Understanding Remontant Flowering in *Hydrangea macrophylla*©

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There has, over the past several years, been a great deal of interest and discussion about remontant flowering (repeat flowering on current season's growth) driven primarily by the introduction of the remontant flowering *Hydrangea macrophylla* 'Bailmer', Endless Summer™ hydrangea. Although Endless Summer™ hydrangea and other remontant flowering *H. macrophylla* have certainly energized hydrangea interest, the genetic underpinnings of remontant flowering remains unknown. The elucidation of these responsible genetic mechanisms would certainly help to facilitate the introduction of the remontant flowering trait into improved cultivars. A traditional genetic approach could be used; however, this approach is impractical because of the long generation time of *H. macrophylla* and the fact that floral induction is known to be under the control of many genes. The basic pathway and genetic mechanisms involved in floral induction have been revealed in model plants such as *Arabidopsis thaliana*, and this knowledge can be used to develop a reasonable hypothesis for the variation in floral induction among *H. macrophylla*.

A model for the molecular control of flowering in *Arabidopsis* has been developed (Searle and Coupland, 2004). In this model, the 24-h cycle is controlled by a negative feedback loop involving the known clock genes LHY/CCA1 and TOC1. *Arabidopsis*, a facultative long day (LD) plant, flowers rapidly under long-days. According to the model, flowering is controlled by the central oscillator which controls expression of the genes CONSTANS (CO), GIGANTEA (GI), and FLOWERING LOCUS T (FT).

CONSTANS shows a diurnal expression pattern, and its protein requires light-mediated modification for activation. The activated CO protein then induces expression of FT leading to floral induction (Searle and Coupland, 2004). Analysis of the diurnal expression patterns of CO in plants grown under either LD or short day (SD) provided insight into how photoperiodism acts to control floral induction. In *Arabidopsis* plants grown under short days, CO expression and protein accumulation peaks during the dark period when light-mediated modification cannot occur. However, under long days, peak expression and protein accumulation occurs late during the light period and corresponds with increased expression of FT. The FT is dependent of CO for activation and is believed to be act directly on floral meristem identity genes (adapted from Searle and Coupland, 2004).

Can the model for photoperiod controlled flowering in the LD plant *Arabidopsis* be applied to SD plants such as hydrangea? Could this model help explain the natural variation in floral timing observed in *H. macrophylla*? Some data from the SD plant *Ipomoea* (*Pharbitis*) *nil* illustrates some important similarities (Kim et al., 2003; Liu et al., 2001). A single mutation could alter expression of a CO-like gene in hydrangea causing expression under LD (normally non-inductive) to occur during

daylight hours when the CO protein can undergo the needed modification. Similar shifts in CO expression timing have been observed following mutagenic treatments in *Arabidopsis* causing enhanced flowering under SD.

In collaboration with Dr. Tim Rinehart (United States Department of Agriculture – Agriculture Research Service), we are developing expressed sequence tags (ESTs) of genes expressed under either inductive or non-inductive conditions. Once these ESTs are available we will be able to compare expression patterns between remontant flowering and nonremontant flowering hydrangeas. This should lead us to the identity of genes responsible for the variation in floral induction. This information can then be used for marker-assisted breeding of new and improved remontant-flowering hydrangea.

LITERATURE CITED

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