Flowering plants comprise all major crops globally. Understanding the underlying molecular mechanisms behind flowering is imperative to advancing breeding and biotechnology programs for increasing yield of crops to meet the demands of a growing population. The protein FLOWERING LOCUS T (FT) in Arabidopsis is the mobile signal in plants that transitions plants from vegetative growth into reproductive growth, or flowering. The protein TERMINAL FLOWER 1 (TFL1) in Arabidopsis is in the same protein family as FT, and is structurally similar, but instead of promoting flowering TFL1 represses flowering. FT and TFL1 are highly conserved evolutionarily with FT-like and TFL1-like proteins found in all flowering plants searched to date. Our lab has isolated an FT-like gene from sugarcane (ScFT2) that clades with FT-like floral promoter genes but has an extreme floral repression phenotype in Arabidopsis. The high similarity of ScFT2 to FT, coupled with the extreme phenotype makes ScFT2 a good probe to study what is important for floral repression. This project aims to identify some undiscovered molecular component important for floral repression and vegetative growth in flowering plants. ScFT2 will be inserted into the model plants Arabidopsis and tomato (Solanum lycopersicum) under the control of various promoters to identify where it is functioning within the plant, as well as how ScFT2 affects plant architecture. Further, a yeast two-hybrid assay will be conducted testing for protein-protein interactions of TFL1 against a library of all Arabidopsis genes to identify specific proteins that may be important for floral repression.