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Chromatin plays a critical role in the regulation of gene expression. Interactions among chromatin regulators, sequence-specific transcription factors, and cis-regulatory sequence elements are the main driving forces shaping context-specific chromatin structure and gene expression. However, because of the large number of such interactions, direct data on them are often missing in most cellular contexts. The purpose of the present work is to show that, by modeling matched expression and accessibility data across diverse cellular contexts, it is possible to recover a significant portion of the (Kolomeisky, 2011). These well sequenced centromeres provide us a platform to profile chromatin modifications and RNA expression patterns associated with maize centromeres. We developed a high resolution genome-wide map of maize CENH3 nucleosomes based on Illumina sequencing of DNA samples prepared from chromatin immunoprecipitation (ChIP) using a maize anti-CENH3 antibody. These active genes were associated with euchromatic histone modification marks. In addition, maize centromeres lacked both euchromatic histone modifications (except for the regions associated with active genes) and H3K27me₂, a mark of heterochromatin in maize. nature of chromatin modifications with respect to gene expression, it is clear that metazoan transcription factors do not survey the entire genome landscape (Kolomeisky, 2011) and that. This evidence suggests that changes in metabolite availability do influence chromatin modifications and ultimately gene expression. In mammalian cells. In cultured cells, nucleocytoplasmic pools of histone proteins are dynamic. It has been demonstrated during the past decade that the posttranslational modifications of histone proteins within the chromosome impact chromatin structure, gene transcription, and epigenetic information. Multiple modifications decorate each histone tail within the nucleosome, including some amino acids that can be modified in several different ways. Covalent modifications of histone tails known thus far include acetylation, phosphorylation, sumoylation, ubiquitination, and methylation. Highlighted in this review are the recent biochemical, molecular, cellular, and physiological functions of histone methylation and ubiquitination involved in the regulation of gene expression as determined by a combination of enzymological, structural, and genetic methodologies. Histone Modification and Gene Expression. Gene expression is governed by complex mechanisms including transcription factor binding to DNA and coordinated changes in chromatin structure. The primary protein components of chromatin are the histones, which are assembled along with DNA into larger complexes known as nucleosomes. Each nucleosome contains two copies of the core histones, H2A, H2B, H3, and H4, each of which has an accessible amino terminal tail with a high proportion of lysines and arginines. Modifications of histone proteins constitute an important mechanism of gene regulation. Hist