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Comparative transcriptome analysis of the floral transition in *Rosa chinensis* 'Old Blush' and *R. odorata* var. *gigantea*

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The floral transition is a crucial developmental event, but little is known about the underlying regulatory networks in seasonally and continuously flowering roses. In this study, we compared the genetic basis of flowering in two rose species, *Rosa chinensis* 'Old Blush', which flowers continuously, and *R. odorata* var. *gigantea*, which blooms in early spring. Gene ontology (GO) terms related to methylation, light reaction, and starch metabolism were enriched in *R. odorata* var. *gigantea* and terms associated with sugar metabolism were enriched in *R. chinensis* 'Old Blush' during the floral transition. A MapMan analysis revealed that genes involved in hormone signaling mediate the floral transition in both taxa. Furthermore, differentially expressed genes (DEGs) involved in vernalization, photoperiod, gibberellin (GA), and starch metabolism pathways converged on integrators, e.g., *LFY*, *AGL24*, *SOC1*, *CAL*, and *COLs*, to regulate the floral transition in *R. odorata* var. *gigantea*, while DEGs related to photoperiod, sugar metabolism, and GA pathways, including *COL16*, *LFY*, *AGL11*, *6PGDH*, *GASA4*, and *BAM*, modulated the floral transition in *R. chinensis* 'Old Blush.' Our analysis of the genes underlying the floral transition in roses with different patterns of flowering provides a basis for further functional studies.

The floral transition is an important developmental event orchestrated by external and developmental stimuli; for example, photoperiod, vernalization, autonomous, aging, gibberellin (GA), and sugar metabolism pathways[1, 2] interact to activate or inhibit the floral transition via a small set of floral integrators, including *FLOWERING LOCUS T* (*FT*), *CONSTANS-LIKE* (*COL*), *SUPPRESSOR OF OVEREXPRESSION OF CO1* (*SOC1*), *FLOWERING LOCUS C* (*FLC*), and floral meristem identity genes, e.g., *LEAFY* (*LFY*), *APETALA1* (*AP1*), *AGAMOUS-LIKE* (*AGL*), *CAULIFLOWER* (*CAL*), and *SEPALLATA* (*SEP*).

Considerable progress has been made toward identifying the molecular networks underlying the floral transition in the annual plant *Arabidopsis thaliana*[3]. However, relatively little is known about the regulation of the floral transition in perennial plants. In perennials, only a portion of buds have competence to complete the phase transition from vegetative to reproductive growth in inductive conditions, while others remain in vegetative growth, indicating the ability to revert back from reproductive to vegetative growth. In temperate regions, most perennials require a period of winter cold (vernalization) to induce the floral transition and show seasonal flowering. However, a small number of perennials, such as *Rosa chinensis* and *Fragaria vesca*, can flower continuously in advantageous environmental conditions. The duration of flowering is crucial for the value of ornamental plants, such as modern roses and chrysanthemums.

Some progress has been made in understanding flowering perennials. Vernalization and sugar metabolism, which interacts with ABA signaling and aging pathways, are key factors inducing the floral transition in *Malus × domestica*[4, 5]. The photoperiod-mediated *CO/FT* modules function as activators in the induction of the floral transition in chrysanthemums and poplars[6, 7]. Different from other species in the genus *Camellia*, the floral transition in *C. azalea* occurs in the spring; it is regulated by low temperatures, photoperiod, and hormone

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