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Upstream regulatory mechanisms of a cold-induced epigenetic switch in plants

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Proper timing of the flowering transition in plants is a key developmental process necessary for adaptation to various ecological niches. Many plant species require exposure to the prolonged cold of winter to flower, a temperature-sensing process referred to as vernalization. In *Arabidopsis thaliana*, prolonged exposure to cold epigenetically represses the expression of a floral repressor, *Flowering Locus C (FLC).* This cold-mediated repression occurs through an evolutionarily conserved Polycomb repressive complex 2 (PRC2) associated with the vernalization-unique protein Vernalization Insensitive 3 (VIN3) and long noncoding RNAs (lncRNAs) complementary to *FLC*. The vernalization-specific PRC2 complex results in increased deposition of an epigenetic silencing mark H3K27me3 at *FLC* chromatin. However, the system by which cold perception leads to the induction of vernalization-specific factors involved in FLC targeting is largely unknown. In this study, we describe the first example of a vernalization-hypersensitive mutant in which the period of cold exposure required to saturate the vernalization response is shortened. This is also the first example of a potential upstream regulator of VIN3 and lncRNAs complementary to *FLC*. The causative locus encodes a methyltransferase, Set Domain Group7 (SDG7) that is required for proper timing of expression of vernalization specific factors in cold-induced polycomb silencing. In summary, our work is an important contribution to the understanding of how environmental signals result in epigenetic gene silencing.

Biography

Joohyun Lee has obtained a PhD in Biological Sciences at Dartmouth College under the supervision of Professor Mary Lou Guerinot. He had worked with Professor Richard Amasino as a Post-doctoral Associate in the Department of Biochemistry at University of Wisconsin (UW)-Madison. He is currently operating his own research group and teaching several courses as a Research Assistant Professor in the Biology Department at University of Massachusetts (UMass) Amherst. The cold-induced epigenetic switch is an important factor that affects the yield of various agricultural crops, because certain plants cannot flower at the proper time without vernalization. In *Arabidopsis thaliana*, prolonged exposure to cold epigenetically represses the expression of a floral repressor, Flowering Locus C (FLC). This is achieved by the increase of the evolutionary conserved Polycomb Repressive Complex2 (PRC2)-mediated epigenetic silencing mark, trimethylation of histone H3 at lysine 27 (H3K27me3), at FLC. However, how plants sense the prolonged cold and measure the duration of cold exposure are not known. Therefore, his research aims to identify and characterize the network of genes controlling a cold-induced epigenetic switch in plants.

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