REGULATION OF FLOWING BY HDA6 IN ARABIDOPSIS

Keqiang Wu and Chun-Wei Yu

Institute of Plant Biology, College of Life Science, National Taiwan University, Taipei 10617, Taiwan

ABSTRACT
Posttranslational modifications of histones including acetylation play a key role in modulating dynamic changes in chromatin structure and gene activity. The reversible acetylation and deacetylation of specific lysine residues on core histone N-terminal tails is catalyzed by histone acetyltransferases (HATs) and deacetylases (HDACs). The competing action of both enzymes generates patterns of acetylation that may specify downstream biological processes such as transcriptional regulation. In general, hyperacetylated histones are associated with gene activation, whereas hypoacetylated histones are related to gene repression. Recent work has demonstrated that histone acetylation is an integral part of transcriptional regulatory systems in yeast and animal cells. Limited information is available regarding the involvement of HDACs in plants. HDA6 is a RPD3-type HDAC in Arabidopsis. The Arabidopsis hda6 mutant, axe1-5, and HDA6 RNA-interfering (HDA6-RNAi) plants displayed late-flowering. The expression of FLC was upregulated and hyperacetylated in axe1-5 and HDA6-RNAi plants, suggesting that HDA6 is required to deacetylate FLC chromatin and thereby repress its expression. Our results suggest that HDA6 is involved in flowering in Arabidopsis.