

Fine mapping and candidate gene analysis of DTF9.4, a QTL that promotes flowering in common bean (*Phaseolus vulgaris*) under long day photoperiod

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Abstract

Flowering time and maturity are important agronomic traits for common bean (*Phaseolus vulgaris*), a short day species in order to adapt to different latitudes and achieve optimal yield. In 2021, a QTL for flowering time, DTF-9.4 was mapped on chromosome 09, explaining more than 30% phenotypic variance. Although the studies indicated functional genes exist in this region that controls flowering time, it has not been deciphered at high resolution. In this study, genotyping and phenotyping of recombinant plants within the QTL region allowed us to narrow down the QTL region to 200 kB, in which two candidate genes were annotated, *PvFUL1* y *PvE1*. The development of near isogenic lines has allowed us to eliminate the effect of other major genes that segregated in the population (such as *PvCOL2*), *dtf-9.4* lines had a lower flowering node and early flowering time (node 8 and 40 d) compared with 'DTF-9.4 lines (node 15 and 54 d) in long day conditions (14 h light). This finding showed the possible involvement of other circadian clock gene in flowering time regulation in common beans. To determine the effects of these candidate genes underlying QTL, we will analyze gene expression within the DTF-9.4 in an effort to link markers, RNA expression, and the phenotype.

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