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HISTONE DEACETYLATION, MAIZE DEVELOPMENT AND EPIGENOME REGULATION

FORESTAN C.*, FARINATI S.*, ROUSTER J.**, VICELLI B.*, LAURIA M.***, VAROTTO S.*

*) Department of Agronomy Animals Food Natural Resources and Environment (DAFNAE), University of Padova, Viale dell'Università 16, 35020 Legnaro (Italy)
**) Biogemma, ZI du Brézet, 8, Rue de Frères Lumière, 63028 Clermont Ferrand (France)
***) Institute of Agricultural Biology and Biotechnology (IBBA) - CNR, Via E. Bassini 15, 20133 Milano (Italy)

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Histone acetylation is a Post-Transcriptional-Modification (PTM) that occurs at the amino groups of the lysine residues on the N-terminus of histone tails. The dynamic PTM histone lysine acetylation is governed by histone acetyltransferases (HATs) and histone deacetylases (HDAs). HATs transfer an acetyl moiety of acetyl coenzyme A (acetyl CoA) to the Ɛ-amino group of specific lysine residues; histone acetylation promotes RNA polymerase and other transcriptional factor complexes to interact with DNA, and leads to active gene expression. In contrast, HDACs remove acetyl modifications from histones, leading to a tight chromatin structure associated with gene transcriptional repression. Histone modification patterns are also thought to generate a "histone code" that provides signals for the recruitment of specific protein complexes, which alter chromatin states and affect transcription. HATs and HDACs gene families are evolutionarily conserved in eukaryotes and in playing a crucial role in transcriptional regulation.

We report the characterization of the *HDA108* gene, a member of the maize Rpd3/HDA1 family of histone deacetylases through the analysis of a Mutator insertional line. The phenotype of maize *hda108/hda108* mutant plants indicates that the *hda108* gene knockout is correlated with many developmental defects, such as a reduction in plant height, alterations of shoot and leaf development, alterations in both male and female inflorescence patterning and fertility. Immunolocalization experiments revealed an evident increase in acetylated histone H3 and H4 in homozygous mutant nuclei compared with wild types and alterations in other histone modifications, namely H3K9me2 and H3K4me3. DNA methylation, histone acetylation and transcript level of ribosomal sequences were also affected in mutant plants.

In defective mutant tissues, differential expression analysis showed the altered expression of many transcription factors involved in different aspects of plant development and identified putative HDA108 targets. Transcriptome analysis also highlighted thousands of genes misregulated in *hda108* mutant anthers: the failure to express pollen-specific genes and the ectopic activation of genes normally not expressed in fertile siblings results in the complete disruption of the transcriptional and developmental patterning in mutant anthers The double mutant lines *hda101AS*/*hda108hda108* and *rmr6rmr6*/*hda108hda108* were also produced to investigate redundancy and hierarchy in gene silencing pathways. Taken together our results showed that

HDA108 is involved in plant development, affecting male gamete formation and epigenetic regulation.