

Gene regulation

3

OM3.1 ALTERNATIVE SPLICING OF FLOWERING LOCUS M AND THE TEMPERATURE DEPENDENCE OF FLOWERING TIME

Many *Arabidopsis* accessions flower more rapidly at the higher temperature of 27°C than they do at the moderate temperature of 23°C. Characterization of mutants in which flowering is always rapid, even at 23°C, revealed that the transcription factor FLM (FLOWERING LOCUS M) is required for slower flowering at lower temperatures. FLM and another transcription factor SVP (SHORT VEGETATIVE PHASE) form a repressive complex that delays flowering at moderate temperatures, by binding to the promoters of key flowering-time regulatory genes.

As temperature increases, the profile of splice variants generated from FLM changes (Figure OM3.1-1). The dominant variant at lower temperatures is *FLM-β*, in which exon 3 is skipped during mRNA processing. The protein product of *FLM-β* can form repressive complexes with SVP that prevent expression of flowering-time genes. As temperature increases, the abundance of other splice variants increases, in particular *FLM-δ* in which exon 2 instead of exon 3 is skipped. The protein product of *FLM-δ* can form a complex with SVP, but the complex does not bind to promoters of flowering-time genes so flowering can occur.

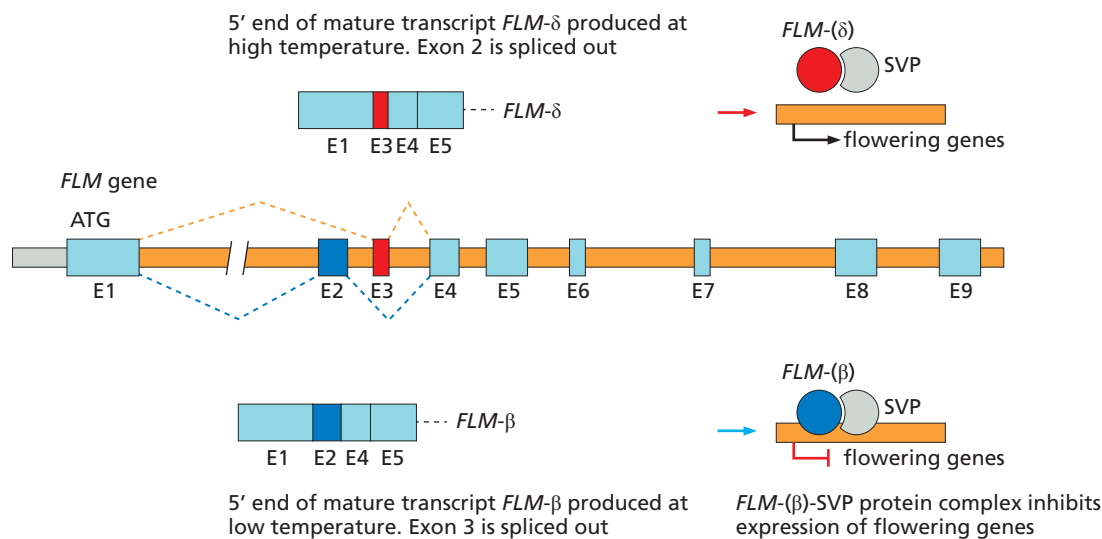


Figure OM3.1-1 Control of flowering by temperature-dependent alternate splicing. *FLM* and *SVP* encode MADS-domain transcription factors. They interact to form a **transcription repressor** complex that regulates genes required for the developmental transition from vegetative to reproductive growth. Depending on the **ambient** temperature, different exons are selected through alternative splicing as the second exon of *FLM*, resulting in the production of *FLM-β* and *FLM-δ* proteins at low and high temperature, respectively. The patterns of alternative splicing that result in exclusion of introns 3 or 2 giving rise to *FLM-β* and *FLM-δ*, respectively, are shown by the blue and orange dashed lines (central part of figure). At lower temperatures (bottom) SVP/*FLM-β* binds to the promoters of flowering genes to inhibit flowering. At higher temperatures (top), SVP/*FLM-δ* does not form a repressive complex and flowering can occur. (Adapted from Gomes E *et al.* (2021) *Front Plant Sci* 12:633846. Distributed under CC BY 4.0.)

Initially, researchers thought that the FLM- δ protein outcompeted the FLM- β protein for FLM-SVP complex formation at higher temperatures, resulting in a decline in the fraction of the complex capable of inhibiting expression of flowering-time genes. However, further research suggested a different explanation. As temperature goes up, the amount of FLM- β goes down as it is increasingly replaced by other splice variants such as FLM- δ . The amount of FLM- β protein declines, so less of the inhibitory form of the FLM-SVP complex can be formed and repression of flowering is relieved. Thus more rapid flowering at higher temperatures results largely from the decline in FLM- β production, rather than from direct effects of other splice variants.

OM3.2 TRANSLATION OF mRNAs AND PROTEIN SYNTHESIS

Initiation factors bound to the 5' cap of the mRNA produced by RNA Pol II load it onto the small subunit of the ribosome (**Figure OM3.2-1**). The small subunit, together with guanosine triphosphate (GTP)-bound initiation factors, scans the mRNA for the AUG **translation start codon** that is recognized by methionine (M or Met) tRNA. When a match is found, GTP is hydrolyzed and the initiation factors dissociate from the small subunit, to which the ribosomal large subunit (LSU) binds. The LSU includes an A site that is occupied by an aminoacyl-tRNA attached to a growing polypeptide chain (shown as M-aa), a P or peptidyl site where successive peptide bonds are formed during protein synthesis, and the exit site (E) for the tRNA after dissociation from its amino acid. During translation, the ribosome moves along the mRNA in the 5'- to 3'-direction one codon (3 nt) at a time, while aminoacyl-tRNA anticodons matching each successive codon progress through the A-P-E sites to build up the polypeptide chain. When one of the three possible **translation termination codons** is reached, the ribosomal subunits release the newly made polypeptide chain and dissociate from the mRNA, which can go through further rounds of translation.

