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Poster Abstract - B.26

THIRTY GENOMIC SEQUENCES IN MAIZE CODING FOR FIVE miRNAs

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In recent years microRNAs (miRNAs) have polarized the interest of the scientific community as new categories of gene expression regulators, present both in plants and animals. These small molecules (20-24 nt), codified by MIR genes and processed from longer primary transcripts folded in stem-loop structures, act via mRNA degradation or translational control of target genes.

Plant miRNAs are involved in processes such as plant development, organ identity and stress response. Nonetheless the knowledge about their functions is still incomplete, and it is conceivable that new processes in which they are involved will be further discovered. This thesis is also supported by the indication that miRNAs can represent up to 1% of all predicted genes in animals and in plants.

For these reasons, structural and functional characterization of MIR genes, also in crop species such as *Z. mays* L., becomes instrumental to address genetic and molecular mechanisms controlling phenotype determination and phenotypic adaptation to growing condition.

Here we contribute to the characterization of miRNAs in maize, by identifying thirty genomic sequences (MIR genes) which putatively code for 5 different microRNAs, identical in sequence to the corresponding rice and arabidopsis ones. These thirthy genomic sequences were obtained either by cloning or by applying a bioinformatic approach. MIR genes were all placed onto maize chromosomes and their putative transcripts were validated as miRNA precursors, due to their characteristic secondary structures. Expression pattern of miRNAs was also determined in different maize tissues and genotypes.

Giving the number of precursors producing these five miRNAs, we are currently investigating their precise role and their expression pattern.

In addition, since phylogenetic conservation of miRNA sequence and its predicted precursor secondary structure is considered an important criterion for validation for MIR genes, the relationship between maize, rice and sorghum MIR genes was also addressed.

To provide data for evolutionary studies on MIR genes in cereals, *Sorghum bicolor* genomic clones containing putative MIR genes were identified, and sequence homology was determined by reciprocal best BLAST hit approach, to define groups of homologous genes.