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MAIZE RPD3-TYPE HISTONE DEACETYLASES

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Post-translational modifications of histones, including acetylation, methylation, phosphorylation, and ubiquitination, establish an epigenetic histone code that is recognized and interpreted by transcriptional regulators and chromatin remodeling factors. Histone acetylation is one the best-characterized type of histone modifications. The enzymes responsible for maintaining the steady-state balance of histone acetylation are the histone acetyltransferases (HATs) and histone deacetylases (HDACs). Mechanisms and factors controlling gene activity by affecting chromatin structure are largely conserved in eukaryotes, including plants. However, the sessile nature of plants, which makes them more sensitive to environmental signals, and the relative plasticity of their cell fate suggest that specific features of the chromatin-mediated control of gene transcription exist in plants. Interestingly marked differences, reflected by specific patterns of histone acetylation and by novel classes of HDACs not identified in other experimental systems, have been reported (Loidl, 2004 Trends Plant Sci 9: 84-90). Different HDAC genes have been identified in plants and their classification into three distinct gene families has been proposed by The Plant Chromatin Initiative (http://www.chromdb.org). The first family, named HDA gene family, contains members related to the yeast sequences Rpd3 and Hda1. Studies in our laboratory focused on functional characterization of maize Rpd3-type HDACs (ZmRpd3s).

Analysis of gene expression and protein accumulation indicates that different members of ZmRpd3 family are ubiquitously expressed but their amount and cellular localization changed during development. Phenotypic and cytological analysis of maize plants over-expressing (OE) and antisensing (AS) one member of ZmRpd3 family (ZmRpd3/101) indicate various defects in plant development and architecture. Molecular characterization of these mutants reveals changes in the global level of histone acetylation, methylation and phosphorylation as well as differences in their nuclear localization. Results obtained with chromatin immunoprecipitation assays and microarray analysis point out that ZmRpd3/101 does not alter histone modification pattern and expression of repetitive regions in maize genome, while appears to be involved in the regulation of various genes controlling different metabolic pathways.