



Control of Flowering and Cell Fate by LIF2, an RNA Binding Partner of the Polycomb Complex Component LHP1

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Polycomb Repressive Complexes (PRC) modulate the epigenetic status of key cell fate and developmental regulators in eukaryotes. The chromo domain protein LIKE HETEROCHROMATIN PROTEIN1 (LHP1) is a subunit of a plant PRC1-like complex in *Arabidopsis thaliana* and recognizes histone H3 lysine 27 trimethylation, a silencing epigenetic mark deposited by the PRC2 complex. We have identified and studied an LHP1-Interacting Factor2 (LIF2). LIF2 protein has RNA recognition motifs and belongs to the large hnRNP protein family, which is involved in RNA processing. LIF2 interacts *in vivo*, in the cell nucleus, with the LHP1 chromo shadow domain. Expression of LIF2 was detected predominantly in vascular and meristematic tissues. Loss-of-function of LIF2 modifies flowering time, floral developmental homeostasis and gynoecium growth determination. *lif2* ovaries have indeterminate growth and produce ectopic inflorescences with severely affected flowers showing proliferation of ectopic stigmatic papillae and ovules in short-day conditions. To look at how LIF2 acts relative to LHP1, we conducted transcriptome analyses in *lif2* and *lhp1* and identified a common set of deregulated genes, which showed significant enrichment in stress-response genes. By comparing expression of LHP1 targets in *lif2*, *lhp1* and *lif2 lhp1* mutants we showed that LIF2 can either antagonize or act with LHP1. Interestingly, repression of the FLC floral transcriptional regulator in *lif2* mutant is accompanied by an increase in H3K27 trimethylation at the locus, without any change in LHP1 binding, suggesting that LHP1 is targeted independently from LIF2 and that LHP1 binding does not strictly correlate with gene expression. LIF2, involved in cell identity and cell fate decision, may modulate the activity of LHP1 at specific loci, during specific developmental windows or in response to environmental cues that control cell fate determination. These results highlight a novel link between plant RNA processing and Polycomb regulation.

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