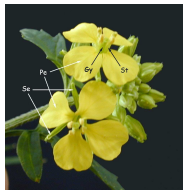
LEAFY expression and temporal sequence of floral transition in *Sinapis alba L.*



BONHOMME Delphine and PERILLEUX Claire
Laboratory of Plant Physiology, Department of Life Sciences, University of Liège,
B22 Sart Tilman, B-4000 LIEGE, BELGIUM. cperilleux@ulg.ac.be

Introduction

The shoot apical meristem (SAM) of *Sinapis alba* can be switched from vegetative to reproductive fate by exposure of 2-month old plants to a single long day (LD). Floral transition then occurs in good synchrony within the population, and a number of biochemical, cellular, and morphological changes have been described whose timing is strictly reproducible. Our aim is to integrate gene expression patterns into this timing. We report here the analysis of *SaLFY*, orthologous to the floral meristem identity gene *LEAFY* of *Arabidopsis*.

Material and methods

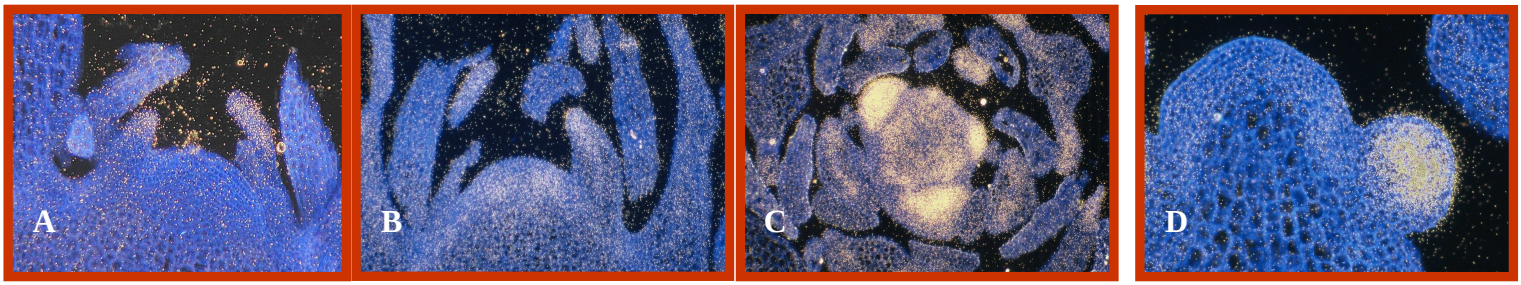
Plants of *Sinapis* were grown in 8-h short days (SD) for two months before being induced to flower by one 22-h LD, then returned into SD. Shoot apices were harvested 24, 32, 40, 48, 56 and 80 h after start of the LD, and prepared for *in situ* hybridization with a [^{35}S]*SaLFY* antisense RNA probe.

Abbreviations

LD : long day; SD : short day

Results and discussion

As expected, the expression of *SaLFY* was found to be very strong in flower primordia, which were clearly identified in SAM sections 80h after start of the LD (picture D). More surprisingly, *SaLFY* was expressed well before the initiation of flowers. First, a strong signal was detected in the tip of youngest leaf primordia of vegetative plants, and this pattern was amplified 24h after start of the LD (picture A). Secondly, *SaLFY* was transiently expressed in the SAM of induced plants, from 32h after the start of the LD. The signal was higher in L3 cells of the peripheral zone (picture B) and formed, in transverse sections, a discontinuous ring with activation where last leaves were to be initiated (picture C). This expression pattern of *SaLFY* followed by ~8h the expression of *SaMADSA*, orthologous to *SOC1*, which was previously reported to be activated from 24h after start of the LD, starting in the central zone of the SAM before extending to the flanks (Bonhomme et al., 2000).



Early and transient expression of *SaLFY* in the SAM of *Sinapis* during the transition to flowering, observed between h 32 and 56 after start of the LD. Here, at h 40 in longitudinal (B) and transversal (C) sections. In C, note that the expression follows the phyllotaxic spiral. Activation in the SAM was not observed in SD-controls (A) .

(D) Typical expression of *SaLFY* in flower primordia at h 80.

Interestingly, the early activation of *SaLFY* in the SAM matched in time and space early growth changes previously described during the transition to flowering, namely an increase in cell proliferation, in leaf primordia growth and an acceleration of last leaf initiation (Bernier, 1997), suggesting that *SaLFY* may have dual functions in fate specification during the floral transition of the SAM.

References

Bernier, G. 1997. Growth changes in the shoot apex of *Sinapis alba* during transition to flowering. J Exp Bot 48; 1071-1077.

Bonhomme, F., Kurz, B., Melzer, S., Bernier, G. Jacqmard, A. 2000. Cytokinin and gibberellin activate *SaMADSA*, a gene apparently involved in regulation of the floral transition in *Sinapis alba.* Plant J 24; 103-111.