

MAIZE HISTONE DEACETYLASE *HDA101* IS INVOLVED IN PLANT DEVELOPMENT, GENE TRANSCRIPTION, AND SEQUENCE-SPECIFIC MODULATION OF HISTONE MODIFICATIONS OF GENES AND REPEATS

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Enzymes catalyzing histone acetylation and deacetylation contribute to the modulation of chromatin structure, thus playing an important role in regulating gene and genome activity. We showed that down-regulation and over-expression of the maize (*Zea mays*) Rpd3-type *HDA101* histone deacetylase gene induced morphological and developmental defects. Nuclear distribution and total levels of acetylated histones, as well as histone acetylation of both repetitive and non repetitive sequences were affected in *HDA101* transgenic mutants. However, only transcript levels of genes but not repeats were altered. Perturbation of *HDA101* expression also affected histone modifications other than acetylation, including histone H3 di-methylation at lysine 4 and lysine 9 and phosphorylation at serine 10. Our results indicate that *HDA101* acts as a general transcriptional repressor and provide evidence of its involvement in setting the histone code, thus mediating developmental programs. Our results furthermore suggest a functional difference between maize and *Arabidopsis thaliana* *Rpd3-like* genes, probably related to differences in chromatin organization.