

## GENOME EDITING PROTOCOLS AND GENETIC DIVERSITY TOOLS FOR FLOWERING TIME ADAPTATION IN ASTERACEAE

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Climate change is leading to a negative alteration of ecological balances and consequently in yield and quality of crops. Therefore, it is necessary developing new fast and precise breeding techniques to select more robust and tolerant crops with increased quality and yields under more extreme conditions. Genome editing is a molecular tool allowing to accelerate breeding processes and the study of important agronomic traits.

The purpose of our work is to develop new efficient genome editing (GE) protocols, including DNA-free GE techniques, for *Lactuca sativa* and *Cichorium endivia* to improve important adaptation traits such as flowering time.

Both species, belonging to the *Cichoriae* tribe in the *Asteraceae* family, are particularly interesting for their agronomical characteristics. Lettuce is one of the most popular leafy vegetables. It represents a genetic model for leafy species due to the small size of its genome (2.5 Gb), short reproductive cycle and suitability for tissue culture. Moreover, a reference sequenced genome with detailed genetic maps is available. *C. endivia* (endive and escarole), a traditional horticultural species, has received increasing interest for the vegetable market for its nutritional value and valuable properties for human health. Although its genome sequence is not public yet, several features make it also a suitable model for leafy crops.

The time at which flowering occurs plays a major role in leafy crops production, it affects the quality and quantity of leaves as well as adaptation to different environmental conditions. The transitioning to reproductive growth is marked by the elongation of the stem (bolting), that renders the crop bitter and unmarketable. Heat-accelerated bolting and flowering is a common phenomenon that impacts agricultural production of diverse lettuce and *Cichorium* spp. cultivars.

As important GE targets for flowering time, our work focused on *SOC1*, a MADS box transcription factor that integrates flowering signals with environmental cues, and *STM*, a *KNOTTED1*-LIKE homeobox protein involved in apical transition from vegetative to reproductive phase. As genetic diversity constitutes a source of allelic variants "tested" naturally in the field of evolution, we first searched for *SOC1* and *STM* allelic variants that could fine tune these genes function in 1135 accessions of *A. thaliana*. Polymorphisms were searched in both coding sequences (CDS) and regulatory promoter regions. Comparative analyses were performed in the genomes of *L. sativa* cultivars and wild relatives.

In order to study the function of *SOC1* and *STM* homologs in *L. sativa* and *C. endivia*, the obtainment of overexpression and GE constructs is in progress. Furthermore, efficient hairy root transformation protocols have been set up to test the efficiency of GE constructs.

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