

MAIZE TRANSCRIPTOME DEEP SEQUENCING: FROM CODING GENES TO THE DARK MATTER OF THE GENOME

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Plant genome heterochromatinization in specific regions using epigenetic marks represents a mechanism to silence gene expression and protect the genome by selfish DNA. Anyway, the idea that the heterochromatin is not subject to gene transcription is now changing. Both the characterization of the chromatin landscapes and application of transcriptomic deep sequencing technologies have revealed that the majority of the genome is pervasively transcribed in many eukaryotes, including plants. The large number of identified transcripts with no apparent coding capacity has been defined as the ‘dark matter’ of the genome. In Arabidopsis, which has a relatively small genome, less than 50% of its genome is capable of coding proteins. More recently, it has been showed that up to 90% of eukaryotic genomes are transcribed into both protein-coding and non-protein-coding RNAs, although as little as 1–2% of the genome has protein coding capacity.

Our aim is to investigate the possible role of the so called ‘dark matter’ of the genome on chromatin conformation and gene transcription in maize under stress condition. In detail, plant of B73 reference and *rmr6* mutant line were grown under drought and salinity stresses. The *rmr6* mutant presents a mutation in the largest subunit of PolIV, involved in the small interfering RNAs (siRNAs) formation. We are monitoring, by RNA-seq, the transcription of genes, transposons and long non-coding RNAs (lncRNAs) at different time points after stress application and during recovery stages. In particular, lncRNAs are a very abundant class of non-coding RNAs, often expressed in a tissue- and stress-specific manner, recently identified as involved in gene epigenetic regulation. How lncRNAs control transcription however is mostly unknown. We intend to verify their role in maize transcription regulation by altering chromatin properties. Since transcription regulation mechanisms play an important role in maize abiotic stress response, it will be interesting to see how lncRNA function intersects with others epigenetic mechanisms (Cp_methylation and histone modifications) in epigenetic pathways (sRNA pathway and DNA methylation), already known to be involved in plant stress response. To this end data obtained from RNA deep sequencing, Chromatin Immuno Precipitation and DNA bisulfite conversion will be integrated.