

STRESS-INDUCED AND EPIGENETIC-MEDIATED TRANSCRIPTIONAL REGULATION AND MEMORY IN MAIZE

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Plant's response and adaptation to abiotic stresses involve sophisticated genetic and epigenetic regulatory systems, which result in both spatiotemporal gene expression changes and activation of transposable elements usually silenced. To obtain a global view of plant's molecular regulation and response to osmotic stresses, including the non-coding portion of genome, we conducted a total leaf transcriptome analysis on maize plants subjected to prolonged drought and salt stresses and after a complete recovery from the stresses. Stress application to both B73 wild type and the epiregulator mutant *rpd1-1/rmr6* (a PolIV subunit mutant involved in siRNA biogenesis and in the RNA-directed DNA methylation -RdDM- pathway) allowed dissection of the epigenetic component of stress response.

The total RNA-Seq approach resulted in the identification of 25,444 new maize transcripts, including 2,664 new intergenic transcripts and 391 antisense transcripts mapping with opposite orientation in respect to reference transcripts. Application of a computational pipeline allowed the systematic identification of 13,387 long non-coding RNAs (lncRNAs) that may play critical roles in regulating gene expression through multiple RNA-mediated mechanisms. Differential expression analysis revealed hundreds of genes differentially expressed in response to long-term stress application, also highlighting several lncRNAs and transposable elements specifically expressed after osmotic stresses application and the recovery period. The amplitude of the stress-modulated gene set and the expression dynamics of stress recovery are very different between B73 wild type and *rpd1-1/rmr6* mutant plants, as result of stress-like effect on genome regulation caused by the epiregulator mutation itself, which appears to activate many stress-related genes even in control growth condition.