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**Poster Abstract – C.31**

# CHARACTERIZATION OF AtMYB59 TRANSCRIPTION FACTOR

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*Myb transcription factor*

MYB proteins are a superfamily of transcription factors involved in plant developmental processes and defense responses. In contrast to animals, plants contain a MYB factor subgroup that is characterised by the R2R3-type MYB domain. Members of this group play a role in plant secondary metabolism and in the specification of cell fate and identity. Our work is focusing on the study of an *Arabidopsis* Myb transcription factor: AtMyb59.

AtMyb59 encodes a transcription factor belonging to the R2R3MYB family and it is present in three splicing variants (Myb59.1, Myb59.2, Myb59.3). By Real Time-PCR analysis performed with specific primers, we measured transcription levels of the three splicing forms in plant organs.

The ectopic expression of Myb59 had an effect on vegetative growth: in fact transgenic plants over-expressing Myb59.1 showed an increased leaf area, whereas the ectopic expression of Myb59.2 induced a decrease of leaf area compared to control plants. Plants over-expressing Myb59.3 are under investigation. Promoter studies revealed that the expression of the three splicing variants has different localization in plant tissues.

Furthermore, we investigated the role of this gene in response to abiotic stresses: we observed that Myb59.1 is not modulated by abiotic stresses, whereas Myb59.2 is induced by ABA, cold and drought treatments and the expression of Myb59.3 is only modulated by drought treatment.

We also analysed a *myb59* knock-out mutant. The comparison between mutant and WT plants will be discussed, considering a putative phenotype not only under standard growth conditions, but also in response to abiotic stresses.

Furthermore, to verify the correspondence between mRNAs and proteins, we induced in *E.coli* the expression of the three proteins derived from the three mature RNAs fused to a flag-tag. The migration patterns of these proteins in SDS-PAGE, will be helpful during the analysis of protein extracts obtained from the *myb59* mutant background complemented with the complete genomic sequence of *Myb59* under the control of its native promoter. This test will allow to indentify which of the three splicing variants actually occurs.