

# CONSTANS-like genes are associated with flowering time in sesame

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## Abstract

Sesame (*Sesamum indicum* L.) is an oilseed crop with high concentration of unsaturated fatty acids. It is produced in many developing countries of the tropical and subtropical regions. Despite its economic and social importance, limited genetic analyses were conducted on sesame to improve its yield. One of the yield-related traits is flowering time, which is crucial for the adaptation of crops to local environments and changing climatic conditions. To gain further insights into the molecular mechanisms behind the control of flowering in sesame, we searched homologs of FLOWERING LOCUS T (FT) and circadian clock-associated genes in the sesame genome. Then we compared their expression between early- and late-flowering sesame varieties before (10 days post-emergence [dpe]), around (20 dpe), and after flowering (30 dpe). Four copies of FT-like genes were found in sesame: SiFTL1/SiFT was up-regulated at 20 and 30 dpe and SiFTL2 at 30 dpe. SiFTL3 was poorly expressed throughout the three stages, and SiFTL4 was highly expressed at 10 dpe but not at later stages. These results suggest that SiFTL1/SiFT acts as florigen, and SiFTL4 could be a floral repressor. The CONSTANS-like genes SiCOL1 and SiCOL2 were highly expressed at 20 dpe suggesting its role as an inducer of florigen. In addition, the early-flowering sesame variety presented higher expression of SiFTL1/SiFT, SiFTL2, and SiCOL2 than the late-flowering variety at 20 dpe. The expression of SiGIs and circadian clock-related genes were similar between the two varieties. Our results suggest that SiCOLs or their regulator might be the causal gene for flowering time variation between the two sesame varieties studied.