Molecular Pathways: The Complexity of the Epigenome in Cancer and Recent Clinical Advances

Mariarosaria Conte and Lucia Altucci

Abstract

Human cancer is causally linked to genomic and epigenomic deregulations. Epigenetic abnormalities occurring within signaling pathways regulating proliferation, migration, growth, differentiation, transcription, and death signals may be critical in the progression of malignancies. Consequently, identification of epigenetic marks and their bioimplications in tumors represents a crucial step toward defining new therapeutic strategies both in cancer treatment and prevention. Alterations of writers, readers, and erasers in cancer may affect, for example, the methylation and acetylation state of huge areas of chromatin, suggesting that epi-based treatments may require “distinct” therapeutic strategies compared with “canonical” targeted treatments. Whereas anticancer treatments targeting histone deacetylase and DNA methylation have entered the clinic, additional chromatin modification enzymes have not yet been pharmacologically targeted for clinical use in patients. Thus, a greater insight into alterations occurring on chromatin modifiers and their impact in tumorigenesis represents a crucial advancement in exploiting epigenetic targeting in cancer prevention and treatment. Here, the interplay of the best known epi-mutations and how their targeting might be optimized are addressed. Clin Cancer Res; 18 (20); 1–9. ©2012 AACR.

Background

A number of epigenetic deregulations, such as DNA methylation, histone modifications, and microRNA-based modulation, have been progressively reported as causally involved in tumorigenesis and progression. In the past decade, several chromatin-modulating enzymes have been discovered and classified, and their aberrations linked to cancer. The state of chromatin is widely controlled by specific DNA- and protein-related modifications. Understanding the histone code and its crucial role in biology led to the study of enzymes that “write” these modifications, the so-called writers, those that recognize modified chromatin, termed readers, and erasers, which are able to remove a specific modification (1). The interpretation of epigenetic changes underlines the phenotypic variability of cells belonging to the same genome. Therefore, identification of epigenetic marks and their bio-implications in tumors represents a crucial step toward defining new therapeutic strategies both in cancer treatment and prevention (2). Alterations of writers, readers, and erasers in cancer may affect the status of chromatin in vast areas of the epigenome, thus suggesting that epi-based treatments may require “distinct” therapeutic strategies compared with “canonical” targeted treatments (3).

Chromatin modifiers and cancer

Chromatin structure can be remodeled by covalent modifications of DNA involving methylation of cytosine within CpG islands and a multitude of histone modifications in both their N-terminal and C-terminal tails, or even in their globular domains. Histone modifications dynamically change chromatin structure (so-called “epigenetic plasticity”). Histone modifications are involved in the neutralization/deneutralization of the positive charges present on histones and alter chromatin structure by determining an on–off state of transcription. In particular, histone acetylation is conducted by histone acetyltransferase enzymes (HAT), an example of writers. HATs acylate conserved amino acids on histones through the transfer of an acetyl group from Acetyl-CoA to form e-N-acetyl-lysine, thus neutralizing positive cells. Histone acetylation is a posttranslational modification linked to transcriptional activation. Conversely, histone deacetylases (HDAC), an example of erasers, define the removal of acetyl groups from an e-N-acetyl-lysine amino acid on a histone, thus preventing transcription by increasing positive charges of histone tails and thus determining high-affinity binding with DNA. The fact that modulation by writers and erasers can also involve nonhistone substrates adds a further level of complexity (4).
Therefore, a great deal of attention has been focused on chromatin-modifying enzymes to define their deregulation in cancer and their potential as therapeutic targets.

**HATs and cancer**

HATs belong to one of two main categories. A-type HATs acylate nucleosomal histones within chromatin, whereas B-type HATs play a much broader role in the cell. A-type HATs are classified into 4 families sharing sequence homology within the HAT domain and include Gcn5/P300/CBP-associated factor (PCAF; ref. 5), MYST (6), p300/CBP (7), and Rtt109, the latter reported to be mycotic specific (8). In prostate cancer both p300 and CREB-binding protein (CBP) are overexpressed, thus altering androgen receptor-responsive gene modulation. CBP is also involved in transcriptional regulation (9;16) in which monocyotic leukemia zinc finger protein (MOZ), an acetyltransferase localized on 8p11, is fused to CBP (9). Mutations in p300 (more frequently C-terminal truncations) have been found in many tumors such as breast, pancreatic, colorectal, gastric, cervical, and ovarian cancers (10–12). Recently, downregulation of PCAF has been correlated to gastric carcinoma progression linked to poor clinical outcome. Mutation in Tip60 is associated with the development of prostate cancer through deregulation of DNA repair and resistance to apoptosis. PCAF and Gcn5 are overexpressed in diseases of the central nervous system in pediatric patients and Wilms tumors (13). Rtt109, correlated to modifications of histones H3 in K9, K27, and K56, plays a critical role in nucleosome assembly (Supplementary Table S1 and Fig. S1).

**Global (de)acetylation, HDACs, and cancer**

The balance between HDAC and HAT activities plays a crucial role in regulating gene expression. Future studies will be needed to verify whether the modulation of chromatin acetylation is causally linked to cancer development or if it is caused by complex epi-deregulations. Whether cancers characterized by global alterations of chromatin acetylation state may benefit (and how) from an epi-based therapeutic approach is an issue that still needs to be addressed further (Supplementary Table S2). HDACs play a key role in gene regulation and therefore in human cancers, such as leukemia (14). HDACs are divided into 4 classes: class I HDACs (HDAC1, 2, 3, and 8), which are homologous to *Saccharomyces cerevisiae* Rpd3; class II (further divided into class IIA and IIB) HDACs (HDAC4, 5, 6, 7, 9, and 10), which are homologous to yeast Hda1; class III HDACs (sirtuins) including enzymes homologous to yeast Sir2 involved in modulation of longevity, metabolism, and physiology; class IV comprising only HDAC11, which shares homology with class I and II. HDACs are overexpressed in several cancers. In particular, HDAC1 is highly expressed in many malignancies including gastric, colorectal, hepatic, breast, and pancreatic cancer (15–17). HDAC2 has been found mutated in colon cancer and is overexpressed in esophageal, prostate, and gastrointestinal carcinomas (18–20). Many other cancers associated with poor prognosis, such as prostate, gastric, colorectal cancer, and chronic lymphocytic leukemia (CLL; 17, 19, 21, 22) have been reported to display HDAC3 overexpression. The class Ia histone deacetylase HDAC4 is expressed in a tissue-specific manner and promotes the growth of colon cancer cells through repression of the cell-cycle regulator p21 (23). HDAC5 downregulation has been reported in lung cancer (24), although its overexpression has been found in colon cancer (25). Downregulated expression levels of HDAC6 have been observed in lymphoma (26), whereas higher expression levels are associated with oral squamous cell cancer (27). The role of HDAC8 has been investigated in CLL (chronic lymphoid leukemia) in children (28). Of the class III HDACs, SIRT1 is involved in carcinogenesis and above all in age-related neoplasms. In particular, sirtuins are correlated to aging, cancer, and stress response. SIRT1 overexpression has been found in prostate, colon, and skin cancers as well as in acute myeloid leukemia (AML; 29). In addition to SIRT1, other sirtuins (such as SIRT4 and 7) are linked to cancer development (30). Conversely, low levels of SIRT2 have been observed in gastric carcinoma and in gliomas. For some sirtuins, such as SIRT3, the scenario is complicated by the fact that both upregulation and downregulation have been reported in different forms of breast cancer. SIRT4 loss may contribute to diabetes, a major risk factor for cancer. SIRT6, which also displays ADP-ribosyltransferase activity, is widely overexpressed in brain and skeletal muscle. Finally, SIRT7 promotes active transcription of rRNA genes and lower levels of this enzyme have been found in nonproliferating tissues such as heart, brain, and skeletal muscle (Table 1).

**PRMTs, KMTs, KDMs, and cancer**

Histones are methylated by enzymes including arginine methyltransferases (PRMT) and lysine methyltransferases (KMT). The presence or absence of methyl marks on specific histones is crucial for gene expression regulation and has implications in carcinogenesis. PRMT1 is an important component of mixed-lineage leukemia (MLL) oncogenic fusion proteins (31). PRMT6 is responsible for H3R2 (histone H3 Arginine 2) methylation, counteracting H3K4me3 (histone H3 lysine 4 trimethylation) deposition. High levels of PRMT1 have been observed in breast and colon cancers (32). PRMT2 can interact with estrogen receptor and acts as a strong coactivator of androgen receptor. PRMT3 is involved in the regulation of protein synthesis, whereas PRMT4 (CARM1, coactivator-associated arginine methyltransferase1) is known to control the arginine-regulated mechanism of transcription. CARM1 methylates histone H3, and the mutation in the presumed binding domain decreases methyltransferase and p160 coactivator regulation (33). CARM1 is overexpressed in breast tumors and is essential for estrogen-induced cell-cycle progression (34). PRMT5 is highly expressed in a wide variety of lymphoma and leukemia cells as well as in gastric carcinoma and immortalized fibroblast cells (35).

Many KMTs are strongly associated with cancer. Lysine methylation occurs in a very large number of histones, deposited by KMTs and removed by lysine demethylases.
DNA methylation and cancer

DNA methylation has frequently been described as a static silencing event. DNA methylation is not, however, static, as recently shown by the variable 5mC-oxidation kinetics at distinct genomic/functional loci and by the fact that 2HG (product of IDH-1 and -2) mutation has been found in leukemia (42).

In recent years genome-scale mapping of methylation has revealed that DNA methylation is involved in different (epi)-genetic settings. Methylation is catalyzed by DNA methyltransferases (DNMT). Several cancers are associated with quantitative or positional alterations of DNA methylation. Furthermore, DNMT3a mutations have been found in AML (43). Thus, DNA methylation is the subject of intense studies aimed at better understanding alterations in tumors via trimethylation of H3K9. Numerous mutations and rearrangements of MLL1 (KMT2A) have been observed in leukemia/myeloma. MLL4 (KMT2D) is involved in liver oncogenesis. MLL4 has been identified as powerful p300 and PCAF inhibitors. However, their metabolic instability precludes their use as anticancer drugs. Other PCAF inhibitors include isoazolones and analogs that act as specific acetylation inhibitors in a dose- and time-dependent manner, and their anticancer properties have been studied in liver cancer cells. Polysoprenylated benzophene derivatives (PBD) have been proposed as candidates for HAT modulation. Garcinol is a B-type PBD active against viruses, bacteria, gastric ulcers, and cancer, such as colon adenocarcinoma (50). Garcinol derivatives based on iso-garcinol have been synthesized. These include LTK-13, -14, and the disulphonyl-substituted derivate LTK-19. Another promising HAT inhibitor is angucyclol, the main component of cashew nut shell liquid. This compound is able to reduce breast cancer cell proliferation in vitro and in vivo (53).

Clinical-Translational Advances

HDAC inhibitors

Much attention has been focused on HDAC inhibitors mainly because HDACs are often overexpressed in cancer. HDAC inhibitors are therefore considered a potential strategy to reverse epigenetic aberrations associated with cancer, and many compounds have been tested in clinical trials (46). For an in-depth description of the role of HDAC inhibitors in cancer we refer the reader to refs. 47–49 and references therein. Whether isotype-selective HDAC inhibitors offer greater therapeutic benefits (or lower adverse effects) than broadly acting HDAC inhibitors (pan HDAC inhibitors) remains one of the issues to be addressed in the clinic (Supplementary Table S3 and Fig. S1).

HAT inhibitors

Few and poorly validated small molecules modulating HATs are currently available. In the past decade, 2 substrates analogous to peptide-CoA conjugates, Lys-CoA and H3-CoA-20, have been identified as powerful p300 and PCAF inhibitors. However, their metabolic instability precludes their use as anticancer drugs. Other PCAF inhibitors include isoazolones and analogs that act as specific acetylation inhibitors in a dose- and time-dependent manner, and their anticancer properties have been studied in liver cancer cells. Polysoprenylated benzophene derivatives (PBD) have been proposed as candidates for HAT modulation. Garcinol is a B-type PBD active against viruses, bacteria, gastric ulcers, and cancer, such as colon adenocarcinoma (50). Garcinol derivatives based on iso-garcinol have been synthesized. These include LTK-13, -14, and the disulphonyl-substituted derivate LTK-19. Another promising HAT inhibitor is angucyclol, the main component of cashew nut shell liquid. This compound is able to reduce breast cancer cell proliferation in vitro and in vivo (53). Whether isotype-selective HDAC inhibitors in cancer we refer the reader to refs. 47–49 and references therein. Whether isotype-selective HDAC inhibitors remain one of the issues to be addressed in the clinic (Supplementary Table S3 and Fig. S1).

PRMT, KMT, and KDM inhibitors

PRMT alterations correlate with many cancers. Hence, molecules able to modulate methyltransferase activity are desirable for cancer treatment. Chaetocin, a fungal mycoxin, is an SU1V39H1 methyltransferase inhibitor reported to exert antitymelyoma activity in interferon 6-dependent and -independent myeloma cell lines, and in vivo (53). BIX01294 was the first small-molecule inhibitor of G9a and GLP. BIX01294 has been reported to inhibit the histone methyltransferase EHMT2, which acts as a corepressor for...
Figure 1. Schematic representation of histone acetylation and methylation: chromatin marks and epi-enzyme deregulation in cancer. Chromatin enzymes able to deposit or erase an epigenetic mark are indicated as writers (teal blue) and erasers (purple), respectively. Epi-drugs able to inhibit the activity of chromatin enzymes are indicated as blockers (brown). For histone methylation: Ash1, absent, small, or homeotic discs 1G9a; EED-EZH2, enhancer of zeste homolog 2; EHMT2, euchromatic histone-lysine N-methyltransferase 2; MLL1/2, lysine N-methyltransferase 2; PRMT1 and PRMT6, protein arginine N-methyltransferase 1 and 6; Set1 and Set2, spin echo T1 and T2 sequences; SETDB1, SET domain bifurcated 1; Smyd3, SET domain-containing protein with histone methyltransferase activity on histone H3 K4; SUV39H1/2, suppressor of variegation 3 to 9 (Drosophila) homolog 1/2; SUZ12, suppressor of zeste 12 protein homolog. For histone acetylation: CBP, CREB binding protein; Gcn5, general control of amino-acid synthesis, yeast, homolog-like 2; p300, protein 300; MOZ, monocytic leukemia zinc finger protein; MYST3 and MYST4, MYST histone acetyltransferase (monocytic leukemia) 3 and 4; PCAF, p300/CBP-associated factor; Rtt109, regulator of Ty1 transposition protein 109; Tip60, HIV1 Tat interacting protein. For histone demethylation: JKDM8, jumonji domain of human lysine-specific demethylase 8; JMJD5, jumonji domain-containing protein 5; KDM1 and KDM2B, lysine-specific demethylase 1 (LSD1 and LSD2B); M1B, methylation-inhibited binding protein 1; SET8, SET domain-containing protein 8; SUV4, suppressor of variegation 4 homolog 2. For histone deacetylation: HDAC1, HDAC2, and HDAC3; SIRT1, silent information regulator 1.
specific transcription factors and is strongly overexpressed in bladder carcinomas (54). A large virtual screening effort has been carried out to identify PRMT inhibitors using the ChemBridge compound collection containing more than 300,000 compounds. Among these, acyl derivatives of p-aminosulfonamides and dapsone have been selected. In particular, dapsone has been suggested for the treatment of glioblastoma (55). Intensive efforts are currently ongoing for the identification of novel selective PRMT inhibitors.

Tranylcypromine (trans-2-phenylcyclopropylamine) and its analogues are among the best known LSD1 (or KDM1) inhibitors. Tranylcypromine has been proposed for the treatment of sarcomas as well as fibrous and peripheral nerve sheath tumors (56). Furthermore, the therapeutic potential of these 2 inhibitors has been reported for the treatment of promyelocytic leukemia (57). The KMT inhibitor 3-Deazaneplanocin A (DZNep) interferes with the polycomb-repressive complex 2 and induces apoptosis in

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cancer cells, for example in AML. Moreover, inhibition of EZH2 by DZNep reduces proliferation in breast cancer cell lines (58). In AML, cotreatment with DZNep and panobinostat, an HDAC inhibitor, exerts an apoptotic effect on primary leukemia cells but not on normal cells (59).

**DNMT inhibitors**

The Food and Drug Administration has approved the DNMT inhibitors 5-azacytidine (azacytidine) and 5-aza-2-deoxycytidine (decitabine) for myelodysplastic syndromes (60). Decitabine has also been used to force reexpression of silenced estrogen receptor in triple-negative breast cancer. Another important DNMT inhibitor is zebularine, which is selectively incorporated into malignant cells but not into normal cells. Cancers such as ovarian and cervical carcinomas can be treated with the DNMT inhibitor hydralazine (61). Besides nucleoside DNMT inhibitors, nonnucleoside targeted molecules directly inhibiting DNMTs have been developed. Among these, the phosphorothioate antisense oligonucleotide MG98, currently being investigated in a phase I study, has been tested in patients with high-risk myelodysplasia and AML (62). RG108 displays demethylating activity comparable with that of zebularine in lymphoid, myeloid, and colorectal cancers. The quinoline-based compound, SGI-1027, inhibits DNMT1, DNMT3a, and DNMT3b and has been proposed for hepatocellular, cervical, prostate, and breast cancer in vitro (63). Finally, the antibiotics mithramycin A and nanaomycin have recently been reported to inhibit DNMT3B reactivation (64).

**Targeting the complexity of epigenetic modifications**

Misregulation of the physiologic pattern of chromatin modifications (mainly DNA methylation and histone modifications) can induce the promotion and progression of cancer. Chromatin modifications may be regulated by writers and erasers and interpreted by readers. These events give rise to a complex epi-modulated scenario, where both single modifications/single enzymes and the interplay with other histone marks/enzymatic complexes (possibly mutually exclusive or additive) need to be taken into account to achieve a better understanding of epigenetic deregulation in malignancies. In recent years a large number of high-throughput screening-based studies in cancer models have highlighted both the importance of specific histone marks and epi-enzymes in cancer and their interconnection with other marks in wide areas of chromatin, suggesting the importance of the positioning (potentially mutually exclusive) of marks and chromatin modifiers in cancer pathogenesis and progression. Such scenarios point to the existence of a very complex "code" of mechanisms and their deregulation in cancer, underlining the difficulties involved in evaluating these mechanisms as therapeutic targets. Additional complexity arises from the difficulty in determining a hierarchy in epigenetic mark deposition. The fact that new modifications are still being uncovered makes the combinatorial repertoire of epigenetic marks appear endless. Currently, detailed knowledge of a hierarchy—mutual exclusiveness or interdependence—is restricted to a handful of well-studied marks such as histone methylation on H3K4 or DNA methylation. Only in a few cases has a "true" hierarchy been successfully established, such as the requirement of H2B ubiquitylation for the deposition of the active histone mark H3K4me3 (65). Mutual exclusiveness has been reported for repressive DNA methylation and histone H3 lysine 27 trimethylation (H3K27me3) on CpG-islands (66). A well-known example of hierarchy is the dependence of 5-hydroxymethylation of cytosines on 5-methylcytosine as its substrate.

Translating our current knowledge from bench to bedside will involve identifying and developing new forms of "targeted" treatment, where large areas of chromatin within cancer cells are likely to be influenced by the forced modification of their epigenetic status. This consideration should lead to a reevaluation of the therapeutic scheme for existing epi-based cancer treatments as well as to a cautious patient stratification currently complicated by the presence of very few, if any, epi-biomarkers of response to treatment and prognosis. For example, only the predictive power of HR23B for clinical response to HDAC inhibitors in cutaneous T-cell lymphoma seems to be confirmed (67). Whether within this complex framework the anticancer action of epi-based modulators can be linked to "pure" epi-effects alone and/or to what extent nonepigenetic action needs to be evaluated remains unclear. Furthermore, the fact that apparently opposite deregulations of the same epi-target have been reported complicates the interpretation of the cancer epigenome. These contradictory findings might be explained by the hypothesis that opposite quantitative epi-alterations may lead, in some cases, to similar readouts in cancer, causing or contributing to a complex disorder of chromatin (and related gene expression) and its potential combinatorial patterns. As things stand, further knowledge is needed to mine the real value of some of the epi-target deregulations in cancer as well as to identify differences and specificities both for cancer disease and epi-modifiers. An additional and largely unexplored level of complexity is presented by the modulation of nonhistone targets by small epi-molecules and by the fact that very few epi-based treatments (mainly HDAC inhibitors and DNA demethylating agents) have actually entered the clinic. Lessons learned from the use of HDAC inhibitors in cancer treatment suggest, for instance, that modulation of histone acetylation should be considered as a readout of the effects of treatment and not, as initially proposed, as a parameter of clinical response to treatment. Thus, one parameter of choice might be represented by the quantitatively unbalanced presence of writers/readers/erasers (overexpression or silencing) or by a specific mutation in one of these enzymes. However, although the selection of patients on the basis of HDAC expression levels might prove useful, at least in in vitro settings, this parameter does not always seem to be predictive of a better response. The scenario might, however, be different when epi-enzymes are mutated in cancer. This type of epigenetic modification is currently under investigation to identify and validate biomarkers and may allow patient stratification. It also offers the exciting possibility of synthesizing
selective small molecules able to modulate only the mutated enzyme, thus acquiring features of tumor-selective action. Interestingly, different categories of enzymes appear to act differently: HDACs, for example, are more often quantitatively modulated in cancer (with the exception of HDAC2 mutation), whereas HATs seem more frequently mutated. However, the implications of this difference still need to be investigated. Moreover, a further level of complexity is added by new discoveries continuously being made in this field: Novel chromatin marks are identified and the efforts for mining these targets (alone and within the context of others) may rapidly change our view. For example, hydroxymethyl cytosine, along with its modulation, is at present the focus of discussions aimed at understanding its mode of action and its potential role in cancer.

Finally, it is debated whether more selective or broader-acting chromatin modulators should be chosen as an approach to epi-treatment in cancer. Although mutated targets might benefit from a selective epi-drug approach (better if active exclusively on the mutant), a broad modulator might present greater advantages in the case of concomitant alterations of different chromatin modifiers and marks. Multiple epi-modulators (targeting more than one class of enzymes, for instance) may also represent a promising approach (68), as could the creation of hybrid molecules able to act broadly on a class of epi-modifiers and to simultaneously mark a specific non–epi-target within cancer cells. This last approach, which still needs to be fully validated, might “remodulate” chromatin in a more targeted manner.

Disclosure of Potential Conflicts of Interest
No potential conflicts of interest were disclosed.

Authors’ Contributions
Conception and design: L. Altucci Writing, review, and/or revision of the manuscript: M. Conte, L. Altucci Study supervision: L. Altucci

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