(5): 194-205 (doi: 10.5376/pgt.2025.16.0021)

Abstract *Rosa chinensis* serves as a model for studying floral transition in perennial woody ornamentals. This study explores how light and temperature regulate flowering patterns, floral quality, and genotype × environment interactions under controlled and field conditions. Molecular analysis shows that the Rc*CO*-Rc*FT* module and *RcPIF*-FLC-like axis integrate environmental cues, with *RcPHYA*, *RcCRY2*, *RcPIF4*, and *RcHsfA6* acting through downstream regulators such as RcSOC1. Transcriptomic and epigenetic data confirm convergence of these networks, enabling synchronized flowering, while high temperature and short-day conditions disrupt activators. Phenotypic trials demonstrate that temperature and light shape floral morphology, longevity, and symmetry. A case study at the Royal Botanic Gardens Kew illustrates how precise environmental management ensures display value and conservation. The findings support breeding climate-resilient rose cultivars using marker-assisted selection, transcriptome-based screening, and CRISPR/Cas9 editing, providing practical strategies for sustainable cultivation, ornamental display, and adaptation to climate change.

Keywords *Rosa chinensis*; Flowering regulation; Photoperiod; Temperature; CO-FT module; RcSOC1; Glasshouse cultivation; Molecular breeding

1 Introduction

Rosa chinensis, commonly known as the Chinese rose, has emerged as an increasingly important model for exploring flowering time regulation in woody perennial species. The plant maintains its flowering ability throughout the year because it does not require photoperiod or vernalization to bloom like most temperate deciduous ornamentals. The plant maintains its flowering ability throughout the year because it does not need photoperiod or vernalization to bloom like most temperate deciduous ornamentals. The plant *R. chinensis* provides an excellent system for studying environmental responses and gene regulation because it does not follow traditional seasonal patterns.

The availability of genomic and transcriptomic resources for *R. chinensis* has grown substantially since the last decade. The first high-quality reference genome appeared in 2018 which enabled scientists to precisely locate *CO* and *FT* and *SOC1* and *FLC-like* genes. The subsequent population resequencing and transcriptome studies have shown the allelic diversity and expression patterns that determine floral behavior in different rose cultivars (Guo et al., 2017; Hibrand Saint-Oyant et al., 2018; Raymond et al., 2018). The perennial growth pattern of *R. chinensis* along with its secondary growth enables scientists to investigate environmental memory effects and re-blooming mechanisms and epigenetic control in wood tissues which cannot be studied in annual models like *Arabidopsis thaliana*.

R. chinensis has commercial value and breeding potential which makes it suitable for research applications. The plant *R. chinensis* connects scientific research to practical horticulture because it possesses specific traits and grows well in outdoor and greenhouse conditions and displays wide genetic diversity. Research on *R. chinensis* floral timing and scent biosynthesis and petal pigmentation and abiotic stress tolerance will help develop similar enhancements for other floricultural plants.

The species *R. chinensis* has been cultivated for a long time in both Eastern and Western horticultural traditions which makes it an excellent subject for studying domestication-related traits. Research shows that *RoKSN* (a TFL1 homolog) deficiency leads to perpetual flowering which differentiates contemporary roses from their original seasonal flowering ancestors (Soufflet-Freslon et al., 2021). *R. chinensis* serves multiple purposes because it is easy to work with in experiments and holds importance for cultural practices and economic activities and environmental conservation.

Plants undergo their vegetative to reproductive transition through internal genetic controls and external environmental cues. Light and temperature stand out as the primary environmental elements which determine when plants will produce flowers. Specialized photoreceptors detect 24-hour photoperiod duration to activate gene expression pathways through the circadian clock system according to Gendron and Staiger (2023). The *CO-FT* module functions as a core module that allows different plant species to convert photoperiod signals into flowering initiation.

The process of flowering is heavily influenced by temperature conditions. Plants that undergo vernalization need to spend time in cold temperatures before they can produce flowers. Plants that experience high temperatures will start flowering more quickly because these conditions activate temperature-sensitive transcription factors and repressors (Han et al., 2018). The plant *R. chinensis* undergoes changes in flowering time and floral form and gene expression patterns when subjected to both heat and cold temperatures (Han et al., 2019; Shin et al., 2023).

Light and temperature operate as separate elements which influence the process. The current scientific studies demonstrate that these signals operate through a common genetic pathway which controls *FT* and *SOC1* floral promoters (Sun et al., 2021). The photoperiodic and thermal signals interact in complex ways to create a multilayered regulatory system that adapts to environmental changes which becomes crucial during climate change.

The research investigates the biological processes by which *Rosa chinensis* flowers under controlled conditions when exposed to light and temperature variations. The research uses genomic analysis together with phenotypic assessment and environmental treatments to fulfill three main objectives: characterization of the photoperiod perception and circadian regulation in *R. chinensis*; investigate the plant's temperature-mediated flowering responses at phenotypic and molecular levels; explore the interactive effects of light and temperature; and identify candidate genes and pathways for horticultural breeding. The detailed methodology shows how *R. chinensis* uses environmental cues to control flowering which delivers important knowledge for plant science investigations and ornamental horticulture applications.

2 Photoperiod and Flowering Pathways in *Rosa chinensis*

2.1 Photoperiod perception mechanisms: *CO-FT* module and circadian clock genes

The photoperiod perception mechanisms in plants use the *CO-FT* module and circadian clock genes to control flowering based on day length. The CONSTANS (CO) and FLOWERING LOCUS T (FT) module functions as the main photoperiod pathway output that controls flowering in plants. Research on *Rosa chinensis* shows that *CO-like* genes operate differently between long and short days to enable the plant to maintain day-neutral flowering (Lu et al., 2020). The activation of *RcFT*, the *R. chinensis* homolog of *FT*, is highly responsive to *RcCO* levels, whose expression is tightly regulated by the circadian clock.

The circadian clock system contains core elements *RcLHY, RcTOC1, RcGI* and *RcFKF1* which link internal biological rhythms to external light information. The genes operate as linked feedback systems which use natural light-dark cycles to regulate *RcCO* expression (Gendron and Staiger, 2023). The process of *RcCO* transcript accumulation under long-day conditions during the light phase leads to *RcFT* activation which starts the floral induction process. The suppression of *RcFT* induction occurs because *RcCO* expression does not follow light exposure patterns during short-day conditions until alternative *CO-like* genes become active (Lu et al., 2020).

Emerging evidence suggests that post-translational regulation plays a crucial role in this pathway as well. *RcSRR1* disrupts *COP1-CO* regulation under red light conditions which results in *RcCO* instability and subsequent changes in *RcFT* expression levels. The proteasome system degrades RcCO through a process that responds to different light qualities which are detected by red/far-red phytochrome signals. The system includes time and frequency components to control plant flowering behavior. The CONSTANS family proteins serve as essential regulators of light-dependent flowering according to Gendron and Staiger (2023) which directs most research on *Rosa chinensis*.

2.2 Rose-specific responses under long-day vs. short-day conditions

The flowering behavior of *R. chinensis* remains constant under various photoperiods because it displays continuous flowering patterns regardless of long-day or short-day plant classification which applies to most temperate species. The system shows flexibility because it contains different *CO-like* and *FT-like* genes which express at distinct times (Sun et al., 2021). The CONSTANS-LIKE 4 (COL4) gene becomes the most abundant under short-day conditions to help replace RcCO function while sustaining RcFT activation (Lu et al., 2020).

The continuous-flowering genotypes lack *RoKSN* floral repressors which results in the loss of seasonal regulation that wild-type and early domesticated roses display (Soufflet-Freslon et al., 2021). The plant *R. chinensis* shows features which make it suitable for studying day-neutral flowering patterns. Experimental data also show cultivar-specific photoperiod sensitivity. Modern cultivars now show two different flowering responses to photoperiod extension because *RcFT* expression levels vary between them. The first group of cultivars flowers quickly when exposed to longer photoperiods because of increased *RcFT* expression. The second group of cultivars maintains their flowering ability under both long-day and short-day photoperiods. The breeding process has modified photoperiodic regulators through selection which resulted in commercial production having a broader flowering period.

2.3 Role of photoreceptors (PHYs, CRYs) in regulating flowering

Research shows that far-red light speeds up flowering in ornamental plants when the daily light integral reaches a specific minimum value (Owen et al., 2018; Whitman et al., 2022). The research by Sun et al. (2021) shows that *RcPHYA* and *RcCRY2* in *R. chinensis* stabilize RcCO protein when light is present which leads to increased *RcFT* expression. The process requires exact control through Phytochrome-interacting factors (RcPIFs) which work together with *RcCO*. The study shows that *RcPIFs* act to reduce *RcCO* activity which leads to extended flowering time (Sun et al., 2021).

The light spectrum functions as a vital component in this process. The activity of *RcPHYA* depends on the ratio of red to far-red light but RcCRY2 responds to blue light. The knowledge gained through this research allows growers to use LED lighting for photoreceptor pathway control which leads to flowering regulation. The researchers evaluated the applications through protected cultivation systems which employed red-enriched light to speed up flowering and blue light to improve morphological precision (Sun et al., 2021). Research now shows that *RcPHYA* and *RcCRY2* affect the strength of circadian outputs which indicates their function extends past their role in flowering initiation. *R. chinensis* achieves its complex flowering control system through its ability to connect light signal transduction pathways with circadian and hormonal networks.

3 Temperature-Mediated Flowering Regulation

3.1 Phenotypic responses to low, moderate, and high temperatures

The plant development of *Rosa chinensis* shows different flowering patterns when exposed to low, moderate and high temperature conditions. Floral initiation experiences a delay when temperatures drop below 15°C and certain cultivars will completely stop flowering due to chilling stress. Plants experience color loss and fragrance changes and structural damage to their flowers when chilled according to Han et al. (2018) and Ouyang et al. (2022). The ideal temperature range for commercial rose cultivation spans from 18 to 25 degrees Celsius because it enables both flower development and produces premium flower quality. Plants that receive these specific growing conditions develop symmetrical flowers with vibrant colors and strong fragrances that stay fresh for longer periods. The combination of long-day photoperiods with moderate temperatures leads to better uniformity of flowers between branches which results in synchronized blooming (Figure 1) (Shin et al., 2023).

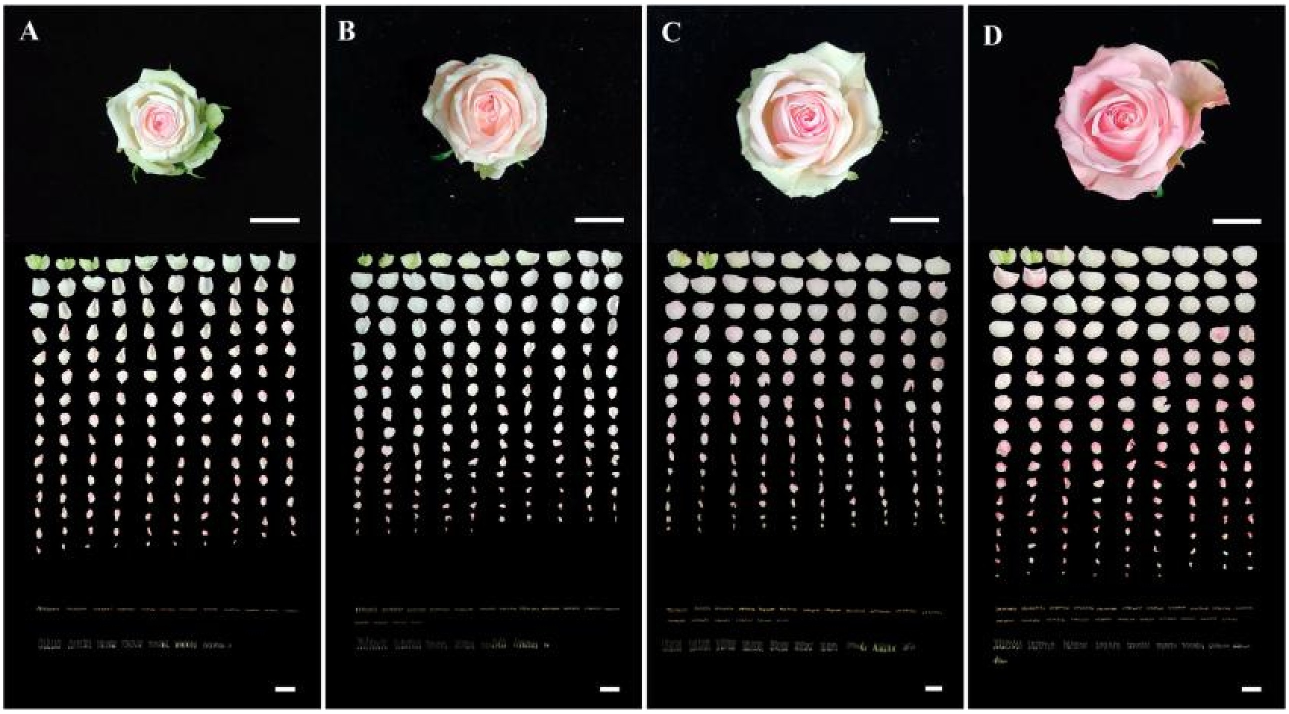

Figure 1 Visual changes in the size and color of a flower and separated floral organs in the spray-type cut rose 'Pink Shine' by temperature conditions: (A) 25/20°C (day/night, OT); (B) 20/20°C; (C) 20/15°C; (D) 15/15°C. These photos represent floral organs under a flower, in order of petals (including petaloid stamens), stamens, and carpels by each column. Scale bars mean 2 cm (Adopted from Shin et al., 2023)

The environment experiences various impacts when temperatures rise above 30°C. The particular genotypes produce early flowering but this leads to smaller flowers with deformed petals and reduced fragrance (Shin et al., 2023). Heat stress causes damage to floral symmetry while simultaneously reducing vase life which results in decreased ornamental value. The prolonged exposure to hot temperatures leads to decreased flower bud development in non-thermotolerant cultivars according to Wang et al. (2024). The observed phenotypic results show why scientists need to identify the genetic factors that control heat tolerance and flower quality. Research shows that different plant cultivars react differently to temperature changes. The reproductive activity of continuous-flowering genotypes persists under heat stress because *RoKSN* expression is suppressed and *RcFT* expression is increased. Seasonal-flowering cultivars show delayed bud emergence and complete floral abortion when they encounter the same environmental conditions. The genetic networks show different thermal response thresholds because of their distinct characteristics.

3.2 Molecular pathways: roles of *FLC-like* genes and temperature sensors

The molecular basis of thermal responses depends on temperature-sensing pathways which use essential regulatory genes. *FLOWERING LOCUS C (FLC)* functions as a floral repressor in Arabidopsis which shows decreased expression during vernalization. *R. chinensis* contains *FLC-like* homologs which show temperature responses through mechanisms that differ from those of Arabidopsis (Antoniou-Kourounioti et al., 2018).

Research shows that *FLC-like* genes in roses operate outside of the typical vernalization process. The expression of these genes seems to be controlled by epigenetic mechanisms which use histone methylation and DNA methylation to modify their activity in response to short-term temperature fluctuations. DNA demethylation at *FLC-like* promoters under heat stress conditions results in delayed flowering and decreased *RcFT* expression according to Yu et al. (2023). The results show that temperature adaptation in roses functions through two distinct mechanisms which include transcriptional and epigenetic regulation.

Heat stress responses include heat shock transcription factors (Hsfs) which include RcHsfA6 that controls protective gene expression and has been shown to cause delayed flowering under stress conditions (Wang et al., 2025). Scientists have confirmed *RcHSP70* functions as a crucial gene which provides thermotolerance to transgenic plants after researchers introduce it (Jiang et al., 2020) and improving flower quality when temperatures rise. The temperature-dependent regulation of flowering in *R. chinensis* involves transcriptional regulators and possibly membrane fluidity changes and reactive oxygen species accumulation and calcium signaling which control flowering-related gene expression. Scientists require more research to understand the connection between upstream signals and downstream floral regulators.

3.3 Evidence from cultivation studies on flowering rate and floral morphology

The controlled greenhouse experiments show experimental results which prove that plant flower production and flower appearance respond to temperature conditions. Flower deformities increased by 30% when the temperature rose from 20°C to 30°C while petal number and color intensity decreased substantially. Research conducted in controlled greenhouses with temperate climates demonstrates that plants produce synchronized flowers when grown at stable light conditions and moderate temperatures which leads to successful commercial yields. Studies have shown that different cultivars exhibit varying levels of genetic variation in thermotolerance which allows certain lines to preserve their floral characteristics when exposed to a 10°C temperature range.

High-throughput imaging and non-invasive sensors allow scientists to study floral organogenesis development through continuous observation under different temperature conditions. These technologies enable real-time stress-induced developmental delay tracking and provide predictive tools for cultivation planning. The integration of phenotypic data with genomic selection models in breeding programs enables breeders to discover genotypes that demonstrate resistance. Temperature determines when flowers bloom and it also determines how well flowers grow and how many flowers will be produced and how consistent the flowers will look. Scientists use these results to build controlled cultivation areas and select plant species that perform best in various environmental settings.

4 Interaction between Light and Temperature Signals

4.1 Synergistic and antagonistic effects of photoperiod and temperature

The flowering in *Rosa chinensis* does not depend solely on photoperiod or temperature but instead comes from the interaction between both environmental signals. The controlled experiments show that the best flowering and highest flower quality occurs when long-day photoperiods coincide with moderate temperatures which shows a synergistic effect. The short-day conditions produce earlier flowering but reduce floral symmetry and pigment accumulation according to Shin et al. (2023).

The interactions depend on cultivar genetics. Research shows that some continuous-flowering cultivars show photoperiod tolerance but remain sensitive to high temperatures. This demonstrates that the photoperiod and temperature regulatory pathways are not completely independent (Wang et al., 2024; Wang et al., 2025). The controlled-environment cultivation studies show that synchronized flowering only occurs when both light and temperature receive precise control which produces optimal commercial results (Figure 2) (Wang et al., 2024).

The mismatch between photoperiod and temperature conditions results in different regulatory outcomes. The high night temperatures combined with short days result in high *RcCO* levels but reduced *RcFT* expression because of signal competition. The cool temperatures combined with long-day photoperiods result in ideal plant development. The current research shows that proper flowering requires signal coordination across both conditions at specific times.

4.2 Crosstalk in molecular networks: PHY-PIF-SOC1-FT integration

The molecular integration of light and temperature occurs through *PHY-PIF-SOC1-FT* networks which use shared transcriptional regulators. The phytochromes (*PHYs*), especially *PHYA*, control *RcCO-RcFT* signaling together with temperature-dependent factors. The PHYs work together with phytochrome-interacting factors (*PIFs)* to connect temperature and light signals to regulate flowering activators and repressors (Sun et al., 2021).

The RcPIF proteins suppress *RcCO* activity especially under high temperatures and low light conditions. The *RcPHYA* activity under favorable light conditions reduces *PIF* activity and relieves suppression of *RcFT*. The downstream integrator *RcSOC1* acts as a central node which combines light and temperature inputs to start flowering.

Transcriptome studies confirm that *RcHsfA6* expression under heat stress affects *RcPIF* stability and activity while *RcCRY2* blue-light responses stabilize *RcCO* which relieve the effects of heat. RNA-Seq shows a circadian-light-temperature regulatory hub that coordinates environmental signals to determine floral gene expression. Researchers also identify long noncoding RNAs (lncRNAs) which regulate *RcFT* and *RcSOC1* chromatin accessibility which enables the system to maintain stability across environmental gradients.

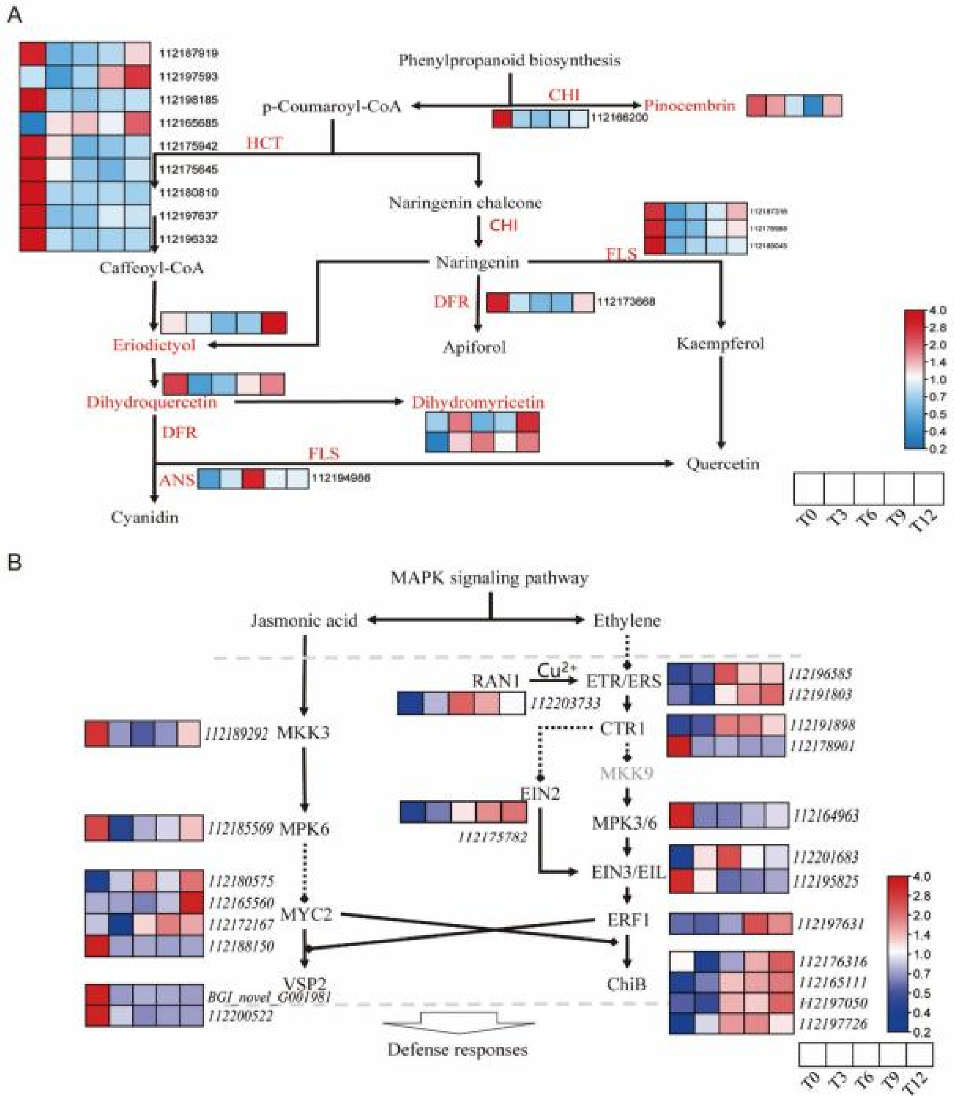

Figure 2 The pathways of flavonoid biosynthesis and MAPK signaling pathway response to heat stress (Adopted from Wang et al., 2024)

Image caption: (A) The flavonoid biosynthesis pathways. HCT: shikimate O-hydroxycinnamoyltransferase; FLS: flavonol synthase; DFR: bifunctional dihydroflavonol 4-reductase/flavanone 4-reductase; ANS: anthocyanidin synthase; CHI: chalcone isomerase. (B) The MAPK signaling pathway. MKK3: mitogen-activated protein kinase kinase 3; MPK6: mitogen-activated protein kinase 6; MYC2: transcription factor MYC2; VSP2: vegetative storage protein 2; RAN1/copA, P-type Cu + transporter; ETR/ERS: ethylene receptor; CTR1: serine/threonine-protein kinase; MPK3: mitogen-activated protein kinase 3; MPK6: mitogen-activated protein kinase 6; EIN2/3: ethylene-insensitive protein 2/3; ERF1: ethylene-responsive transcription factor 1; ChiB: basic endochitinase B. Log2-scaled FPKM or metabolites content are shown in different time points of leaf (here T0-T12, from left to right in each heatmap panel) are presented in the heatmap alongside the gene id. Low to high expression is indicated by a change in color from blue to red (Adopted from Wang et al., 2024)

4.3 Hypothetical model for rose light-temperature interactions

The evidence supports a model in which photoreceptors and thermosensors combine signals through *RcPIFs* and *RcCO* and *RcSOC1* to regulate *RcFT* expression. The model shows that *RcPHYA* and *RcCRY2* maintain *RcCO* stability under long days and moderate temperatures which allows *RcFT* activation and flowering induction. The floral initiation also requires the suppression of temperature-sensitive regulators such as *RcHsfA6* and *FLC-like* genes (Wang et al., 2025).

Stress conditions increase PIF expression which reduces *RcCO* and *RcFT* activity. Epigenetic regulators such as methylation at *FLC-like* loci also contribute to flowering delays. The dual-input control system provides high levels of flowering plasticity that enables *R. chinensis* to adapt to different climates (Yu et al., 2023).

The model requires validation through experiments such as ChIP to confirm *RcPIF4* binding at the *RcFT* promoter and luciferase reporter assays to test *RcCO-RcFT* activation under different conditions. Scientists also require transgenic lines with *RcPIFs* and *RcPHYA* and *FLC-like* knockouts and overexpression to test the architecture of the network. The potential outcome includes the use of molecular breeding and biotechnological techniques to produce stress-resistant cultivars which demonstrates a sustainable path for rose production in unstable climates.

5 Controlled Cultivation and Phenotypic Outcomes

5.1 Advantages of controlled cultivation conditions for flowering research

The controlled environments of glasshouse and greenhouse systems allow scientists to investigate flowering control in *Rosa chinensis* with precision because they can manage environmental parameters. The natural outdoor conditions create unavoidable variations in light intensity and photoperiod and temperature across the seasons and weather changes. The controlled systems allow for precise experimental design.

Scientists investigate photoperiodic responses and thermal sensitivities and synchronous flowering through year-round monitoring which cannot occur in outdoor environments (Cola et al., 2020). The controlled systems also eliminate biological stresses such as pathogens which allows researchers to focus on the influence of abiotic signals such as light spectra and temperature gradients. The systems help identify genotype-environment interactions and test hypotheses about flowering time and morphology and quality.

5.2 Phenotypic outcomes under varying light–temperature combinations

The experimental cultivation of *R. chinensis* under different light and temperature conditions produces phenotypic changes. Plants flower more profusely with larger and more uniform blooms when grown under long-day photoperiods and moderate temperatures. Short-day photoperiods combined with high temperatures cause flowers to develop reduced symmetry and less pigment accumulation according to Wang et al. (2024).

The use of LED lighting systems allows researchers to control light quality manually. The enriched far-red and blue spectra induce specific flowering results. The research demonstrates that these technologies accelerate floral induction and extend vase life for cut roses (*Rosa hybrida*) (Trivellini et al., 2023).

5.3 Implications for year-round flowering and commercial production

The cultivation studies provide significant commercial implications for rose production. The combination of optimized light spectra and temperature buffering systems allows producers to control flowering across different seasons which guarantees continuous supply to meet consumer demand (Sapounas et al., 2020; Hu and You, 2022). These practices reduce energy waste and improve resource efficiency because they often integrate data-driven climate control and renewable energy sources. Controlled cultivation not only serves as a scientific tool but also as a practical requirement for sustainability in high-value horticultural production.

6 Case Study: Flowering Management at the Royal Botanic Gardens, Kew

6.1 Case context

The Royal Botanic Gardens, Kew in London represents one of the most prominent botanical institutions in the world which combines scientific research with conservation and public education. The rose garden forms a central feature during the summer months and attracts high visitor numbers during peak flowering. The flowering management at Kew provides a practical case of environmental control science in action which shows how laboratory findings apply to public garden management.

The model plant *Arabidopsis thaliana* provides a clear understanding of flowering processes through genetic pathways including photoperiodic and vernalization and gibberellin signaling. The *CONSTANS (CO)* gene activates *FLOWERING LOCUS T (FT)* under long-day conditions which then acts as a mobile florigen that moves from leaves to meristems to interact with *FD* to activate *SOC1* and *LFY* which initiates floral identity (Antoniou-Kourounioti et al., 2018; Gendron and Staiger, 2023).

These modules exist in roses and other ornamentals as well. *RcCO*, *RcFT* and *RcSOC1* homologs show similar responses to environmental cues. The practice at Kew benefits from these findings since its light and thermal systems align with the genetic activation times for flowering. The public gardens serve as living laboratories where environmental management connects with genetic knowledge to deliver synchronized floral displays for both education and conservation.

6.2 Management practices

Multiple flowering genes in roses have been identified and functionally characterized. Genomic and transcriptomic studies show that *RcCO*, *RcCOL4*, *RcFT1*, and *RcFT2* express in leaf and shoot apical meristem tissues with photoperiodic dependence (Lu et al., 2020; Sun et al., 2021). *RcCO* expresses highly under long-day conditions with *RcGI* and *RcFKF1* regulation. *RcCOL4* expresses during short days which compensates for reduced *RcCO* expression. *RcFT1* functions as the primary florigen gene while *RcFT2* expresses more broadly. Downstream integrators *RcSOC1a/b* function as central nodes.

Different cultivars show variation at *RoKSN* and *RcFLC-like* loci. Continuous-flowering cultivars lost repressor activity which resulted in perpetual flowering. Epigenetic processes also contribute because temperature variations induce DNA methylation and histone modifications especially at *RcFLC-like* sites. Yu et al. (2023) demonstrate that heat signals increase H3K27me3 marks similar to the cold-induced repression in Arabidopsis. Small RNAs including siRNAs and lncRNAs may also regulate *RcSOC1* and *RcFLC-like* chromatin states under stress.

Photoreceptors and thermosensors regulate these flowering behaviors. *RcCRY2* stabilizes *RcCO* under blue light to promote *FT* activation. *RcPIF4* accumulates during heat stress to repress *RcFT* expression. The system allows *R. chinensis* to adjust flowering with flexibility under variable environmental conditions.

6.3 Practical outcomes

Kew greenhouse experiments confirm the environmental effects on rose flowering gene expression and phenotypes. The combined light and temperature control shortened flowering by 6~8 days and extended display duration by 10~14 days compared to conventional greenhouses (Cola et al., 2020; Sapounas et al., 2020). The treatments altered *RcFT1*, *RcSOC1*, and *RcPIF4* expression patterns and produced significant phenotype improvements for both commercial and public display applications.

Kew combines intelligent sensors and exhibition data to phenotype flowering responses and collaborates with universities to calibrate predictive models of flowering. The gardens function as research-grade testing facilities that transform gene regulatory networks into applied horticultural outcomes (Cola et al., 2020).

The integrated management system allows Kew to align rose flowering with public events. The system ensures dense and colorful floral displays which support education and visitor engagement. The environmental controls extend flower longevity and reduce stress damage. Kew uses the facilities to test new cultivars and climate resilience which links research with practice.

The Kew case shows how light-temperature control systems provide practical horticultural outcomes. The horticultural staff combine environmental control with phenological knowledge and cultivar-specific responses to deliver floral displays which are both aesthetically reliable and stable. The case demonstrates that the application of molecular and physiological research to public garden management produces dependable results. The case places botanical gardens as bridges between science and society.

7 Genetic and Molecular Basis of Flowering Control

7.1 Key genes: *RcCO, RcFT, RcSOC1, FLC-like, PIFs*

The flowering of *Rosa chinensis* depends on multiple environmental cues which activate or repress specific transcription factors that control gene expression. The plant uses a network similar to Arabidopsis which involves *RcCO*, *RcFT, RcSOC1*, FLC-like repressors, and *RcPIFs*. *RcCO* activates *RcFT* whose expression determines floral transition (Lu et al., 2020). RcSOC1 integrates light and thermal and hormonal signals and expresses highly under long-day and moderate temperatures to drive flowering (Sun et al., 2021).

The *FLC-like* genes in roses act as repressors of flowering though their mechanisms differ from Arabidopsis. They do not depend on long-term vernalization but instead link to environmental stress and epigenetic modifications (Yu et al., 2023). *RcPIF4* and *RcPIF5* suppress *RcCO* and *RcFT* under high temperature and low light. They also function in photomorphogenesis and thermal responses which makes them potential breeding targets (Sun et al., 2021; Yu et al., 2023; Lu et al., 2024; Kang et al., 2024).

7.2 Transcriptional regulatory networks integrating light and temperature signals

Genomic and transcriptomic studies show that these flowering regulators belong to a broader network which contains feedback loops and convergence points. *RcCO* expression follows circadian rhythms but its amplitude depends on phytochrome light quality. *RcPIFs* respond to temperature and serve as downstream effectors of heat shock factors.

The transcriptome sequencing of *Rosa chinensis* under heat stress reveals coexpression relationships between *RcPIF4*, *RcHSP70*, and *RcFT* which suggests coordinated regulation of thermotolerance and flowering (Wang et al., 2024). Research also highlights the importance of noncoding RNAs. Long noncoding RNAs such as lncWD83 regulate flowering by altering post-translational states of MYC2 proteins (Chen et al., 2023).

Epigenetic regulation also plays a major role. The expression of *RcFT* and *FLC*-like loci depends on histone modifications and DNA methylation which respond dynamically to environmental stresses. The rose plant adjusts flowering timing by modulating these marks which enables plasticity for survival (Yu et al., 2023).

7.3 Breeding applications: marker-assisted selection and CRISPR editing strategies

The genomic studies of *Rosa chinensis* support new breeding methods. Molecular markers for *RcFT, RcCO*, *RcSOC1*, and *RoKSN* allow rapid identification of traits such as continuous flowering, floral uniformity, and thermotolerance which accelerates breeding cycles (Soufflet-Freslon et al., 2021). Transcriptome-wide association studies (TWAS) and expression QTL mapping identify critical regulators. Epigenetic selection appears promising because heritable DNA methylation at FLC-like genes influences flowering under stress (Yu et al., 2023).

CRISPR/Cas9 genome editing now applies in rose breeding. Researchers target *RcPIF4*, *RcCO, RcFT*, and remove repressors like *RoKSN* to produce early-flowering and repeat-flowering plants which resemble domesticated cultivars. The technology faces limitations such as low tissue regeneration efficiency. Scientists improve success by adjusting hormone levels and using somatic embryogenesis. Non-transgenic editing methods such as ribonucleoprotein delivery and base editing increase acceptance.

Regulatory frameworks vary. The United States and Japan permit fast approval for non-transgenic edited crops while the European Union applies GMO regulations. Consumer perception matters for commercialization. High-value ornamental markets demand aesthetic traits which gene editing can deliver. The integration of marker-assisted selection, high-throughput genotyping, and CRISPR will transform rose breeding by producing cultivars adapted to climates and cultivation systems.

8 Conclusion, Implications, and Future Outlook

8.1 Breeding and horticultural implications

The need for climate-resilient rose cultivars becomes more critical because of climate change. The stability of flower production under heat stress and photoperiod changes depends on four main molecular targets which include *RcCO*, *RcFT*, *RcPIFs and RoKSN*. The combination of marker-assisted selection with multi-omics data enables better thermotolerance prediction and CRISPR-based non-transgenic genome editing shortens breeding times and boosts public acceptance of new crop varieties. The strategies link sustainability to market competitiveness through their ability to meet consumer floral design needs while building business resilience.

Scientists transform genetic and environmental data into sustainable garden designs through their application of horticultural practices. LED lighting systems that work with renewable heating and automated irrigation systems create climate-adaptive gardens which achieve optimal resource management. The Kew case study shows how synchronized flower displays create educational benefits and improve visitor experiences and conservation efforts which can serve as a model for worldwide adaptation programs.

8.2 Integrated conclusion

Research on *Rosa chinensis* shows that *RcCO–RcFT–RcSOC*1 networks receive light and temperature signals which are detected by *RcPHYA, RcCRY2*, *RcPIF4* and *RcHsfA6*. The expression of floral symmetry along with fragrance and longevity depends on how genetic makeup interacts with environmental conditions. The controlled cultivation systems which match environmental signals to genetic pathways produce synchronized and predictable flowering patterns that benefit both scientific research and commercial farming operations.

8.3 Future outlook and challenges

The development of future breeding depends on uniting transcriptomic and epigenomic and metabolomic and phenomic data to generate predictive systems biology models. The implementation of machine learning and AI models for cultivar performance forecasting requires maintaining genetic diversity to prevent uniformity risks. The speed of commercialization depends on regulatory frameworks because fast approval of gene-edited ornamentals would enable companies to achieve global market leadership. Public acceptance requires successful public engagement to achieve its goals. The exact control methods used for rose flowering can serve as a model to improve other ornamental plants while maintaining molecular breeding and environmental control for sustainable horticulture under climate change conditions.

Acknowledgments

Thank supervisors, colleagues, and my family for their guidance and support during this research.

Conflict of Interest Disclosure

The authors affirm that this research was conducted without any commercial or financial relationships that could be construed as a potential conflict of interest.

Reference

Antoniou-Kourounioti R.L., Hepworth J., Heckmann A., Duncan S., Qüesta J., Rosa S., Säll T., Holm S., Dean C., and Howard M., 2018, Temperature sensing is distributed throughout the regulatory network that controls FLC epigenetic silencing in vernalization, Cell Systems, 7(6): 643-655.
https://doi.org/10.1016/j.cels.2018.10.011

Chen Y., Lu J., Wang W., Fan C., Yuan G., Sun J., Liu J., and Wang C., 2023, Rose long noncoding RNA lncWD83 promotes flowering by modulating ubiquitination of the floral repressor RcMYC2L, Plant Physiology, 193(4): 2573-2591.
https://doi.org/10.1093/plphys/kiad502

Cola G., Mariani L., Toscano S., Romano D., and Ferrante A., 2020, Comparison of greenhouse energy requirements for rose cultivation in Europe and North Africa, Agronomy, 10(3): 422.
https://doi.org/10.3390/agronomy10030422

Gendron J.M., and Staiger D., 2023, New horizons in plant photoperiodism, Annual Review of Plant Biology, 74: 481-509.
https://doi.org/10.1146/annurev-arplant-070522-055628

Guo X., Yu C., Luo L.E., Wan H., Li Y., Wang J., Sung T., Pan H., and Zhang Q., 2017, Comparative transcriptome analysis of the floral transition in *Rosa chinensis* 'Old Blush' and *R. odorata* var. *gigantea*, Scientific Reports, 7: 6068.
https://doi.org/10.1038/s41598-017-05850-8

Han Y., Tang A., Wan H., Zhang T., Sung T., Wang J., Yang W., Pan H., and Zhang Q., 2018, An *APETALA2* homolog, *RcAP2*, regulates the number of rose petals derived from stamens and response to temperature fluctuations. Frontiers in Plant Science, 9: 481. https://doi.org/10.3389/fpls.2018.00481

Han Y., Tang A., Yu J., Sung T., Wang J., Yang W., Pan H., and Zhang Q., 2019, *RcAP1*, a homolog of *APETALA1*, is associated with flower bud differentiation and floral organ morphogenesis in *Rosa chinensis*, International Journal of Molecular Sciences, 20(14): 3557. https://doi.org/10.3390/ijms20143557

Hibrand Saint-Oyant L., Ruttink T., Hamama L., Kirov I., Lakhwani D., Zhou N., Bourke P.M., Daccord N., Leus L., Schulz D., van de Geest H., Hesselink T., Van Laere K., Debray K., Balzergue S., Thouroude T., Chastellier A., Jeauffre J., Voisine L., Gaillard S., Borm T.J.A., Arens P., Voorrips R.E., Maliepaard C., Neu E., Linde M., Le Paslier M.C., Bérard A., Bounon R., Clotault J., Choisne N., Quesneville H., Kawamura K., Aubourg S., Sakr S., Smulders M.J.M., Schijlen E., Bucher E., Debener T., De Riek J., and Foucher F., 2018, A high-quality sequence of *Rosa chinensis* to elucidate genome structure and ornamental traits, Nature Plants, 4: 473-484. https://doi.org/10.1038/s41477-018-0166-1

Hu G., and You F., 2022, Renewable energy-powered semi-closed greenhouse for sustainable crop production using model predictive control and machine learning for energy management, Renewable and Sustainable Energy Reviews, 168: 112790. https://doi.org/10.1016/j.rser.2022.112790

Jiang C., Bi Y., Zhang R., and Feng S., 2020, Expression of *RcHSP70*, heat shock protein 70 gene from Chinese rose, enhances host resistance to abiotic stresses, Scientific Reports, 10: 2445. https://doi.org/10.1038/s41598-020-58745-6

Kang Y., Sun P., Yang Y., Li M., Wang H., Sun X., and Jin W., 2024, Genome-wide analysis of the Hsf gene family in *Rosa chinensis* and *RcHsf17* function in thermotolerance, International Journal of Molecular Sciences, 26(1): 287. https://doi.org/10.3390/ijms26010287

Lu J., Sun J., Jiang A., Bai M., Fan C., Liu J., Ning G., and Wang C., 2020, Alternate expression of *CONSTANS-LIKE 4* in short days and *CONSTANS* in long days facilitates day-neutral response in *Rosa chinensis*, Journal of Experimental Botany, 71(14): 4057-4068. https://doi.org/10.1093/jxb/eraa161

Lu J., Wang W., Fan C., Sun J., Yuan G., Guo Y., Yu X., Chang Y., Liu J., and Wang C., 2024, Telo boxes within the *AGAMOUS* second intron recruit histone 3 lysine 27 methylation to increase petal number in rose in response to low temperatures, The Plant Journal, 118(5): 1486-1499. https://doi.org/10.1111/tpj.16691

Ouyang L., Leus L., De Keyser E., and Van Labeke M.C., 2022, Temperature is an important driver for cold acclimation in garden roses, Scientia Horticulturae, 296: 110905. https://doi.org/10.1016/j.scienta.2022.110905

Owen W.G., Meng Q., and Lopez R.G., 2018, Promotion of flowering from far-red radiation depends on the photosynthetic daily light integral, HortScience, 53(4): 465-471. https://doi.org/10.21273/HORTSCI12544-17

Raymond O., Gouzy J., Just J., Badouin H., Verdenaud M., Lemainque A., Vergne P., Moja S., Choisne N., Pont C., Carrère S., Caissard J., Couloux A., Cottret L., Aury J., Szécsi J., Latrasse D., Madoui M.A., François L., Fu X., Yang S.H., Dubois A., Piola F., Larrieu A., Perez M., Labadie K., Perrier L., Govetto B., Labrousse Y., Villand P., Bardoux C., Boltz V., Lopez-Roques C., Heitzler P., Vernoux T., Vandenbussche M., Quesneville H., Boualem A., Bendahmane A., Liu C., Le Bris M., Salse J., Baudino S., Benhamed M., Wincker P., and Bendahmane M., 2018, The *Rosa* genome provides new insights into the domestication of modern roses, Nature Genetics, 50: 772-777. https://doi.org/10.1038/s41588-018-0110-3

Sapounas A., Katsoulas N., Slager B., Bezemer R., and Lelieveld C., 2020, Design, control, and performance aspects of semi-closed greenhouses, Agronomy, 10(11): 1739. https://doi.org/10.3390/agronomy10111739

Shin Y.C., Yeon J.Y., and Kim W.S., 2023, Influence of suboptimal temperature on flower quality and floral organ development in spray-type cut rose 'Pink Shine', Horticulturae, 9(8): 861. https://doi.org/10.3390/horticulturae9080861

Soufflet-Freslon V., Araou E., Jeauffre J., Thouroude T., Chastellier A., Michel G., Mikanagi Y., Kawamura K., Banfield M., Oghina-Pavie C., Clotault J., and Pernet A., and Foucher F., 2021, Diversity and selection of the continuous-flowering gene, *RoKSN*, in rose, Horticulture Research, 8: 76. https://doi.org/10.1038/s41438-021-00512-3

Sun J., Lu J., Bai M., Chen Y., Wang W., Fan C., Liu J., Ning G., and Wang C., 2021, Phytochrome-interacting factors interact with transcription factor CONSTANS to suppress flowering in rose, Plant Physiology, 186(2): 1186-1201. https://doi.org/10.1093/plphys/kiab109

Trivellini A., Toscano S., Romano D., and Ferrante A., 2023, LED lighting to produce high-quality ornamental plants, Plants, 12(8): 1667. https://doi.org/10.3390/plants12081667

Wang H., Xu W., Zhang X., Wang L., Jia S., Zhao S., Li W., Lu R., Ren A., and Zhang S., 2024, Transcriptomics and metabolomics analyses of *Rosa hybrida* to identify heat stress response genes and metabolite pathways, BMC Plant Biology, 24: 874. https://doi.org/10.1186/s12870-024-05543-1

Wang W., Sun J., Fan C., Yuan G., Zhou R., Lu J., Liu J., and Wang C., 2025, RcSRR1 interferes with the RcCSN5B-mediated deneddylation of RcCRL4 to modulate RcCO proteolysis and prevent rose flowering under red light, Horticulture Research, 12(5): uhaf025. https://doi.org/10.1093/hr/uhaf025

Whitman C., Padhye S., and Runkle E.S., 2022, A high daily light integral can influence photoperiodic flowering responses in long day herbaceous ornamentals, Scientia Horticulturae, 295: 110897.
https://doi.org/10.1016/j.scienta.2022.110897

Yu R., Xiong Z., Zhu X., Feng P., Hu Z., Fang R., and Liu Q., 2023, RcSPL1-RcTAF15b regulates the flowering time of rose (*Rosa chinensis*), Horticulture Research, 10(6): uhad083.
https://doi.org/10.1093/hr/uhad083