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Poster Communication Abstract – 1.14

THE MAIZE WD-REPEAT CHROMATIN REMODELING GENE *nfc102* REGULATES THE MAIZE HOMOLOG OF THE *ARABIDOPSIS* FLORIGEN *FT*

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The *nfc102* gene encodes a WD-repeat protein belonging to the *Multicopy suppressor of IRA* (*MSI*) family, originally identified in yeast. In maize, five genes of the *MSI* family have been identified and named *nfc*, because they display homology with one of the NURF complex component, where NURF is the Nucleosome Remodeling Factor: a multi-proteins complex that regulates transcription by catalyzing nucleosome sliding. Among the members of the *MSI* family, the maize *nfc102* gene displays high sequence homology with the Arabidopsis *FVE*, which is a component of the autonomous flowering pathway and that regulates transposons transcription. Although *FVE* is known as a positive flowering regulator, mainly because it inhibits expression of the flowering repressor locus *FLC*, it has been recently shown that *FVE* can also negatively affect transcription of the Arabidopsis florigen *FT*. In all cases, *FVE* acts by affecting histone modification pattern, thus provoking changes in the chromatin structure of its targets.

In maize, none of the several members of the MADS-box transcription factor class identified so far exhibits a functional homology with the Arabidopsis *FLC*. However, the maize homolog of the Arabidopsis *FT* gene has been recently identified and named *ZCN8*. *FT* orthologs from different plant species were shown to behave as a flower-forming signal because they were transcribed and translated in leaves, but their proteins subsequently move through the phloem to the SAM, where they induced the floral transition upon reaching a critical concentration. Interestingly, *ZCN8* transcript is detected almost exclusively in an unspliced form in tissues enriched for meristematic area (MA), while the spliced transcript form is produced only in the leaf blades (LB). Using strand specific RT-PCR we observed that the unspliced *ZCN8* RNA transcript is mainly represented by the antisense *ZCN8* RNA strand, which was named ZAS1. A shorter antisense *ZCN8* RNA strand, named ZAS2, was also detected, corresponding to RNA with alternative splicing with respect to the spliced sense RNA strand. The *ZCN8* sense RNA strand was almost exclusively present in LB as a fully spliced form, with an ORF that encodes for the ZCN8 protein.

Analysis of the *ZCN8* sense and antisense RNA levels in *nfc102* RNAi mutant compared to wild-type plants showed that *nfc102* down-regulation affect the level of both *ZCN8* sense and antisense transcripts and the ratio between the amount of ZAS1 and ZAS2. In this poster we will illustrate in details these findings and we will discuss about the possible role of *nfc102* in controlling *ZCN8* expression by linking changes in chromatin structure with RNA processing.