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IN BRIEF

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 the response to daylength and identify several key regions that play a role in *FT* 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 *A. 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*.

Further experiments teased out other facets of the *FT* promoter, in particular properties of chromatin structure mediated by the chromo domain chromatin-associated protein *LIKE HETERCHROMATIN PROTEIN1* (*LHP1*; also known as *TERMINAL FLOWER2*). *LHP1* is known to negatively influence *FT* expression, since *lhp1* mutants show daylength-independent early flowering due to upregulation of *FT* expression (Kotake et al., 2003). Adrian et al. used a variety of mutants and overexpressors of *LHP1*, together with high-resolution chromatin mapping at the *FT* locus by ChIP-chip experiments, to show that chromatin changes in the *FT* promoter are correlated with its transcriptional state. The results suggest that a reduction in LHP1 binding plays a permissive role at the *FT* locus (i.e., by maintaining chromatin in an open conformation accessible to regulatory factors). The authors further found that chromatin changes during *FT* induction seem to be a delayed response instead of a prerequisite for *FT* transcription. Following the initial CO-mediated induction of *FT*, a loss of repressive chromatin from the entire *FT* promoter could lead to a progressively enhanced flowering response over time. These results provide insight into the interplay between LHP1 and CO in the photoperiod-mediated regulation of *FT* in *Arabidopsis*.

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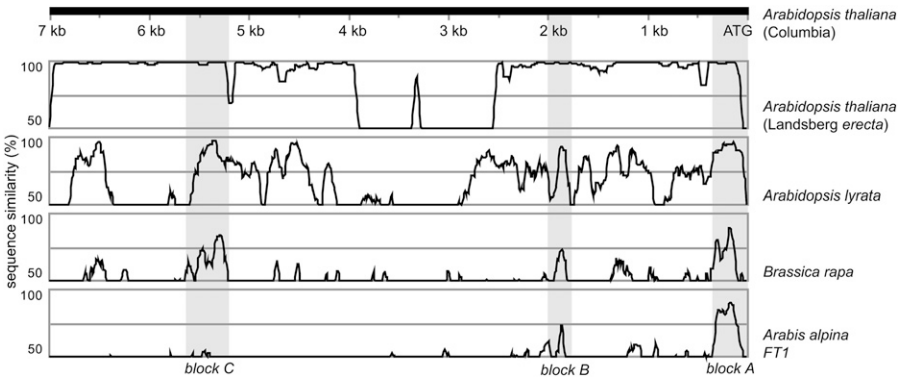

Conservation of *FT* promoter sequences. A pairwise alignment of *FT* promoter sequences from different species to the 7.0-kb *FT* promoter sequence of *A. thaliana* Col. Light-gray areas highlight highly conserved blocks.

REFERENCES

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