

EXPRESSION ANALYSIS OF FLOWERING RELATED GENES IN OLIVE PLANTS TRANSFORMED WITH THE *MEDICAGO TRUNCATULA* FT GENE *MtFTa1*

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Olive tree (*Olea europaea* L.) forms inflorescences in lateral buds that flower in spring. Flowering occurs due to the presence of a mobile flower-promoting factor called florigen, the product of “FLOWERING LOCUS T” (FT). In many plants, FT and TERMINAL FLOWER 1 (TFL1) genes encode related proteins with opposite functions, i.e. FT induces flowering, while TFL1 represses it. Olive flower induction seems to be mediated by an increase in FT levels in response to cold winters. Because of climate change, warmer winters are expected, which can alter flowering time. Three olive transgenic lines containing the *MtFTa1* gene from *Medicago truncatula* were obtained (FT5, FT7 and FT15) to study the effect of FT on flowering time (Haberman et al., 2017). The embryogenic line P1 from a seed of cv. Picual was used for transformation, and also as control (CP1). FT7 flowered continuously; FT5 did not flower and showed a dwarf branching phenotype, and FT15 had a dwarf-branching habit and developed abnormal flowers. The expression of the transgene and three endogenous genes (*OeFT1*, *OeFT2* and *OeTFL1-1*) was analyzed in these juvenile plants throughout the year (autumn, winter and spring). Size of CP1 plants was controlled through successive pruning. CP1 showed high *OeFT2* and *OeTFL1-1* transcript levels in spring. The high expression of *OeTFL1-1*, probably enhanced by successive pruning, could explain why CP1 never flowered despite high *OeFT2* mRNA levels, and confirms its possible role in preventing flowering (Haberman et al., 2016). In the transgenic lines, *MtFTa1* was overexpressed throughout the year, with higher levels of transcripts in spring. The three endogenous genes were under-expressed in autumn and winter. In the flowering period, *OeFT2* and *OeTFL1-1* expression levels were high in FT5, the transgenic line that did not flower. By contrast, the line displaying continuous flowering, FT7, and also FT15, showed increased levels of *OeFT2* and *OeFT1* mRNAs, and low levels of *OeTFL1-1*. These results suggest that FT5 line reveals the effect of FT gene on plant architecture (inhibition of apical dominance and lateral bud induction), while FT7 exhibits its role in flower induction.

References

- Haberman A., Ackerman M., Crane O., Kelner J-J. Costes E. and Samach A. (2016) *The Plant Journal* 87, 161-173.
- Haberman A., Bakhshian O., Cerezo-Medina S., Paltiel J., Adler C., Ben-Ari G., Mercado J.A., Pliego-Alfaro F., Lavee S. & Samach A. (2017) *Plant, Cell and Environment* 40 (8), 1263-1280.

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