

STRESS-INDUCED GENETIC AND EPIGENETIC REGULATION OF MAIZE TRANSCRIPTOME AND GENOME STABILITY: FROM CHROMATIN MODIFICATION TO lncRNAs AND BEYOND

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The plastic adaptability of plants to environmental changes involves sophisticated responses of cellular physiology, gene regulation and genome remodelling. Increasing experimental evidences suggest a predominant role of epigenetic mechanisms, such as DNA methylation, chromatin modifications and non coding RNAs, in abiotic stress responses. Stress-induced epigenetic release may also result in genome destabilization, with the activation and/or the transcription of DNA transposons and retroelements, usually silenced, which may result in novel gene expression and DNA rearrangements.

We used a total RNA-Seq strategy to deeply analyze the leaf transcriptome both of B73 and *Required to Maintain Repression6 (rnr6)*; involved in siRNA biogenesis and in the RNA-directed DNA Methylation pathway) after drought and salt stress application. Our reference annotation based transcript (RABT) assembly approach allowed to identify, in addition to the 133,660 transcripts at 110,191 loci annotated in the *Zea_mays*.AGPv3.20 genome release, 21,471 potential novel isoforms, 992 new transcripts with partial overlap with reference and 2,768 new transcribed loci mapping in intergenic regions. Interestingly, we also found 397 transcripts matching on the opposite strand of annotated loci, which represent potential antisense transcripts. We are now assessing the protein-coding potential of all these new classes of transcribed loci, analyzing their expression modulation as effect of the stress application in B73 and *rnr6* mutant leaves. Preliminary results indicate that the main part of newly identified intergenic transcripts correspond to transposable elements and their characterization is underway. These TE-related sequences are exclusively expressed in *rnr6* mutant and upregulated by the stress application.

In parallel we investigated the genome-wide distribution of histone H3 lysine4 trimethylation (H3K4me3), histone H3 lysine9 acetylation (H3K9ac), histone H3 lysine27 trimethylation (H3K27me3) using ChIP-Seq on B73 drought stressed samples to explore the whole epigenomic landscape of stress response and adaptation in maize. Preliminary analysis are revealing that the stress treatment can alter the epigenomic landscape, showing a direct correlation between H3K4me3 and, to a lesser extent H3K9ac, enrichment with transcription activation in response to stress.

The results obtained by combining these different approaches aim to identify a robust list of sequences targets of epigenetic regulation, building a genome-wide survey of epigenetic regulation of genome transcription and stability under stress conditions.