Dissecting cis-Regulation of FLOWERING LOCUS T

Flowering in many plants is strongly influenced by daylength. Arabidopsis thaliana FLOWERING LOCUS T (FT) encodes a small peptide that is now widely recognized as a major component of florigen, a systemic signal that induces flowering in response to daylength (Turck et al., 2008). FT is expressed in phloem companion cells, and the protein is translocated through the phloem to the shoot apical meristem, where it promotes the transition to flowering by inducing the expression of other floral induction genes, such as SOC1 and AP1. Transcriptional activation of FT under inductive daylength conditions is mediated by CONSTANS (CO), which is itself regulated by a complex interplay of signals in the photoperiod pathway. In a new study, Adrian et al. (pages 1425–1440) analyze the promoter region of FT to define the minimal promoter sufficient to mediate expression of FT in response to daylength and is crucial for regulation of FT by CO. A short block of the promoter 1.0 kb upstream of the start site contains key regulatory elements required to mediate expression of FT in response to daylength and is crucial for regulation of FT by CO. A short block of the promoter 1.0 kb upstream of the start site retained residual activity, and transient assays using reporter constructs with point mutations in block A elements in the context of the 1.0-kb FT promoter suggested that these elements also contribute to cis-regulation of FT.

Further experiments teased out other facets of the FT promoter, in particular properties of chromatin structure and promoter activity. The authors first employed a technique known as phylogenetic shadowing to identify putative regulatory sequences by aligning sequences upstream of FT in Arabidopsis thaliana accession Columbia to the same regions from the accession Landsberg erecta and homologous genes from the closely related species Arabidopsis lyrata, Brassica rapa, and Arabis alpina. This led to the identification of three putative regulatory regions, blocks A–C (see figure). Functional analysis of these regulatory regions was performed by generating a set of deletion constructs and testing complementation of an ft mutant line that remains late flowering under inductive long-day conditions. This showed that the conserved block C 5.7 kb upstream of the translation start site contains key regulatory elements required to mediate expression of FT in response to daylength and is crucial for regulation of FT by CO. A short block of the promoter 1.0 kb upstream of the start site retained residual activity, and transient assays using reporter constructs with point mutations in block A elements in the context of the 1.0-kb FT promoter suggested that these elements also contribute to cis-regulation of FT. Conservation of FT promoter sequences. A pairwise alignment of FT promoter sequences from different species to the 7.0-kb FT promoter sequence of A. thaliana Col. Light-gray areas highlight highly conserved blocks.

REFERENCES


