

# Expression of flowering candidate genes in alfalfa

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## Abstract

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Alfalfa (*Medicago sativa*), a perennial legume, is mainly cultivated as a forage crop. Apart from being the third most important crop in the USA in terms of production, only after wheat and corn, alfalfa is emerging as a potential energy crop. Classical breeding is being used to develop varieties of germplasm that produce large amounts of biomass. Studies in other systems, like Arabidopsis, have shown that manipulating key flowering pathways genes results in extended vegetative growth and thus biomass increase. We hypothesize that a similar approach in alfalfa will provide us with plants with enhanced biomass production. Based on the reports from Arabidopsis, we are focused on three major flowering time control genes, namely *CONSTANS* (*CO*), *FVE* and *FCA* controlling two independent flowering pathways namely photoperiod/light pathway and autonomous pathway. We conducted data mining of *Medicago truncatula* (a close relative of alfalfa) genome and cloned the homologs of these three genes from alfalfa based on the sequence similarity. Since alfalfa has more than one homolog for each gene, we did an expression analysis of the homologs in order to identify the ones that were the most similar to Arabidopsis genes. All three genes showed distinct expression patterns in different tissues and developmental stages. We have prepared several constructs that will be transformed into either Arabidopsis or alfalfa in order to confirm the function of these candidate genes in flowering time control.