

IDENTIFICATION AND PHYLOGENETIC ANALYSIS OF *FT* GENES IN COMMON BEAN (*Phaseolus vulgaris* L.)

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Flowering in many plant species is controlled by photoperiod, which represents the most reliable seasonal change in nature. The availability of crops with different photoperiod responses made it possible to extend their distribution range. The gene network controlling flowering is well studied in the model plant *Arabidopsis thaliana*, where the *FLOWERING LOCUS T (FT)* gene is crucial for the acceleration of flowering. *FT* is part of a gene family that also includes the *TERMINAL FLOWER 1 (TFL1)* gene, which inhibits flowering. Constitutive *FT* expression or loss of *TFL1* function causes early flowering and transition of the shoot apex from vegetative to reproductive identity. *FT* proteins have a conserved role as mobile flowering signals in several different species and promote flowering in long or short days depending on the species. The induction of flowering by *FT* family members has been investigated in legumes such as pea, soybean and *Medicago* but the *FT* family has not yet been characterized in common bean. Increasing knowledge of the identity and regulation of *FT* genes in common bean will be helpful to select variants that are better adapted to changing photoperiod conditions. BLAST searching revealed ten genes with homology to *FT/TFL1* in the common bean genome. The inferred phylogenetic tree from the identified common bean *FT/TFL1* amino acid sequences and sequences of soybean (*Glycine max*), chickpea (*Cicer arietinum*), *Medicago truncatula*, *Lotus japonica*, and pea (*Pisum sativum*) indicated that common bean contains *MFT*-like, *BFT*-like and *FT/TFL1*-like genes. Phylogenetic analyses also revealed substantial levels of microsynteny between *Medicago*, chickpea and pea, and between soybean and common bean, as expected from their proximity within the legume family. These results indicate that the expansion of the *FT* family occurred relatively early in legume evolution.

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