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Transcriptome of the floral transition in *Rosa chinensis* 'Old Blush'

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Abstract

Background: The floral transition plays a vital role in the life of ornamental plants. Despite progress in model plants, the molecular mechanisms of flowering regulation remain unknown in perennial plants. *Rosa chinensis* 'Old Blush' is a unique plant that can flower continuously year-round. In this study, gene expression profiles associated with the flowering transition were comprehensively analyzed during floral transition in the rose.

Results: According to the transcriptomic profiles, 85,663 unigenes and 1,637 differentially expressed genes (DEGs) were identified, among which 32 unigenes were involved in the circadian clock, sugar metabolism, hormone, and autonomous pathways. A hypothetical model for the regulation of floral transition was proposed in which the candidate genes function synergistically the floral transition process. Hormone contents and biosynthesis and metabolism genes fluctuated during the rose floral transition process. Gibberellins (GAs) inhibited rose floral transition, the content of GAs gradually decreased and *GA2ox* and *SCL13* were upregulated from vegetative (VM) meristem to floral meristem (FM). Auxin plays an affirmative part in mediating floral transition, auxin content and auxin-related gene expression levels were gradually upregulated during the floral transition of the rose. However, ABA content and ABA signal genes were gradually downregulated, suggesting that ABA passively regulates the rose floral transition by participating in sugar signaling. Furthermore, sugar content and sugar metabolism genes increased during floral transition in the rose, which may be a further florigenic signal that activates floral transition. Additionally, *FRI*, *FY*, *DRM1*, *ELIP*, *COP1*, *CO*, and *COL16* are involved in the circadian clock and autonomous pathway, respectively, and they play a positively activating role in regulating floral transition. Overall, physiological changes associated with genes involved in the circadian clock or autonomous pathway collectively regulated the rose floral transition.

Conclusions: Our results summarize a valuable collective of gene expression profiles characterizing the rose floral transition. The DEGs are candidates for functional analyses of genes affecting the floral transition in the rose, which is a precious resource that reveals the molecular mechanism of mediating floral transition in other perennial plants.

Keywords: Floral transition, Circadian clock, Sugar signaling, Hormone signaling, Recurrent flowering, Differentially expressed genes

Background

Roses have been used as garden ornamental plants and cut flowers for centuries, which are characterized by recurrent flowering; however, little is known about the genetic and molecular basis of the floral transition in the species. The timing of the floral transition is mediated by complex regulatory networks that constantly monitor environmental and endogenous cues.

Enormous progress has been made in research on the genetic, epigenetic and environmental factors that trigger the transition from vegetative growth to flowering in the model plant *Arabidopsis thaliana*. Environmental factors, photoperiod, and vernalization pathways mediate the transition to flowering in cooperation with diverse exogenous cues, including autonomous, gibberellin (GA), trehalose-6-phosphate (T6P), and age-dependent pathways [1, 2]. In combination, all these pathways converge to mediate a set of "floral integrator genes,"

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