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Three INDETERMINATE DOMAIN transcription factors redundantly regulate flowering in *Arabidopsis*.

Presented by:

Dr. Harumi (Mimi) Tanimoto

Abstract:

Plants have evolved many strategies to ensure optimum reproductive timing and therefore the regulation of flowering is very complex, relying on numerous environmental and developmental signals. In crop plants, flowering time has profound effects on yield, length of growing season and input costs, so understanding the mechanisms that regulate this process offers huge potential for crop improvement. The maize *INDETERMINATE1* (*ID1*) gene promotes floral transition and encodes the founding member of the plant-specific INDETERMINATE DOMAIN (IDD) transcription factor family. Although certain flowering pathways appear to be common to all higher plants and close relatives of *ID1* are found in other grass species, no clear *ID1* orthologue has been described in the dicot, *Arabidopsis*. We show that three *IDD* genes from *Arabidopsis* act redundantly to regulate flowering and our genetic analysis suggests that *AtIDD3*, *AtIDD8* and *AtIDD10* may function in more than one flowering time pathway. Comparison of the transcriptomes in *atidd8* mutants, *AtIDD8* overexpression lines and wild type plants suggests that *AtIDD8* may regulate genes involved in carbohydrate transport or metabolism. These results support the hypothesis that floral transition is tightly coupled with carbohydrate status.