A0311

Mitotic-Specific Methylation in the HeLa Cell through Loss of DNMTs and DMAP1 from Chromatin

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A diversified and concentrative approach of methylation player can be one of the most powerful studies in the understanding of global epigenetic modifications. Previous studies have suggested that DNA methylation contributes to transcriptional silencing through the several DNA methylation-mediated repression systems by hypermethylation, including methyltransferases (DNMTs), DNA methyltransferase association protein 1 (DMAP1), methyl-CpG binding domain (MBD), and histone deacetylases (HDACs). Assembly of these regulatory protein complexes act sequentially, reciprocally, and interdependently on the newly composed DNA strand through S phase. Therefore, these protein complexes have a role in coupling DNA replication to the designed turn-off system in genome. In this study, we attempted to address the role of DNA methylation by the functional analysis of the methyltransferase molecule, we described the involvement of DMAP1 and DNMTs in cell divistion and the effect of their loss. We also described distinct patterns that DMAP1 and DNMTs are spatially reorganized and displaced from condensing chromosomes as cells progress through mitosis in HeLa cell, COS7, and HIH3T3 cell cycle progressions. DNMT1, DNMT3b, and DMAP1 do not stably contact the genetic material during chromosome compaction and repressive expression. These finding show that the loss of activities of DNMTs and DMAP1 occure stage specifically during the cell cycle, may contribute to the integral balance of global DNA methylation. This is consistent with previous studies resulted in decreased histone acetyltransferases and HDACs, and differs from studies resulted in increased histone methyltransferases. Our results suggest that DNA methylation by DNMTs and DMAP1 during mitosis acts to antagonize hypermethylation by which this mark is epigenetical mitotic-specific methylation.

Key words) ***DNA Metylation, DNMTs, DMAP1, Mitosis***