Proceedings of the 52nd Italian Society of Agricultural Genetics Annual Congress
Padova, Italy – 14/17 September, 2008
ISBN **978-88-900622-8-5**

Poster Abstract – D.09

CHARACTERIZATION OF FLC-LIKE SEQUENCES IN *CICHORIUM INTYBUS*

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flowering transition, vernalization, inflorescence, FLC, chicory

In winter annuals ecotypes of *Arabidopsis*, the flowering repressor, *FLOWERING LOCUS C* (*FLC*), a MADS box transcription factor, is expressed at such level as to inhibit flowering in the first growing season. FLC expression is enhanced by *FRIGIDA* (*FRI*) to levels that inhibits the transition to flowering by repressing the expression of the genes often referred to as Floral Pathways Integrators. The main process promoting flowering by the repression of *FLC* is the vernalization and the duration of cold has been shown to be proportional to the degree of down-regulation of *FLC*; such repression is maintained for the rest of the plant life even after cold exposure ends, but is restored after meiosis. The repression involves epigenetically stable modifications in *FLC* chromatin that include a H3 Lys27 trymethylation (H3K27me3) and a H3 Lys9 methylation, (Sung et al, 2006).

Wild chicory (*Cichorium intybus* L.) is a biennial species which requires vernalization to flower. In Italy different types of chicory (the so called Italian red and variegate types) have been selected by farmers as leafy vegetable. These types show quite different classes of precocity in relation to flowering.

In our study, we are investigating the molecular basis that regulate the switch to flower in chicory by vernalization, to verify whether such mechanism is the same that controls flowering in *Arabidopsis*, and, finally, to address the diversity of the classes of precocity to one of the cases known for this model plant. We isolated FLC homologues from chicory and characterized their expression in plant tissues and we studied the pattern of cytosine methylation in chicory genomic DNA in response to vernalization. Given the presence of 4 *Ci*FLC transcript variants in chicory, we tested by Southern blot analysis the number of FLC copies in the *C. intybus* genome of different cultivar of chicory. Souther analysis and GenomeWalking led to the isolation of five sequences: two of them corresponding to intron-less cDNA-like sequences where the start codon ATG was replaced by a TGA stop codon; a third sequence, 439 bp in length, corresponded to the "putative" second exon and the beginning of the second intron of the gene; a fourth genomic sequence of 283 bp, is very peculiar, because it presents a partial duplication of the MADS-domain and the two repetitions are separated by a non-coding 85 bp region. A second southern blot has cleared the presence of multiple copies of the *CiFLC* gene, using as a probe a DNA sequence of 439 bp isolated by genome walking.