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Abstract for GRR

The pathways to flowering are being examined in the model species *Arabidopsis thaliana* and recently in some important woody species. Little is being done to study the induction of flowering on the whole plant level in ornamental woody plants. Our aim is to understand the regulation of flowering as it relates the physiological development of the plant.

We are studying the genes involved in the pathways that integrate the flower inductive signals in *Magnolia virginiana*. There are three genes that are important in the integration of the major pathways to flowering: *SUPPRESSOR OF OVEREXPRESSION OF CONSTANS 1 [SOC1]*, *LEAFY [LFY]* and *FLOWERING LOCUS T [FT]*. We have cloned a putative SOC1 ortholog and a fragment of a putative LFY ortholog from *Magnolia virginiana*. These show 80% and 90% sequence similarity at the gene and protein levels respectively for LFY. Our putative SOC1 ortholog has 74% for the gene and 65% sequence similarity for the protein.

This poster examines the work done to date and the future direction of the research.