A cold-responsive FLC-like gene in kiwifruit is regulated by epigenetic mechanisms to control budbreak

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Program theme: Genetics and Epigenetics

Oral

Abstract

Temperate perennials require an extended period of cold temperatures during winter to resume growth in the following spring. Growth and dormancy cycles are governed by complex genetic regulatory networks and may depend on epigenetic mechanisms, although the specific genes and mechanisms remain poorly understood.

We performed RNA-Seq analysis of buds of the woody perennial vine kiwifruit (*Actinidia chinensis*) in the field and controlled conditions to understand how seasonal changes and chilling regulate dormancy and growth. A MADS-box gene with homology to Arabidopsis FLOWERING LOCUS C was identified and characterized.

Elevated expression of AcFLC-like (AcFLCL) was detected during bud dormancy and upon chilling. We also identified a long non-coding (lnc) antisense transcripts with expression pattern opposite to AcFLCL and shorter sense non-coding RNAs. Furthermore, cold exposure induced an increase in trimethylation of lysine-4 of histone H3 (H3K4me3) in the 5' end of the gene, indicating multiple layers of epigenetic regulation in response to chilling. Overexpression of AcFLCL in kiwifruit hastened budbreak, whilst gene editing using CRISPR-Cas9 resulted in transgenic lines with substantially delayed budbreak, suggesting a role as growth activator.

These findings have implications for future management and breeding of perennials in order to enhance their resilience to a changing climate.