Bookmark Target Genes in Mitosis: A Shared Epigenetic Trait of Phenotypic Transcription Factors and Oncogenes?

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Introduction

Mitosis, the process of cell division, poses a challenge to maintain cellular identity. In normal diploid cells, lineage-restricted transcription must resume in an efficient and faithful manner following mitosis. In tumor and transformed cells, there is an equivalently stringent requirement to sustain the cancer phenotype through successive cell divisions. Genetic information plays a key role in maintaining cellular identity, but it is becoming increasingly evident that epigenetic mechanisms are pivotal to sustaining cellular memory. Studies over the past decade have provided insights into epigenetic mechanisms that maintain cellular identity in lineage-committed as well as in cancer cells. Mitotically heritable posttranslational modifications and stoichiometry among variants of histone proteins, as well as methylation of CpG islands present in DNA-regulatory elements of developmental, phenotypic, and cancer-related genes, are key in marking genes for retention and transmission of cellular expression memory. Evidence is emerging for the presence of distinct transcriptional regulatory microenvironments in mitotic chromosomes in which the genes bookmarked for reactivation postmitotically reside. Importantly, some oncoproteins are present in mitotic microenvironments where they occupy target genes during mitosis and may contribute to perpetuating the transformed phenotype. We discuss emerging regulatory implications of epigenetically bookmarking genes during mitosis for physiologic control as well as for the onset and progression of cancer. Cancer Res; 74(2); 420–5. ©2014 AACR.

Abstract

The regulatory information for phenotype, proliferation, and growth of normal and tumor cells must be maintained through genome replication in the S phase and cell division during mitosis. Epigenetic mechanisms that include DNA methylation, posttranslational modifications of histones, selective utilization of histone variants, and inheritable RNA molecules play pivotal roles in maintaining cellular identity through mitotic divisions. Recent studies demonstrate that mitotic occupancy of genes, which are determinants of cell fate, growth, and proliferation, by lineage-restricted transcription factors is a key epigenetic mechanism for retention and transmission of cellular expression memory. Evidence is emerging for the presence of distinct transcriptional regulatory microenvironments in mitotic chromosomes in which the genes bookmarked for reactivation postmitotically reside. Importantly, some oncoproteins are present in mitotic microenvironments where they occupy target genes during mitosis and may contribute to perpetuating the transformed phenotype. We discuss emerging regulatory implications of epigenetically bookmarking genes during mitosis for physiologic control as well as for the onset and progression of cancer. Cancer Res; 74(2); 420–5. ©2014 AACR.

Mitotic Chromosomal Microenvironment

Chromatin reconfiguration during replication and mitosis poses a major regulatory challenge for cells to perpetuate identity as well as transcriptional regulatory commitment through architectural remodeling that includes chromatin unfolding, replication, condensation, and segregation. Compared with replication, chromatin undergoes striking structural and physical changes during mitosis; the 10-nm nucleosomal fiber condenses more than 70-fold to configure mitotic chromosomes (5). The highly compacted chromatin organization of mitotic chromosomes, combined with historically significant observations from pulse-chase radiolabeling approaches, suggested that transcription is universally inhibited during mitosis, and that the condensed chromosomes are not readily accessible to nuclear proteins (6, 7). Subsequently, experiments carried out on pure mitotic cell populations demonstrated selective nuclear accessibility of mitotic chromosomes, suggesting that components of the mitotic chromatin may not be transcriptionally inert (8). Ligation-mediated PCR (LM-PCR) studies of specific gene promoters during
mitosis further corroborated the observation that regions within mitotic chromosomes are accessible to regulatory proteins (9). Evidence is emerging for specific regulatory microenvironments present in mitotic chromosomes where genes involved in biologic control and cancer are bookmarked for rapid reactivation postmitotically (Fig. 1).

Properties of nuclear proteins that bookmark genes in mitosis

Recent advances in high-resolution microscopy as well as genome-wide biochemical approaches (e.g., chromatin immunoprecipitation followed by high-throughput sequencing) have provided an unbiased and comprehensive assessment of transcriptional dynamics in mitotic cells. Accruing evidence from studies in a variety of lineages suggests that transcription factors that play essential roles in conferring lineage identity often remain associated with target genes on mitotic chromosomes. The evidence is limited but compelling. Here, we outline some of the general properties of nuclear proteins that are retained with target genes during mitosis:

**Sequence specificity.** Although it has been shown that many sequence-specific transcription factors are displaced from condensed chromosomes during mitosis (10), several functionally significant nuclear proteins remain associated with mitotic chromosomes. Mitotically retained nuclear proteins include components of basal transcription machinery, coregulatory proteins that include activators, suppressors, and chromatin remodeling factors, as well as lineage-restricted transcription factors that interact with cognate binding motifs in regulatory elements of target genes. The Runx (AML/Cbfα) family of transcription factors is an initial example of mitotically retained nuclear regulatory proteins (11). Runx factors share a highly conserved DNA-binding domain (designated Runt homology domain for its homology to the Drosophila Runt protein) and exhibit recognition of a unique DNA-binding motif within the regulatory regions of target genes (12). Recently, it has been shown that the liver-related transcription factor FoxA1 and the hematopoietic regulator GATA1 are among many transcription factors that bind to lineage-restricted target genes during mitosis (13, 14). These sequence-specific interactions mediate postmitotic reactivation of their respective differentiation programs. With few exceptions (15, 16), most mitotically retained proteins exhibit sequence-specific recognition of regulatory DNA elements in target genes, indicating that sequence specificity is an important property of nuclear regulatory proteins that remain associated with mitotic chromosomes.

**Scaffolding proteins.** Another shared property of transcription factors that bookmark target genes during mitosis is that these proteins reside in specific nuclear microenvironments in the interphase nucleus and assemble multi-protein regulatory complexes at strategic sites of target gene promoters that often contain chromatin remodeling factors, coactivators, and cosuppressors (17). To what extent...
the cohort of coregulatory proteins is retained on mitotic chromosomes with the scaffolding proteins remains to be determined. Experimental evidence is provided by the Runx2 transcription factor. Runx2 coordinates cell proliferation, growth, and differentiation by regulating both the RNA Pol I and RNA Pol II genes (18, 19). During mitosis, Runx2 selectively occupies target genes regulated by RNA Pol II, as well as the RNA Pol I rRNA genes. Biochemical and in situ studies reveal that Runx2 remains associated with TLE2, a cosuppressor of Runx target genes, but dissociates from HDAC1, another coregulator (20). Additional examples of coregulatory proteins without known DNA-binding activity include bromodomain containing BRD proteins that recognize acetylated histones and remain associated with mitotic chromosomes (15, 16, 21). Global proteomics and multiplex in situ studies are warranted to further explore the complete cohort of coregulators that remain associated with mitotically retained transcription factors.

**Lineage master regulators.** Most of the transcription factors that bookmark target genes during mitosis are also master regulators of respective lineages. For example, GATA1, which remains associated with target genes during mitosis for their reaction after cell division, is a master regulator that controls erythroid lineage differentiation from hematopoietic stem cells (13, 22). Similarly, FoxA1 regulates specification of liver cell differentiation (14, 23). Other examples include Runx factors that regulate the hematopoietic (Runx1), osteogenic (Runx2), and gastrointestinal/neurogenic (Runx3) lineages, the key adipogenic regulator C/EBPα, and MyoD, the master regulator of muscle differentiation (11, 12, 18, 24–29). These observations raise an interesting possibility that lineage identity is, in part, sustained by mitotic gene bookmarking. Additional studies are required to establish whether mitotic bookmarking of genes is a common property of all lineage-determining transcription factors.

**Dynamics of mitotic bookmarking.** It is becoming increasingly evident that mitotic bookmarking of target genes for rapid activation is a shared property of phenotypic transcription factors. However, the mechanistic underpinnings of the process remain underexplored. Insights into the process have been provided by live-cell imaging experiments that combined the power of live cell microscopy and fluorescence recovery after bleach to establish kinetics of gene reactivation postmitotically (21, 30, 31). For example, Prasanth and colleagues have shown that specific gene loci that are active before mitosis exhibit increased kinetics of activation in postmitotic cells (31). Recruitment kinetics for the RNA Pol II and chromatin modifier BRD4 are different in interphase and mitotic cells. Mechanistically, enhanced BRD4 recruitment results from increased levels of H4K5Ac on the previously activated locus. BRD4 accelerated the dynamics of mRNA synthesis by decompacting chromatin and hence facilitating transcriptional reactivation. Previous studies showed that components of the transcriptional regulatory and RNA-processing machineries sequentially enter the telophase nuclei after the nuclear envelope is re-formed (31). These studies reveal that genes activated before mitosis are marked for rapid reactivation following mitosis, and the machinery is assembled in situ to resume transcription immediately after cell division (30). Such single-cell studies elucidate kinetics of gene activation following mitosis. However, use of GFP for live-cell microscopy requires the expression of artificially constructed transgenes ectopically expressed in cells above physiologic levels. It remains to be established whether the endogenous proteins under physiologic conditions follow similar kinetics. Additional considerations include quantitative determination of transcription factor concentration/association/dissociation analyses and mobility of proteins involved in epigenetic bookmarking.

**Properties of genes that are bookmarked in mitosis**

As discussed earlier in this review, for decades, it had been assumed that highly compact and condensed mitotic chromosomes are not accessible to nonhistone proteins to the chromatin. It has, however, become increasingly evident that despite compaction, some regions of the mitotic chromosomes remain in an open conformation and accessible to regulatory proteins and that the mitotically bookmarked genes share several properties:

**Nuclease accessible.** In the mid-1970s, pulse-chase radiolabeling experiments on mitotic chromosomes of the kangaroo rat revealed that the compacted mitotic chromosomes were indeed amenable to nuclease digestion (8). Subsequent studies using LM-PCR identified several genes, including Hsp70 and Myc among others that were accessible to nuclease and were occupied by regulatory proteins (32). For example, the Myc gene, which is repressed during mitosis, is rapidly reactivated after cells divide. Many sequence-specific proteins that recognize and bind to single-stranded DNA (e.g., hnRNP K and FBH) regulate Myc gene transcription. Interestingly, several genes that are rapidly reactivated after mitosis are selectively sensitive to permanganate only during mitosis, but not in other stages of the cell cycle. These observations indicate a unique and selective behavior of bookmarked genes during mitosis, in which they are accessible to single-strand DNA-binding proteins for rapid reactivation postmitotically. Genome-wide studies are required to assess whether nuclease accessibility is a common feature of all mitotically bookmarked genes.

**Enrichment of selective histone modifications and/or histone variants H2A.Z and H3.3 in gene promoters.** There is emerging evidence that the nucleosomes of bookmarked genes are enriched in histone variants, particularly in H2A.Z and H3.3. Ng and Gurdon have shown that the memory for the myogenic gene MyoD expression, in which histone H3.3 has been incorporated into the nucleosomes, can persist through 24 cell divisions in the absence of transcription (33). Mechanistically, the association of a mutated histone H3.3, which lacks the methylatable H3.3 lysine 4, with promoter DNA eliminates memory, indicating a requirement of H3.3 K4 for memory (33). An alternate mechanism of gene bookmarking by histone variants is provided by genome-wide association of H2A.Z (34). Kelly and colleagues have shown that in active gene promoters +1, nucleosomes immediately downstream of the transcription start sites (TSSs) containing H2A.Z, shift upstream to occupy TSSs during mitosis, significantly reducing...
nucleosome-depleted regions (34). This change seems to be specific to active genes that are silenced during mitosis and rapidly reactivated postmitotically (e.g., GRP78 gene). Importantly, these authors find that trimethylation of lysine 4 at histone H3 (H3K4me3) is also maintained enriched at these promoters during mitosis, whereas other epigenetic markers of active chromatin are lost.

Histone modifications play a key role in epigenetically regulating gene expression in the interphase cells and their role in bookmarking genes during mitosis has been well studied (1). Additional evidence for a role of histone modifications in mitotic gene bookmarking is suggested by observations at the level of a higher-order chromosome architecture (35). In this study, Terreno and colleagues have found a striking similarity in the distribution patterns of histone H3K4me3 between interphase and metaphase cells. It is notable that the methylation of histone H3 at lysine 4, in combination with histone H2A.Z variant, provides a mark for activation-associated acetylation of genes in the interphase (36). Although it remains to be investigated whether a gene that is active in G2 cells is selectively marked during mitosis via H3K4me3 modification, and is acetylated before reactivation in G1 cells, these observations suggest that a mitosis-specific histone code may, in part, orchestrate gene bookmarking. Together, these observations indicate that various chromatin marks that include selective incorporation of histone variants and retention of specific epigenetic posttranslational modifications contribute to mitotic gene bookmarking.

Demarking by cohesion. Is bookmarking of genes during mitosis a universal phenomenon? It is unclear, and unlikely, that all genes that are rapidly reactivated postmitotically are occupied by transcription factors during mitosis. In fact, it has been shown that many sequence-specific transcription factors are selectively displaced from mitotic chromosomes (10). Displacement of transcription factors from mitotic chromosomes indicates the presence of additional epigenetic mechanisms that do not involve occupancy of target genes by transcription factors. Recently, genome-wide chromatin immunoprecipitation studies followed by high-throughput sequencing have revealed binding patterns for hundreds of transcription factors (37). These studies show that bound transcription factors are highly clustered and that these clusters are enriched in binding motifs for several major transcription factor classes. Strikingly, most clusters are formed around cohesion, a protein required for chromosome condensation during mitosis (38). Mechanistically, cohesion plays two key roles: During the S phase of the cell cycle, it holds the replicating strands together at the transcription factor cluster sites, and during mitosis, it remains bound to the clusters even when the transcription factors have been displaced from target genes. Functionally, loss of cohesion decreases both DNA accessibility and binding of transcription factors to clusters. These results provide a mechanistic explanation of a decades-long observation that mitotic chromosomes are nucleosome accessible (8). Furthermore, these observations suggest that cohesion binding promotes reestablishment of transcription factor clusters and reactivation of target genes after DNA replication as well as after mitosis, thus providing a secondary mechanism for maintaining cellular memory through cell divisions.

Implications of Mitotic Gene Bookmarking

Sustained lineage identity

In committed cells, lineage identity must be sustained as cells replicate and equally distribute genetic information to progeny. Mitotic gene bookmarking by transcription factors, in combination with DNA methylation and histone modifications as well as selective incorporation of histone variants in the chromatin of bookmarked genes, provides a mechanistic basis for sustained lineage identity through cell divisions. Studies over the past decade have demonstrated that several phenotypic transcription factors remain associated with target genes during mitosis for rapid transcriptional control postmitotically. So far, more than 15 transcription factors including many lineage-determining factors have been reported to be associated with mitotic chromosomes (39). Examples include the basic helix–loop–helix myogenic regulatory factors in muscle cell differentiation, CCAAT/enhancer-binding protein β in the adipocyte differentiation program, FoxA1 in liver cells, GATA1 and Runx1 in hematopoietic lineage differentiation, and Runx2 in osteoblast differentiation (11, 13, 14, 24, 25, 27). Frequently, these phenotypic transcription factors associate with selected target genes involved in cell growth, proliferation, and differentiation, thus coordinating maintenance not only of lineage identity but also cellular potential for a physiologic balance between growth and proliferation. Despite the growing list of mitotically retained transcription factors, our current understanding for functional role(s) of mitotic gene bookmarking remains minimal. For example, it is not clear if mitotic occupancy of a target gene by the transcription factor is a prerequisite for reactivation postmitotically. Furthermore, are all mitotically retained transcription factors functional immediately after mitosis or is the mitotic retention merely a mechanism to equally distribute regulatory proteins to progeny cells? Genome-wide experimental approaches involving endogenous transcription factors in biologically relevant systems will provide mechanistic insights into functional relevance of mitotic gene bookmarking in maintaining epigenetic cell memory in progeny cells.

Maintenance of stem-cell niches

It is hypothesized that, in contrast with embryonic stem cells, adult stem cells undergo at least one round of asymmetric cell division to generate lineage-committed cells and maintain the stem-cell pool. We have discussed recent observations that lineage-determining transcription factors associate with target genes during symmetrical cell division to maintain cellular identity. We suggest a requirement for asymmetric bookmarking of target genes in lineage-committed stem cells by phenotypic transcription factors or by oncogenes in cancer stem cells to generate committed or transformed cells. Despite broad-based relevance, asymmetric cell division has been predominantly studied in yeast or Drosophila. For example, in budding yeast, the Ace2 chromatin-remodeling factor is asymmetrically accumulated in the nucleus of the daughter cell, perhaps regulating gene expression that is restricted to the progeny cell (40). During Drosophila neurogenesis, Numb, an attenuator of Notch signaling, and the Prospero transcription factor are
selectively distributed to progeny cells as a mechanism to maintain the stem-cell population and to give rise to committed cells (41). Similar mechanisms may be operative in mammalian cells. In fact, there is compelling evidence for asymmetric orientation of the mitotic spindle in gut epithelium as well as in muscle stem cells that dictates lineage commitment as well as maintenance of the stem-cell pool (42–44). However, experimental evidence and a model system to establish the existence of asymmetrical mitotic gene bookmarking in mammals are lacking. To which extent cancer stem cells undergo asymmetric and/or symmetric cell division remains open ended and clinically and biologically relevant. This may have important implications for developing therapeutic strategies that target the persistent tumor progenitor pool or actively dividing tumor cells that have escaped from the cancer stem-cell niche. Despite current experimental limitations, epigenetic bookmarking provides a flexible, yet cell type–specific and context-dependent mechanistic dimension to gene regulation.

Propagation of disease phenotype

Evidence is accruing that mitotic gene bookmarking may have an important role in the onset, progression, and perpetuation of disease. This is illustrated by the leukemic fusion protein AML1-ETO that blocks myeloid differentiation and enhances proliferative potential (27). Interestingly, mitotic association of the leukemic AML1-ETO with the rRNA genes, as well as with genes controlling cell proliferation and myeloid cell differentiation, upregulates rRNA and cell proliferation-related genes, but downregulates gene mediators of myeloid cell differentiation, promoting and or supporting transformed phenotype. Another recent example of cancer-related mitotic gene bookmarking is the mixed lineage leukemia (MLL) protein. MLL is a chromatin-remodeling factor that is associated with leukemia and regulates transcription by recruiting chromatin modifying machinery to target genes. This mitotic retention favors rapid reactivation of target genes required for the onset and progression of MLL postmitotically (45). It will be informative to establish whether mitotic bookmarking of cancer-related genes is a shared trait of all sequence-specific oncogenic proteins.

Concluding Remarks

Mitotic bookmarking of target genes by sequence-specific transcription factors is emerging as a frequently invoked epigenetic mechanism to sustain lineage identity in normal cells and to perpetuate the transformed phenotype. Further insights into mechanistically understanding bookmarking requires addressing questions such as the following: (i) Is mitotic retention of regulatory proteins a transcriptional regulatory mechanism to reactivate gene expression postmitotically, or do some mitotically retained proteins merely use dividing chromosomes as vehicles for equal distribution into progeny cells? (ii) Do signaling pathways operative before mitosis dictate which genes will be bookmarked? (iii) What are the dynamics of coregulatory protein complex organization and activity during mitosis? (iv) Does the cohort of coregulatory factors that remain associated with transcription factors define the postmitotic transcriptional status of bookmarked genes? (v) Does colocalization of genes in the chromatin microenvironment contribute to mitotic gene bookmarking? and (vi) Can the accumulation of transcription factors on mitotic chromosomes be therapeutically targeted in dividing cells? Additional studies will be necessary to further elucidate a functional link between mitotic gene bookmarking and maintenance of cellular memory within the context of biologic control and pathology of cancer.

Disclosure of Potential Conflicts of Interest

No potential conflicts of interest were disclosed.

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Grant Support

These studies were in part supported by the grants from the NIH (P01 CA098233 and P01 AR48818 to G.S. Stein; R01 AR039588 to G.S. Stein and J.B. Lian; R03 CA167726 to S.K. Zaidi; and R37 DE 012528 to J.B. Lian) and FONDAP (15090007 to M. Montecino).

Received October 1, 2013; revised November 1, 2013; accepted November 4, 2013; published OnlineFirst January 9, 2014.

References

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