

## REVIEW

# Writing, erasing and reading histone lysine methylations

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Histone modifications are key epigenetic regulatory features that have important roles in many cellular events. Lysine methylations mark various sites on the tail and globular domains of histones and their levels are precisely balanced by the action of methyltransferases ('writers') and demethylases ('erasers'). In addition, distinct effector proteins ('readers') recognize specific methyl-lysines in a manner that depends on the neighboring amino-acid sequence and methylation state. Misregulation of histone lysine methylation has been implicated in several cancers and developmental defects. Therefore, histone lysine methylation has been considered a potential therapeutic target, and clinical trials of several inhibitors of this process have shown promising results. A more detailed understanding of histone lysine methylation is necessary for elucidating complex biological processes and, ultimately, for developing and improving disease treatments. This review summarizes enzymes responsible for histone lysine methylation and demethylation and how histone lysine methylation contributes to various biological processes. *Experimental & Molecular Medicine* (2017) 49, e324; doi:10.1038/emm.2017.11; published online 28 April 2017

## INTRODUCTION

In eukaryotic cells, genetic information stored in DNA is present in a highly organized chromatin structure. The nucleosome, the basic unit of chromatin, is composed of two copies of each core histone, H2A, H2B, H3 and H4, wrapped by about two turns of DNA.<sup>1</sup> Protruding unstructured N-terminal tails as well as structured globular domains of each histone are subject to post-translational modifications that include methylation, acetylation, phosphorylation and ubiquitylation, among others.<sup>2,3</sup> These histone modifications affect chromatin structure and also provide binding platforms for diverse transcription factors, such as chromatin remodelers, histone chaperones, DNA/histone-modifying enzymes and general transcription factors.<sup>2,3</sup> Thus, histone modifications have important roles in many cellular events, including gene expression, DNA replication and repair, chromatin compaction and cell-cycle control.<sup>2,3</sup> Misregulation of histone modifications has been implicated in the pathogenesis of cancer and in developmental defects, further emphasizing the importance of the regulation of histone modifications.<sup>4,5</sup>

Although histone methylation and its involvement in transcription were first reported in the 1960s,<sup>6</sup> it was only about 15 years ago that the first histone methyltransferase, SUV39H1, containing a catalytic SET (Su(var)3-9, Enhancer of Zeste, and Trithorax) domain, was identified,<sup>7</sup> igniting

discoveries of numerous histone methyltransferases based on SET-domain homology searches.<sup>8</sup> Until the discovery of an H3K4 demethylase LSD1 (lysine-specific histone demethylase 1),<sup>9</sup> histone methylations had been thought to turn over more slowly than other histone modifications. The subsequent discovery of the JmjC (jumonji C) domain as a key signature of demethylating enzymes<sup>10</sup> has substantially broadened our repertoire of histone demethylases.

There are three lysine methylation states—mono-, di- and trimethylation (me1, me2 and me3, respectively)—none of which changes the electronic charge of the amino-acid side chain; therefore, histone lysine methylation functions are considered to be mainly exerted by effector molecules that specifically recognize the methylated site.<sup>11</sup> These 'reader' proteins contain methyl-lysine-binding motifs, including PHD, chromo, tudor, PWWP, WD40, BAH, ADD, ankyrin repeat, MBT and zn-CW domains, and also have the ability to distinguish target methyl-lysines based on their methylation state and surrounding amino-acid sequence.<sup>12</sup>

Unlike other histone modifications, which simply specify active or repressed chromatin states, histone lysine methylations confer active or repressive transcription depending on their positions and methylation states.<sup>13</sup> Generally, H3K4, H3K36 and H3K79 methylations are considered to mark active transcription, whereas H3K9, H3K27 and H4K20 methylations

are thought to be associated with silenced chromatin states.<sup>13</sup> These histone lysine methylations also interact with other histone modifications as well as DNA methylation to regulate precisely gene expression. For example, H3K4 and H3K79 methylations are known to require prior H2B ubiquitylation in yeast.<sup>14</sup> Also, bivalent chromatin marked simultaneously by H3K4 and H3K27 methylations have an important role in shifting gene expression from a poised state to active or inactive states in embryonic stem cells (ESCs).<sup>15</sup>

Numerous studies have shown that mutation or misregulation of histone methylation, methyltransferases, demethylases and methyl-lysine-binding proteins are associated with various diseases.<sup>16</sup> Therefore, many histone methylation-related proteins are being studied as potential therapeutic targets.<sup>17</sup> Recent advances in next-generation sequencing, mass spectrometry, X-ray crystallography and cryo-EM techniques for analyzing histone modification-related proteins have allowed a more detailed understanding of relationship between histone methylation and diseases.<sup>3,18</sup>

In this review, we summarize how histone lysine methylations are regulated by histone methyltransferases ('writers') and demethylases ('erasers'), as depicted in Figure 1. We also discuss the biological roles of histone lysine methylations and associated diseases caused by misregulation of histone lysine methylations, as summarized in Table 1.

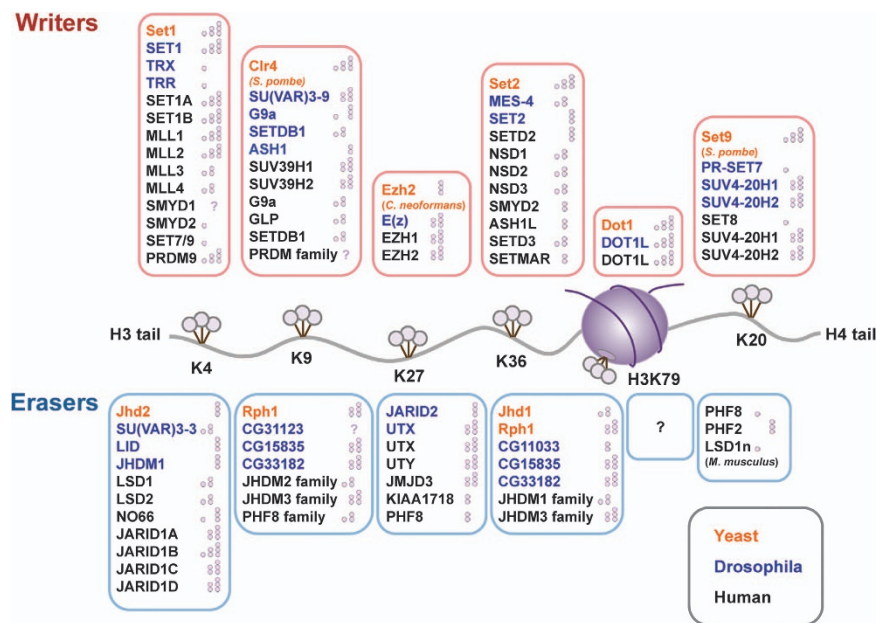
### H3K4 METHYLATION

#### H3K4 methyltransferases

H3K4 methylation is an evolutionarily conserved histone modification that marks active transcription and is highly enriched at the promoter region and transcription start site.<sup>19</sup> In yeast, all H3K4 methylations are carried out by Set1

methyltransferase, which forms a multisubunit Set1 complex, also known as COMPASS, with seven other subunits: Swd1, Swd3, Bre2, Sdc1, Swd2, Spp1 and Shg1.<sup>20–22</sup> Set1 contains a catalytic SET domain, in which H3K4 methyltransferase activity is assisted by associated Swd1, Swd3, Bre2 and Sdc1 subunits. The loss of individual Set1 complex subunits differentially affects Set1 stability, complex integrity, global H3K4 methylation level and distribution of H3K4 methylation along active genes.<sup>23</sup> H3K4 methyltransferases are highly conserved from yeast to human. *Drosophila melanogaster* contain three Set1 homologs (SET1, TRX and TRR), whereas mammals have six such homologs (SET1A/KMT2F, SET1B/KMT2G, MLL1 (mixed-lineage leukemia 1)/KMT2A, MLL2/KMT2B, MLL3/KMT2C and MLL4/KMT2D).<sup>19</sup> Each Set1 homolog, which functions as a scaffold protein within the complexes, associates with four common subunits (WRAD: WDR5 (WD repeat domain 5), RbBP5 (retinoblastoma-binding protein 5), ASH2L (absent, small or homeotic-2 like) and DPY30), as well as unique subunits that specify distinct functions.<sup>19</sup>

The association of WRAD with the SET domain of each SET1/MLL family protein (core complex) produces distinct enzymatic properties. The SET domain of MLL1 alone exhibits weak H3K4 monomethylation activity, but complex formation with WRAD allows it to predominantly mono- and dimethylate H3K4 *in vitro*.<sup>24</sup> The interaction of WDR5 with the MLL1 SET domain is crucial for association of ASH2L and RbBP5 with the MLL1 SET domain and H3K4 dimethylation activity of the assembled MLL1 core complex.<sup>25,26</sup> Biochemical analyses with purified proteins have further shown that MLL1/2 core complexes can catalyze H3K4 mono- and dimethylation, whereas the specificity of MLL3/4 core complexes is restricted



**Figure 1** A schematic depiction of a nucleosome showing principal lysine methylation sites on histones H3 and H4. The reported writers (methyltransferases) and erasers (demethylases) for each lysine methylation are also depicted with their methylation state specificities: single circle (○), me1; double circle (⊗), me2; triple circle (⊗), me3.

**Table 1 Summary of principal writer (methyltransferases), eraser (demethylases) and reader proteins for lysine methylation on histones H3 and H4 and their associated diseases**

Writer Name	Diseases	Erasers name	Diseases	Reader name	Domains	Functions	Diseases
H3K4	SET1A/KMT2E SET1B/KMT2F MLL1/KMT2A MLL2/KMT2B	Hepatocarcinogenesis <sup>293</sup> — Leukemia <sup>81</sup> —	Prostate cancer <sup>294</sup> Lung cancer <sup>296</sup> Lung carcinoma <sup>50</sup> Ankylosing spondylitis <sup>50</sup>	CHD1 BPTF TAF3 Sgf29	Chromo PHD PHD Tudor	Chromatin remodeler <sup>67</sup> NURF complex subunit <sup>68</sup> TFIID complex subunit <sup>69</sup> Crosstalk between H3K4me2/3 and H3 acetylation <sup>71</sup>	Prostate cancer <sup>295</sup> Alzheimer disease <sup>297</sup> — Hepatocarcinogenesis <sup>298</sup>
	MLL3/KMT2C MLL4/KMT2D	Urinary bladder <sup>299</sup> Lymphomagenesis <sup>299</sup>	Breast cancer <sup>300</sup> Intellectual disability <sup>50</sup>	ING4 CFP1	PHD PHD	G1M cell cycle arrest <sup>301</sup> Binds to unmethylated CpG <sup>30</sup>	Breast cancer <sup>302</sup> Involved in hematopoietic cell differentiation <sup>303</sup> Breast carcinoma <sup>306</sup>
	SMYD1/KMT3D	Rhabdomyosarcoma <sup>304</sup>	Prostate cancer <sup>50</sup>	PHF2/KDM7C	PHD	Oxygen sensor in normoxia <sup>305</sup>	Liposarcoma <sup>310</sup>
	SMYD2/KMT3C	Pancreatic and gastric cancers <sup>307,308</sup>		SPIN1	PHD	Senescence and apoptosis <sup>309</sup>	
	SET7/9/KMT7 PRDM9/KMT8B	Gastric cancer <sup>311</sup> Childhood leukemogenesis <sup>313</sup>		PHF23 PYGO2	PHD PHD	Autophagy <sup>312</sup> Self-renewal of mammary progenitor cells <sup>5</sup>	Myeloid leukaemia <sup>5</sup> Malignant breast tumor <sup>5</sup>
H3K9	SUV39H/KMT1A-B	Blood cell defects, <sup>314</sup> chromosome instability <sup>315</sup>	Malignant colorectal cancer, <sup>316</sup> prostate adenocarcinoma metastasis, <sup>317</sup> renal cell carcinoma <sup>318</sup>	HP1 $\alpha/\beta$	Chromo	Heterochromatin formation <sup>121</sup>	Breast cancer, <sup>319</sup> medulloblastoma, <sup>320</sup> papillary thyroid carcinoma <sup>321</sup>
	G9a/KMT1C GLP/KMT1D SETDB1/KMT1E	Breast and ovarian cancers <sup>149,152</sup> Kleefstra syndrome <sup>323</sup> Huntington disease <sup>148</sup>	Myeloid leukemia <sup>322</sup> — Bladder and breast cancers <sup>325,326</sup>	HP1 $\gamma$ UHRF1	Chromo TTD	Transcription elongation <sup>137</sup> DNA methylation <sup>115</sup>	— Gastric cancer <sup>324</sup>
	PRDM family	Breast and liver cancers, <sup>327</sup> AML, <sup>328</sup> myelodysplastic syndrome <sup>329</sup>	Peripheral nerve sheath tumor <sup>330</sup>				
			Esophageal and breast cancers, <sup>331,332</sup> medulloblastoma, <sup>333</sup> lymphoma <sup>330</sup>				
			X-linked mental retardation <sup>334</sup> Breast carcinoma <sup>306</sup>				
H3K27	EZH1/KMT6B	—	Kabuki syndrome <sup>50</sup>	CBX7	Chromo	Transcriptional depression of PRC complex target gene. <sup>180</sup>	Involved in glioma cell growth and migration <sup>335</sup>

**Table 1 (Continued)**

Writer Name	Diseases	Erasers name	Diseases	Reader name	Domains	Functions	Diseases
EZH2/KMT6A	Prostate cancer <sup>336</sup>	UTY/KDM6C	Prostate cancer <sup>337</sup>	EED	WD40	Spreads H3K27 methylation <sup>162</sup>	Colorectal cancer <sup>338</sup>
H3K36		JMJ3/KDM6B	Hodgkin's lymphoma <sup>50</sup>	BAHD1	BAH	Facultative heterochromatin formation <sup>339</sup>	—
NSD1/KMT3B		KIAA1718/KDM7A	—	NSD2	PWWP	Transcriptional elongation <sup>340</sup>	Wolf-Hirschhorn syndrome, <sup>186</sup> myeloma <sup>207</sup>
SETD2/KMT3A	Renal cell carcinoma <sup>341</sup>	PHF8/KDM7B	X-linked mental retardation <sup>334</sup>				
NSD1/KMT3B	Sotos syndrome, <sup>205</sup> myelodysplastic syndrome, <sup>343</sup> AML, <sup>206</sup> neuroblastoma <sup>344</sup>	JHDM1A/KDM2A	—	DNMT3A	PWWP	DNA methylation <sup>195</sup>	AML <sup>342</sup>
NSD2/KMT3G	Wolf-Hirschhorn syndrome, <sup>186</sup> myeloma <sup>207</sup>	JHDM1B/KDM2B	Leukemia, <sup>345</sup> bladder carcinoma <sup>346</sup>	LEDGF	PWWP	DNA repair (HR) <sup>201</sup>	Medulloblastoma, <sup>347</sup> prostate cancer <sup>348</sup>
NSD3/KMT3F	Breast cancer, <sup>350</sup> AML, <sup>351</sup> myelodysplastic syndrome <sup>352</sup>	JHDM3A/KDM4A	Bladder and breast cancers <sup>325,326</sup>	NBS1	—	DNA repair (NHEJ) <sup>200</sup>	Gastric cancer <sup>349</sup>
SMYD2/KMT3C	Pancreatic and gastric cancers <sup>307,308</sup>	JHDM3B/KDM4B	Peripheral nerve sheath tumor <sup>330</sup>	Ku70	—	DNA repair (NHEJ) <sup>200</sup>	Colorectal cancer <sup>353</sup>
ASH1L/KMT2H	Leukemia <sup>354</sup>	JHDM3C/KDM4C	Esophageal cancer, <sup>331</sup> breast cancer, <sup>332</sup> medulloblastoma, <sup>333</sup> lymphoma <sup>330</sup>	MRG15	Chromo	RNA splicing <sup>139</sup>	—
SETD3	B-cell lymphoma <sup>356</sup>	JHDM3D/KDM4D	—	ZMYND11	PWWP	RNA splicing <sup>203</sup>	Breast cancer <sup>355</sup>
SETMAR	AML <sup>357</sup>	—	—	TP53BP1	Tudor	DNA damage response <sup>232</sup>	B-cell lymphoma, <sup>358</sup> breast cancer <sup>359,360</sup>
H3K79	MLL-rearranged leukemia <sup>245,251–254</sup>	PHF8/KDM7B	X-linked mental retardation <sup>334</sup>	TP53BP1	Tudor	DNA damage response <sup>276</sup>	B-cell lymphoma <sup>358</sup> breast cancer <sup>359,360</sup>
H4K20	Breast cancer <sup>361</sup>	PHF2/KDM7C	Breast carcinoma <sup>306</sup>	L3MBTL1	MBT	Chromatin compaction <sup>279</sup>	—
SUV4-20H1/KMT5B	—	LSD1n	—	ORC1	BAH	Replication <sup>282,283</sup>	Microcephalic primordial dwarfism <sup>363</sup>
SUV4-20H2/KMT5C	Liver and lung cancers <sup>290,362</sup>	—	—	ORCA	WD repeat	Replication <sup>283</sup>	—
				Pdp1	PWWP	Chromatin localization of H4K20 methyltransferase <sup>364</sup>	—

Abbreviations: AML, acute myeloid leukemia; HR, homologous recombination; MLL, mixed-lineage leukemia 1; NHEJ, non-homologous end joining; NURF, nucleosome remodeling factor; PRC, polycomb repressive complex; TFIIID, transcription factor IID.

to H3K4me1.<sup>27</sup> These observations indicate that WRAD proteins participate differentially in H3K4 methylation process in each SET1/MLL complex. How SET1/MLL family complexes differentially regulate H3K4 methylation is not precisely known. One possible mechanism is that distinct amino acids within the SET domain of each SET1/MLL proteins, in conjunction with WRAD proteins, create different active sites that differentially modulate H3K4 methyltransferase activity.

In addition to WRAD proteins, unique subunits in each SET1/MLL complex also have roles in regulating H3K4 methylation. For example, it has been shown that WDR82 (WD repeat domain 82) and CFP1 (CXXC finger protein 1) are required for appropriate levels of SET1A/B complex-mediated H3K4 trimethylation.<sup>28,29</sup> More specifically, CFP1 directly binds to unmethylated CpG islands through its CXXC domain and regulates the genome-wide distribution of H3K4me3 in ESCs.<sup>30,31</sup> H3K4me3 levels in specific genes are dependent on the MLL1/2-specific subunit menin during initiation and progression of sporadic pancreatic endocrine tumors.<sup>32</sup> PTIP (Pax transactivation domain-interacting protein), a unique subunit of MLL3/MLL4, has been shown to regulate H3K4me3 levels at the *Ntrk3* (neurotrophic tyrosine kinase receptor, type 3) locus, whose function is important for podocyte foot process patterning.<sup>33</sup> These results indicate that unique subunits in SET1/MLL complexes interact with distinct transcription factors and thus have important roles in the expression of specific target genes for given SET1/MLL complexes.

Structural analyses have recently begun to aid our understanding of the detailed molecular mechanism of H3K4 methylation. A cryo-EM analysis of partial yeast Set1 (SET domain plus Swd1, Swd3, Bre2 and Sdc1) and human MLL1 (SET domain plus WRAD) complexes revealed that the two subunits, Swd1 (RbBP5) and Swd3 (WDR5), are positioned in the top lobe of the Y-shaped structure, whereas Bre2 (ASH2L) and Sdc1 (DPY30) occupy the bottom base.<sup>34</sup> A recent X-ray crystallographic analysis of human MLL1-SET/RbBP5/ASH2L and MLL3-SET/RbBP5/ASH2L complexes found that association of heterodimeric RbBP5/ASH2L with the MLL SET scaffold stabilizes the catalytic SET domain and further showed that substrate binding induces a conformational change in the active site that facilitates H3K4 methylation.<sup>35</sup> A structural understanding of H3K4 methyltransferase complexes has only begun to be established. Notably, difficulties in biochemical purification of high-molecular-weight and multisubunit complexes have hampered structural analyses of any holo-H3K4 methyltransferase complex. Continuing efforts should ultimately afford a detailed understanding of the mechanism of action of H3K4 methyltransferase complexes.

H2B ubiquitylation-dependent H3K4 methylation in yeast was the first-discovered histone trans-tail relationship, where H3K4 di- and trimethylation were shown to require prior monoubiquitylation at lysine 123 (corresponding to lysine 120 in mammalian cells) of histone H2B.<sup>36–39</sup> Following up on this interesting relationship, two groups reported that Swd2 is a key player in this process, although through different

mechanisms.<sup>40,41</sup> However, this assertion was challenged by a biochemical analysis showing that the Set1 complex lacking Swd2 exhibits even higher H2B ubiquitylation-dependent H3K4 methylation activity.<sup>42</sup> Instead, the authors of this latter study showed that the n-SET domain within Set1 is essential for H2B ubiquitylation-mediated H3K4 methylation activity of the Set1 complex.<sup>42</sup> The H2B ubiquitylation dependence of human H3K4 methyltransferases is unclear, because reducing H2B ubiquitylation by knocking down the human homologs of Bre1 (BRE1A/RNF20 and BRE1B/RNF40) results in only a partial decrease in H3K4 methylation in human cells.<sup>43–45</sup> The incompleteness of this decrease is probably attributable to inefficient knockdown of Bre1 proteins. Interestingly, however, these studies also suggest that six human H3K4 methyltransferase complexes may differentially require H2B ubiquitylation for their H3K4 methylation activity.

### H3K4 demethylases

Until the identification of the FAD (flavin adenine dinucleotide)-dependent nuclear amine oxidase LSD1 (also known as KDM1A), the first histone H3K4 demethylase discovered,<sup>9</sup> histone methylation was believed to be stable and inheritable. LSD1, and the related LSD2/KDM1B, can demethylate H3K4me1 and H3K4me2.<sup>9,46</sup> It has been shown that LSD1 is recruited to target genes by CoREST-, BHC80- and SFMBT1-containing repressive complexes and members of the zinc-finger transcription factor family, Snail.<sup>47–49</sup> In addition to amine oxidases, JARID1 (jumonji AT-rich interactive domain-1) family proteins (JARID1A/KDM5A, JARID1B/KDM5B, JARID1C/KDM5C and JARID1D/KDM5D) and the JmjC domain-containing protein NO66 (also known as MAPJD)<sup>50</sup> were found to demethylate H3K4. NO66 is able to demethylate all three states of H3K4 methylation using  $\alpha$ -ketoglutarate and Fe(II) as cofactors,<sup>51</sup> whereas JARID1A, JARID1B, JARID1C and JARID1D were shown to be specific for demethylation of H3K4me2 and H3K4me3.<sup>52–55</sup> These proteins function as transcriptional corepressors by demethylating H3K4 or recruiting other corepressors.<sup>56,57</sup>

### Distribution of H3K4 methylation

Gene expression is associated with the position of histone methyl-lysine residues within genes and their degree of methylation. H3K4me1, H3K4me2 and H3K4me3 have been shown to differentially mark actively transcribing genes. H3K4me1 is highly enriched at enhancers, H3K4me2 is highest toward the 5' end of transcribing genes, and H3K4me3 is a hallmark of the promoters of actively transcribing and poised genes.<sup>58–61</sup> Although the strong correlation between H3K4 methylation and active transcription is well documented, how SET1/MLL methyltransferase complexes are recruited to specific gene loci is still an open question. However, it has been shown that SET1/MLL complex subunits HCF-1 (host cell factor-1) and menin are required for proper recruitment of these complexes to herpesvirus immediate early promoters and *HOX* genes, respectively.<sup>62,63</sup> In addition, cell-type-specific transcription factors and cofactors were also shown to mediate



recruitment of H3K4 methyltransferases. For example, the transcription factors bZIP28 and bZIP60 bring SET1/MLL complexes to endoplasmic reticulum stress-responsive genes through interactions with Ash2 and WDR5a.<sup>64</sup> A direct interaction with p53 was shown to be responsible for recruitment of the SET1 complex to DNA damage-responsive genes.<sup>65</sup> In addition, it was reported that the Paf1 transcription elongation complex mediates interactions between Set1 and the C-terminal domain of RNA polymerase II such that the Set1 complex can be recruited to transcribing genes.<sup>66</sup>

### Transcriptional coactivators that recognize H3K4 methylation

Each state of H3K4 methylation recruits distinct downstream effectors containing specific 'reader' domains that further regulate gene expression. Several chromatin remodelers are known to read H3K4 methylation and participate in the regulation of gene expression. For example, the ATP-dependent chromatin-remodeling enzyme, CHD1, recognizes H3K4me2 and H3K4me3 through its two N-terminal chromodomains.<sup>67</sup> In addition, BPTF (bromodomain PHD finger transcription factor), a subunit of the ATP-dependent chromatin remodeling complex NURF (nucleosome remodeling factor), was shown to interact with H3K4me3 via its PHD domain.<sup>68</sup> As an example of a general transcription factor that binds to H3K4 methylation, transcription factor IID was shown to be recruited to H3K4me3 through its PHD domain-containing TAF3 subunit, resulting in more efficient preinitiation complex formation.<sup>69,70</sup>

The activity of several histone-modifying enzymes is modulated by recognition of H3K4 methylation. For instance, the yeast SAGA complex binds to H3K4me2 or H3K4me3 through its Sgf29 subunit, which contains a C-terminal H3K4me2- or H3K4me3-binding tudor domain, and thus efficiently acetylates neighboring histones.<sup>71</sup> The acetyltransferase activity of the NuA3 histone acetyltransferase complex can be efficiently targeted to H3K14 through recognition of H3K4me3 by the Yng1 subunit, which contains a PHD domain.<sup>72</sup> In addition, the HBO1 histone acetyltransferase complex was reported to acetylate histone H3 in a manner that depends on the PHD domain-containing ING4 (inhibitor of growth family member 4) subunit and facilitates apoptosis by enhancing the expression of genotoxic stress-responsive genes.<sup>73</sup>

In addition, H3K4 methyl-binding domains within H3K4 methyltransferase complexes further contribute to the precise regulation of their enzymatic activities. For example, the PHD domain-dependent binding of CFP1 to H3K4me3 is responsible for recruitment of SET1A/B complexes to H3K4me3-containing chromatin regions.<sup>74</sup> CFP1 was also found to be required for deposition of H3K4me3 near the promoters of DNA damage-responsive genes in ESCs.<sup>75</sup> Among MLL family H3K4 methyltransferases, only MLL1 is recruited through its PHD domain to regulate *HOX* gene expression. The roles of PHD domains within other MLL family proteins remain to be characterized.<sup>76,77</sup>

### H3K4 methylation and cancers

Mutations in H3K4 methyltransferases highly increase the susceptibility to various cancers.<sup>78</sup> About 70% of infant leukemia is related to chromosomal translocation of MLL1 genes, which results in fusion of its N-terminal fragment to more than 50 partner proteins. MLL1 translocations are also frequently found in mixed-lineage leukemia, acute lymphoblastic leukemia and acute myeloid leukemia.<sup>79</sup> Interestingly, aberrant H3K4 methylation caused by MLL1-AF9 fusion proteins was shown to require an intact MLL1 protein.<sup>80</sup> Therefore, considerable effort has been devoted to developing inhibitors that target MLL1 as a cancer therapy strategy. Although inhibitors that directly target the MLL1 SET domain have not yet been discovered, the chemical compounds MM102 and MM-401, which specifically disrupt the interaction between WDR5 and MLL1, but not other SET1/MLL family methyltransferases, has been reported to inhibit proliferation of leukemia cells.<sup>81,82</sup>

Mutations in H3K4 demethylases are also related to a number of diseases. JARID1 family proteins often function as transcriptional corepressors that are important for expression of development-related genes. JARID1A was shown to be important in regulating *HOX* gene expression in *Caenorhabditis elegans*.<sup>52</sup> It has also been reported that cryptic fusion of NUP98 (nucleoporin 98) and JARID1A causes *HOXA/B* gene overexpression and results in pediatric acute leukemia in humans.<sup>83</sup> Increased expression of JARID1B, often found in breast carcinomas and testicular cancer, causes misregulation of *14-3-3σ*, *BRCA1* (breast cancer 1, early onset), *CAV1* (caveolin 1) and *HOXA5* (homeobox A5) genes.<sup>53</sup> X-linked mental retardation patients have a large number of sense or missense mutations in *JARID1C* genes, implying an important role for the encoded protein during brain development.<sup>84</sup> In addition, a number of inhibitors have been developed for LSD1, which is involved in embryonic development and hematopoiesis, and many types of cancer. Some of these inhibitors were designed to irreversibly deactivate LSD1 by forming a covalent adduct with the cofactor FAD within LSD1.<sup>85</sup>

### H3K4 and H3K27 methylations and bivalent domains in ESCs

Bivalent chromatin has an important role in regulating changes in gene expression from poised to active or inactive states in ESCs.<sup>15</sup> In bivalent promoters, coenrichment of active H3K4me3 and repressive H3K27me3 marks was shown to be responsible for differentiation into specific cell types.<sup>61,86</sup> It was further found that MLL2 is mainly responsible for H3K4 methylation on bivalent promoters.<sup>87,88</sup> H3K27 methylation is an abundant modification that is crucial for fate determination in ESCs. In embryonic fibroblast cells, H3K27me3 was shown to be highly enriched at the promoters of thousands of genes that are responsible for embryonic development and differentiation.<sup>89</sup> Subunits of the H3K4 methyltransferase complex also participate in ESC fate determination. For example, WDR5 interacts with Oct4 (octamer-binding transcription factor 4) and mediates H3K4 methylation at

key development loci in ESCs.<sup>90</sup> During ESC differentiation, ASH2L downregulation correlates with decreased expression of pluripotent transcription factors and increased expression of differentiation-related genes.<sup>91</sup> In addition, a specific role for DPY30 in the differentiation of ESCs, but not the maintenance of their self-renewal capacity, has also been reported.<sup>92</sup>

## H3K9 METHYLATION

### H3K9 methyltransferases

H3K9 methylation is a histone modification that is a well-known indicator of silenced transcription and heterochromatin structure.<sup>86</sup> Fission yeast has a single H3K9 methyltransferase (Clr4/KMT1) that is responsible for all three states of H3K9 methylation<sup>93</sup> and regulates silencing at pericentromere and mating-type loci.<sup>94,95</sup> In mammalian cells, several H3K9 methyltransferases—SUV39H1/KMT1A, SUV39H2/KMT1B, SETDB1/KMT1E, dimeric G9a/KMT1C-GLP (G9a-like protein)/KMT1D and PRDM family—with different catalytic activities and target genes, have roles in diverse cellular events.<sup>96</sup> SUV39H1 and SUV39H2 catalyze H3K9 di- and trimethylation in constitutive heterochromatin, including the pericentromeric region.<sup>7,97</sup> Recombinant SUV39H1/2 proteins were shown to possess H3K9 mono-, di- and trimethylation activity;<sup>98</sup> however, a cell line lacking SUV39H1/2 proteins was shown to lose H3K9me2 and H3K9me3, but not H3K9me1, marks.<sup>99</sup> SETDB1 catalyzes H3K9 monomethylation at the pericentromeric region and provides a substrate for SUV39H1/2 to produce H3K9me3.<sup>100</sup> Another H3K9 methyltransferase, a heterodimer of G9a and GLP (G9a-GLP), mono- and dimethylates H3K9 in euchromatin regions to repress gene expression.<sup>101</sup> When either G9a or GLP is deleted, H3K9me1 and H3K9me2 levels are reduced in euchromatin. Interestingly, *in vitro* analyses have shown that G9a and GLP can individually form homodimers that exhibit H3K9 mono-, di- and trimethylation activity.<sup>98,102</sup> In a related observation, the multi-zinc-finger-containing protein Wiz interacts with the G9a-GLP heterodimer and stabilizes its conformation,<sup>103</sup> indicating that Wiz-assisted G9a-GLP heterodimer formation is crucial for modulation of G9a-GLP enzymatic activity *in vivo*.<sup>104</sup> Several PRDM (PRDI-BF1 and RIZ homology domain) proteins also contribute to H3K9 methylation. Among 17 members of the PRDM family (PRDM1–17), all of which contain a PR domain similar to the SET domain,<sup>105</sup> several are known to possess intrinsic H3K9 methyltransferase activity, whereas the remaining members regulate H3K9 methylation by interacting with other H3K9 methyltransferases, such as G9a.<sup>106</sup> However, whether PRDM protein-mediated regulation of H3K9 methylation is direct or indirect is still controversial, and more detailed biochemical studies are necessary to clarify this issue.

### H3K9 demethylases

Three classes of mammalian proteins—JHDM2/KDM3, JHDM3(JMJ2)/KDM4 and PHF8/KDM7—have H3K9 demethylation activity. Three JHDM2 (jumonji domain-containing histone demethylase-2) family proteins (JHDM2A–C) have the ability to demethylate H3K9me1 and

H3K9me2<sup>107</sup> and regulate hormone-dependent transcriptional activation.<sup>108</sup> JHDM3 family proteins can demethylate H3K9me2 and H3K9me3 in addition to H3K36me2 and H3K36me3 *in vitro*.<sup>107–109</sup> PHF8, a member of the PHF (PHD finger) protein family that acts as a demethylase for H3K9me1 and H3K9me2,<sup>110</sup> is a mononuclear Fe(II)-dependent hydroxylase that uses 2-oxoglutarate and oxygen as cosubstrates.<sup>111</sup> Because PHF8, like other members of the PHF family, contains a PHD domain, it preferentially removes H3K9 methylations from H3K4me3-containing histone peptide substrates.<sup>112</sup> This activity would largely account for the mutually exclusive distribution of H3K4 and H3K9 methylations.

### Cross-talk between H3K9 methylation and DNA methylation

A number of studies have reported physical and functional interactions between H3K9 methyltransferases and DNA methyltransferases (DNMTs). For example, SUV39H1/2 and DNMT3A/B interact with each other and can be recruited via their interaction with HP1 (heterochromatin protein 1) to methylate H3K9-enriched constitutive heterochromatin regions, thereby reinforcing the condensed chromatin structure.<sup>113,114</sup> In addition, DNMT3A/B interacts with G9a-GLP and is involved in facultative heterochromatin formation in ESCs.<sup>115,116</sup> Moreover, the fact that G9a, DNMT1 and PCNA (proliferating cell nuclear antigen) are colocalized at the replication fork<sup>117</sup> implicates H3K9 methylation in the maintenance of DNA methylation during DNA replication. UHRF1 (ubiquitin-like, containing PHD and ring finger domain 1) also has been reported to have a role in maintaining DNA methylation by bringing DNMT1 to the replication fork through its interaction with methylated H3K9, hemimethylated CpG and DNMT1.<sup>117,118</sup> Furthermore, the methyl-CpG-binding protein MBD1 was shown to recruit SETDB1 to the chromatin assembly complex CAF-1, facilitating SETDB1-mediated methylation of H3K9 on newly deposited nucleosomes.<sup>119</sup>

### Establishment of pericentromeric heterochromatin

SETDB1 and SUV39H1/2 are recruited to pericentromeric heterochromatin and catalyze H3K9 methylation.<sup>7,100,120</sup> HP1 $\alpha$  and HP1 $\beta$  bind to H3K9me3 through their chromodomains and form multimers that interact with SUV39H1/2. As SUV39H1/2 also contains a chromodomain, they can be further recruited to methylated H3K9 at the pericentromeric region by HP1 $\alpha/\beta$  as well as by themselves.<sup>97,121</sup> These multiple interactions enable SUV39H1/2 to spread H3K9me3 to neighboring nucleosomes.<sup>122</sup> HP1 $\alpha/\beta$  contributes to heterochromatin formation by recruiting many other proteins involved in heterochromatin formation, such as histone deacetylase, transcriptional repressors and chromatin remodelers.<sup>123–125</sup> H3K9 methylation also increases nucleosome occupancy and has an important role in maintaining transposon repression in pericentromeric heterochromatin.<sup>126</sup> In fission yeast and plants, heterochromatin formation mediated by interactions of

methylated H3K9 with the RNA interference machinery has been well established.<sup>127,128</sup>

### H3K9 methylation-mediated transcriptional repression

The G9a-GLP heterodimer deposits H3K9me1 and H3K9me2 and represses target gene expression.<sup>101</sup> G9a-GLP can be recruited to target gene promoters through direct interactions with diverse DNA-binding proteins.<sup>103,129–131</sup> Once it binds and methylates H3K9 on target genes, G9a-GLP recruits additional dimers through its ankyrin repeat domain and spreads H3K9me1 and H3K9me2 to neighboring nucleosomes.<sup>101</sup> The resulting repression of gene expression is crucial in many biological processes, such as memory formation, immune responses and differentiation.<sup>132–134</sup> During ESC differentiation, G9a/GLP-mediated facultative heterochromatin formation silences Oct3/4 and Nanog.<sup>101</sup> Furthermore, G9a-GLP regulates H3K9me2 and represses different sets of genes in a tissue-specific manner. G9a/GLP-mediated silencing also represses non-neuronal genes in neurons<sup>135</sup> and skeletal muscle genes in brown adipose tissue.<sup>136</sup> In the immune system, H3K9me2 inhibits uncontrolled interferon induction and regulates naïve T-helper cell differentiation.<sup>133</sup> Moreover, H3K9me2 is dynamically altered in the hippocampus and entorhinal cortex in response to contextual fear conditioning, and mediates memory formation.<sup>132</sup> These observations indicate that the distribution of H3K9me2 in euchromatin is dynamically altered according to cell type and external stimuli. Collectively, the results of these studies imply that G9a-GLP interacts with a large number of DNA-binding proteins in different contexts. Numerous studies have revealed that diverse biological processes are regulated by H3K9 methylation. However, only a few downstream target genes, and no upstream regulators of H3K9 methyltransferases, have been identified. Clarifying the detailed molecular mechanisms by which H3K9 methyltransferases mediate transcriptional repression will require a greater effort to identify upstream regulators that bring H3K9 methyltransferases to target genes.

Interestingly, it has been reported that H3K9me3 and HP1 $\gamma$  are enriched in the coding region of certain active genes in several cell lines.<sup>137</sup> In contrast to HP1 $\alpha/\beta$ , HP1 $\gamma$  recruits elongating RNA polymerase II and induces gene expression.<sup>137</sup> Consistent with this, the *D. melanogaster* HP1 $\gamma$  homolog, HP1c, recruits the histone chaperone FACT to RNA polymerase II and enhances transcription elongation of heat-shock genes.<sup>138</sup>

### H3K9 methylation and alternative splicing

Alternative splicing is regulated by nucleosome occupancy and post-translational modifications in transcribing genes.<sup>139,140</sup> A recent study has revealed that local increases in H3K9me2 and H3K9me3 enhance exon inclusion, whereas H3K9 demethylation correlates with exon skipping. Moreover, a genome-wide study showed that H3K9me2 and H3K9me3 are enriched in internal exons.<sup>141</sup> Although how H3K9 methylation facilitates exon inclusion is not fully understood, two hypotheses have

been proposed. First, H3K9 methylation-bound HP1 $\gamma$  could recruit the splicing regulatory protein SRSF1 for efficient splicing.<sup>142</sup> Alternatively, H3K9 methylation would increase nucleosome occupancy and slow down RNA polymerase II elongation, prolonging the time for RNA splicing.<sup>143,144</sup>

### H3K9 methylation-related diseases

H3K9 methylation is often misregulated in various diseases, such as neurodegenerative diseases, drug addiction and cancer.<sup>145,146</sup> In a mouse Alzheimer disease model, aberrantly increased H3K9 methylation levels in the *BDNF* (brain-derived neurotrophic factor) gene leads to downregulation of BDNF expression in neurons. BDNF is critical for synaptic plasticity; hence, reduced BDNF levels are thought to be an important contributor to the pathogenesis of Alzheimer disease.<sup>147</sup> In addition, overexpression of SETDB1 and elevated levels of H3K9 methylation are often found in Huntington disease patients.<sup>148</sup> Although a correlation between abnormal H3K9 methylation and neurodegenerative diseases is well established, more studies are required to identify target genes through which misregulated H3K9 methylation causes these diseases.

Uncontrolled H3K9 methylation is also linked to cancer. In particular, G9a is often overexpressed in various types of cancer.<sup>149–151</sup> Overexpression of G9a hypermethylates H3K9 on tumor suppressor genes and thus represses their expression. The tumor suppressors, *DSC3* (desmocollin 3) and *MASPIN* (mammary serine protease inhibitor) in breast cancer<sup>152</sup> and *CDH1* (cadherin 1), *DUSP5* (dual specificity phosphatase 5) and *SPRY4* (sprouty homolog 4) in ovarian cancer,<sup>149</sup> are often silenced by G9a. These results suggest that H3K9 methyltransferases could be good therapeutic targets in cancer treatment.

## H3K27 METHYLATION

### H3K27 methyltransferases

H3K27me3 is a hallmark of transcriptional repression. The EZH2 (enhancer-of-zest homolog 2) subunit (also known as KMT6A) within PRC2 (polycomb repressive complex 2) complex, an evolutionarily conserved class of polycomb group proteins, is an H3K27 methyltransferase<sup>153</sup> responsible for all three states of H3K27 methylation.<sup>154–156</sup> The mammalian PRC2 complex is composed of four core subunits: EZH1/2, SUZ12, EED and RbAp46/48.<sup>157,158</sup> PRC2 can also associate with other accessory proteins, such as AEBP2 (AE binding protein 2), JARID2 and PCLs (polycomb-like proteins).<sup>159</sup> These accessory proteins are thought to be involved in recruiting PRC2 to target genes and regulating its activity.<sup>158</sup> EZH1/2 alone has no enzyme activity, but incorporation into a PRC2 complex with other subunits enables it to methylate H3K27.<sup>160,161</sup> The PRC2 subunits SUZ12 and EED have the ability to bind the histone H3 N-terminal tail and H3K27me3, respectively. Thus, a positive feedback mechanism is used to spread H3K27me3-repressive marks to adjacent gene loci.<sup>162–164</sup>



### H3K27 demethylases

UTX/KDM6A, UTY/KDM6C and JMJD3/KDM6B demethylate H3K27me<sub>2</sub> and H3K27me<sub>3</sub> and are primarily involved in gene derepression.<sup>165–167</sup> UTX contains six TPR (tetratricopeptide repeat) domains and one JmjC domain. The evolutionarily conserved TPR domain mediates multisubunit complex assembly.<sup>165</sup> UTX, one of the subunits in the MLL4 H3K4 methyltransferase complex, mediates crosstalk between H3K4 and H3K27 methylations.<sup>168</sup> Interestingly, UTX target genes responsible for cancer proliferation and invasiveness are also regulated by MLL4, as evidenced by the fact that individual knockdown of UTX or MLL4 phenocopies the traits of breast cancer cells.<sup>169</sup> JMJD3, a JmjC-domain-containing protein that catalyzes demethylation of H3K27me<sub>2</sub> and H3K27me<sub>3</sub>,<sup>165</sup> activates transcription of development-related genes and directs differentiation of ESCs into definitive endoderm.<sup>170</sup> Microbial stimuli cause nuclear factor- $\kappa$ B-mediated enrichment of JMJD3 at the transcription start site of lipopolysaccharide-responsive genes in macrophages.<sup>171</sup> PHF subfamily proteins, including KIAA1718/KDM7A and PHF8, also demethylate H3K27 using  $\alpha$ -ketoglutarate and iron as cofactors. KIAA1718 contains PHD and JmjC domains, which allow selective demethylation of H3K27me<sub>2</sub> on H3K4-trimethylated nucleosomes.<sup>112</sup> The JmjC domain-containing PHF8 is specific for H3K27me<sub>2</sub>.<sup>110</sup>

### Maintenance of gene repression

The PRC2 subunit EED also binds to H3K27me<sub>3</sub> through its WD40 domain, and disruption of this interaction leads to reduced H3K27 methylation and developmental defects.<sup>162</sup> Binding of PRC2 to H3K27me<sub>3</sub> spreads H3K27 methylation to neighboring nucleosomes, and thus has an important role in the maintenance of gene-expression status. Consistent with a repressive role of H3K27 methylation, the inactivated X chromosome in mammalian cells is highly enriched for H3K27 methylation, which stabilizes the inactive chromatin structure.<sup>172</sup>

### H3K27 methylation and cancers

Misregulation of H3K27 methylation is associated with tumorigenesis as well as metastasis. In this context, over-expression of the PRC2 subunit EZH2 has been reported in human breast and prostate cancers as well as lymphoma.<sup>173–176</sup> For instance, an Y641F mutation in the EZH2 SET domain increases H3K27me<sub>3</sub> levels and contributes to the pathogenesis of germinal center B-cell lymphomas.<sup>177</sup> In addition, another EZH2 mutant lymphoma cell line harboring an A677G mutation shows elevated levels of H3K27me<sub>3</sub> and decreased levels of H3K27me<sub>2</sub> and H3K27me<sub>1</sub>. A structural study reported that the A677G mutation enlarges the lysine tunnel, enhancing the ability of PRC2 to catalyze H3K27 dimethylation.<sup>178</sup> These results suggest that inhibition of hyperactive PRC2 could be a potential treatment strategy for specific types of lymphoma. In this regard, several EZH2 inhibitors that target B-cell and follicular lymphomas have been developed.<sup>17</sup> For example, the EZH2 inhibitor GSK126 was shown to decrease global levels of H3K27 methylation,

reactivate PRC2 target genes, and decrease tumor progression in a mouse model.<sup>179</sup>

H3K27 methylation can be recognized by chromodomain- and WD40 domain-containing proteins. Among several chromodomain-containing proteins that bind to H3K27 methylation, the PRC1 complex subunit CBX7 (chromobox 7) has received attention as a therapeutic target owing to its involvement in tumorigenesis as well as stem cell self-renewal and differentiation. The recently developed chemical compound, MS37452, binds the methyl-binding pocket of the chromodomain of CBX7, resulting in transcriptional derepression of PRC1 complex target genes and inhibition of the proliferation of prostate cancers.<sup>180</sup>

### H3K36 METHYLATION

#### H3K36 methyltransferases

In yeast, a single H3K36 methyltransferase, Set2/KMT3, catalyzes all three states of H3K36 methylation.<sup>181</sup> The SRI (Set2 Rpb1 interacting) domain in Set2 enables it to interact with the S2- and S5-phosphorylated C-terminal domain of RNA polymerase II and methylate H3K36 during transcriptional elongation.<sup>181</sup> Mammalian cells contain at least eight H3K36 methyltransferases: NSD1/KMT3B, NSD2/KMT3G, NSD3/KMT3F, SETD2/KMT3A, SETD3, SETMAR, SMYD2/KMT3C and ASH1L/KMT2H.<sup>182</sup> Among these, NSD1–3 and SETD2 are considered major H3K36 methyltransferases. Only SETD2 can catalyze H3K36 trimethylation, whereas the methyltransferase activity of the other seven enzymes is restricted to H3K36 mono- and/or dimethylation.<sup>183</sup> NSD (nuclear receptor-binding SET domain) enzymes have additional methylation sites on histones as well as non-histone target proteins.<sup>184</sup> Biochemical analyses have shown that NSD enzymes lose their H3K36 specificity if histone octamers are used as a substrate instead of physiologically relevant nucleosomes.<sup>184</sup> From a structural perspective, NSD1–3 enzymes have an autoinhibitory loop that blocks the substrate-binding site. Interaction of a short segment of nucleosomal DNA appears to interact with the autoinhibitory loop, dislodging it from the substrate-binding site. Therefore, H3K36 located close to the nucleosome core region can enter the substrate-binding site, thus imparting H3K36 specificity on NSD enzymes.<sup>185</sup> The H3K36 trimethyltransferase SETD2 has important roles in many biological processes.<sup>186–189</sup> Although recombinant SETD2 was shown to generate all three states of H3K36 methylation *in vitro*, only H3K36me<sub>3</sub> levels were found to decrease in SETD2-knockdown cells.<sup>186,187</sup> In addition, it was reported that not only H3K36me<sub>1</sub> and H3K36me<sub>2</sub> levels but also H3K36me<sub>3</sub> levels are decreased in NSD1–3-deficient cells.<sup>190</sup> These results suggest that NSD enzymes provide H3K36me<sub>1</sub> and H3K36me<sub>2</sub> to SETD2, which then subsequently generates H3K36me<sub>3</sub> *in vivo*.

#### H3K36 demethylases

There are two H3K36 demethylase families in mammalian cells: JHDM1/KDM2A–B and JHDM3/JMJD2/KDM4A–D. The H3K36me<sub>1</sub>- and H3K36me<sub>2</sub>-specific demethylase, JHDM1,

contains multiple histone-binding domains, including a PHD domain,<sup>10,191</sup> and it accounts for mutually exclusive distribution of H3K4me3 and H3K36me3 in same genes.<sup>60,192</sup> JHDM3 is specific for H3K36me2 and H3K36me3 demethylation and has also been shown to demethylate H3K9me2 and H3K9me3 *in vitro*.<sup>109,111</sup>

### Regulation of transcription initiation and elongation

H3K36 methylation has been implicated in preventing abortive initiation of transcription within the gene body and in regulation of transcription elongation. In yeast, Set2 binds to the phosphorylated C-terminal domain of RNA polymerase II and catalyzes H3K36 methylation in newly deposited nucleosomes.<sup>182</sup> The RPD3 deacetylase complex is recruited to nucleosomes through recognition of H3K36me1 and H3K36me2, and then deacetylates histones. Local deacetylation maintains a repressive chromatin state that prevents aberrant transcription initiation.<sup>193</sup> In mammalian cells, different players participate in this process. NSD3, LSD2 (lysine demethylase 2) and G9a form a complex that interacts with transcription-elongation factors and the S2-phosphorylated C-terminal domain of RNA polymerase II. This complex, in turn, maintains newly incorporated nucleosomes in a repressed state by methylating H3K9 and H3K36, and demethylating H3K4.<sup>194</sup> Moreover, PWWP domain-containing NSD2 and DNMT3A bind to H3K36-methylated nucleosomes and further contribute to repression of aberrant transcription.<sup>194,195</sup> Collectively, these observations indicate that H3K36 methylation, H3K9 methylation and DNA methylation simultaneously accumulate in newly incorporated nucleosomes to control accurate transcription elongation in mammalian cells.

In addition to its preferential localization to the gene body, H3K36 methylation is also enriched in the promoter region of several genes.<sup>196</sup> Promoter-enriched H3K36 methylation inhibits activity of the PRC2 complex and prevents PRC2-mediated expansion of H3K27 methylation.<sup>197</sup> This observation is further supported by chromatin immunoprecipitation sequencing analyses showing a mutually exclusive distribution H3K27 methylation and H3K36 methylation.<sup>198</sup>

### DNA damage responses

Several studies have demonstrated roles of H3K36 methylation in DNA damage repair. SETD2 induces DNA mismatch repair by catalyzing H3K36me3 at mismatch sites.<sup>199</sup> In addition, the H3K36 dimethyltransferase, SETMAR, facilitates non-homologous end joining at DNA double-strand break (DSB) sites.<sup>200</sup> When a DSB occurs, SETMAR is recruited to DSB sites and catalyzes H3K36 methylation. NBS1, a subunit of the MRN complex, and Ku70 recognize H3K36 methylation and stabilize DSB until other non-homologous end-joining-related proteins are recruited. Homologous recombination is also known to be regulated by H3K36me3.<sup>201</sup> If a DSB occurs, the H3K36me3-interacting protein LEDGF/p75, also known as PSIP1 (PC4- and SFRS1-interacting protein 1), recruits CtIP (C-terminal-binding protein-interacting protein), which carries out DSB resection. RPA (replication protein A) and RAD51

are then recruited to the site and promote homologous recombination repair.<sup>201</sup> In the absence of SETD2, homologous recombination repair cannot be performed properly because reduced H3K36me3 levels lead to dissociation of LEDGF from chromatin. This explains why SETD2 functions as a tumor suppressor. Homologous recombination repair is a very accurate DNA-repair process, and it is usually carried out in H3K36me3-enriched coding regions.<sup>183</sup> Therefore, H3K36me3 seems to function as surveillance for DNA damage in coding regions to maintain genome stability.

### H3K36 methylation and exon exclusion

Similar to H3K9 methylation, H3K36 methylation also has a role in alternative splicing.<sup>139</sup> For example, SETD2-mediated H3K36 trimethylation stimulates exon exclusion.<sup>202</sup> H3K36me3-bound MORF4L1 (mortality factor 4-like 1; also known as MRG15) recruits PTB (polypyrimidine tract binding protein), which is a well-known exon-inclusion repressor.<sup>139</sup> In addition, a recent study showed that H3.3K36me3-recognizing ZMYND11 protein causes large-scale intron retention.<sup>203</sup> These studies imply that H3K36me3 exclusively marks exons in the alternative splicing process. In support of this, H3K36me3 levels are very low in intron-less genes.<sup>204</sup> Alternative splicing is also regulated by the level of SETD2.<sup>189</sup> Specifically, downregulation of SETD2 levels by polyubiquitylation mediated by the E3 ubiquitin ligase complex, SPOP/CUL3, reduces H3K36me3 on SETD2 target genes and induces their splicing alternatively. Taken together with studies on H3K9 methylation, these results indicate that various histone modifications participate actively in RNA splicing processes.

### H3K36 methylation-related diseases

Misregulation of H3K36 methylation often leads to various diseases.<sup>182</sup> A defect in NSD1 was reported to cause Sotos syndrome, a neurological disorder characterized by macrocephaly and cognitive and motor skill deficiencies.<sup>205</sup> In addition, *Ndh2*-knockout mice die shortly after birth with symptoms of Wolf-Hirschhorn syndrome.<sup>186</sup> These studies suggest that a deficiency of H3K36 methyltransferases disrupts neuronal development, although additional investigation will be required to elucidate the detailed molecular mechanism. The *NSD* genes also often function as oncogenes when overexpressed or translocated to other genes.<sup>206,207</sup> For instance, a fusion protein caused by joining of the *NSD1* gene with the *NUP98* gene causes acute myeloid leukemia.<sup>208</sup> This NSD1–NUP98 fusion protein facilitates H3K36 methylation and induces inappropriate activation of *HOX* genes.<sup>206</sup> In addition, NSD2 overexpression induces multiple myelomas by promoting the expression of several oncogenes, such as *TGFA* (transforming growth factor alpha), *MET* and *p21*.<sup>207</sup> Thus, their causal role in such distinctive diseases strongly suggests that NSD1 and NSD2 have different downstream target genes, despite sharing a common methylation site on histones. Moreover, the fact that a loss-of-function mutation of SETD2 causes renal cell carcinoma development implies that

SETD2 acts as a tumor suppressor<sup>209,210</sup> reflecting its roles in DNA repair and alternative splicing.

## H3K79 METHYLATION

### H3K79 methyltransferases

Unlike other histone lysine methylations, which are located on unstructured histone tail domains and are catalyzed by SET domain-containing methyltransferases, H3K79 methylation occurs on the globular domain of histone H3 and is mediated by Dot1, which lacks a SET domain.<sup>211</sup> Dot1 was originally identified as a disruptor of telomeric-silencing genes in yeast,<sup>212</sup> and subsequent genetic and biochemical studies showed that Dot1, as well as evolutionarily conserved homologs, including human DOT1L (DOT1-like)/KMT4, are responsible for all three states of H3K79 methylation.<sup>213–217</sup>

On the basis of structural studies, Dot1 homologs are categorized as a class I S-adenosyl methionine-dependent methyltransferase.<sup>218,219</sup> Despite structural similarities between human DOT1L and the arginine methyltransferase PRMT1,<sup>211</sup> Dot1 homologs exhibit methyltransferase specificity toward lysine rather than arginine.<sup>213,214,220</sup> In this context, it will be interesting to determine whether Dot1 homologs methylate arginine rather than lysine residues, if present, on novel target proteins.

Intriguingly, *in vitro* histone methyltransferase assays have demonstrated that Dot1 proteins preferentially methylate nucleosomal substrates rather than free histone H3.<sup>214,220,221</sup> In addition, it has been shown that a positively charged region within human DOT1L (amino-acid residues 390–407) is required for direct interaction with nucleosomes and histone methyltransferase activity.<sup>218</sup> These observations suggest that a newly created surface on the nucleosome produced by participation of histones and DNA provides an environment preferential for recognition and methylation by Dot1 proteins.

Another interesting feature of H3K79 methylation, like that of H3K4 methylation, is the *trans*-tail histone modification relationship with H2B ubiquitylation. Yeast genetic studies have demonstrated that defects in H2B ubiquitylation cause the complete disappearance of H3K79me2 and H3K79me3.<sup>39,222,223</sup> Importantly, biochemical approaches have further shown that H2B-ubiquitylated recombinant nucleosomes serve as a preferential substrate for human DOT1L,<sup>217,224</sup> indicating that H2B ubiquitylation directly stimulates the H3K79 methylation activity of human DOT1L. The Muir group has made a number of important observations that have helped elucidate the molecular mechanism underlying this interesting *trans*-tail histone modification. An enzyme kinetic analysis suggested that human DOT1L undergoes a conformational change in the presence of H2B-ubiquitylated nucleosomes.<sup>217</sup> In addition, mutation analyses of the surface of ubiquitin linked to nucleosomes have suggested communication of specific amino-acid residues on ubiquitin with human DOT1L.<sup>225</sup> Furthermore, a targeted photocrosslinking study provided evidence that H2B ubiquitylation 'corrals' human DOT1L into an H3K79-proximal orientation.<sup>226</sup> Collectively, these studies support the proposition that

installation of ubiquitin on nucleosomes converts dominant, but unproductive, interactions between DOT1L and the nucleosome into less dominant, but productive, interactions that allow H3K79 methylation.

In addition to H2B ubiquitylation, another *trans*-tail mechanism for regulating H3K79 methylation has been reported. An *in vitro* analysis showed that a direct physical interaction between Dot1 and the histone H4 N-terminal tail is required for Dot1-mediated H3K79 methylation.<sup>227</sup> In a related observation, increased H4K16 acetylation induced by SAS2 (something about silencing 2) overexpression was shown to cause upregulation of H3K79 methylation by inhibiting the interaction between Sir3 (silent information regulator 3) and the histone H4 tail.<sup>227</sup> Collectively, these observations suggest that, not only are structural features of the nucleosome important, surrounding histone modifications also affect the overall H3K79-methylation activity of Dot1.

### Unidentified H3K79 demethylase

Although many demethylating enzymes responsible for histone lysine methylations have been reported, the reversibility of H3K79 methylations has not been clarified. The fact that H3K79me2 is reduced to a lesser extent on non-replicating extrachromosomal DNA than on chromosomal loci suggests that removal of H3K79 methylation merely depends on replication-dependent histone exchange.<sup>228</sup> However, several studies have shown that global H3K79 methylation levels change dynamically during the G1/S transition.<sup>214,229</sup> The observed disappearance of H3K79 methylation in the G2 phase also suggests the existence of a demethylation process. Furthermore, treatment of U-87MG cells with the demethylase inhibitor 2-hydroxyglutarate was shown to result in increased H3K79 methylation, strongly suggesting the presence of an H3K79 demethylase.<sup>230</sup> Given that Dot1 homologs preferentially methylate nucleosomal substrates over free histone H3, it is possible that an unidentified H3K79 demethylase may also target only chromatinized H3K79 methylation. These observations argue for the need for a biochemical approach using H3K79-methylated nucleosome substrates to identify the H3K79 demethylase.

### Disruption of telomeric silencing

Dot1 was initially identified as a disrupter of telomeric silencing.<sup>212</sup> Sir proteins, important players in heterochromatin spreading, are mislocalized to the telomeric region following mutation of H3K79 or overexpression or deletion of Dot1.<sup>213,220</sup> More direct regulatory evidence was provided by Côté and co-workers,<sup>227</sup> who showed that an H3K79-methylated peptide exhibits reduced binding to Sir3. Furthermore, a yeast genetic study showed that Dot1 deletion stimulates efficient binding between nucleosome and Sir3.<sup>231</sup> These studies imply that proper H3K79 methylation level is crucial for regulation of heterochromatin formation and stability.



### DNA damage responses

Dot1/DOT1L and H3K79 methylation also serve important functions in DNA damage responses. Recruitment of human TP53BP1 (tumor protein p53 binding protein 1) to DSBs is dependent on H3K79 methylation.<sup>232</sup> Furthermore, DOT1 deletion or H3K79 mutations cause defects in G1/S checkpoint arrest following UV irradiation, ionizing radiation or treatment with a genotoxic agent.<sup>233–235</sup> On the other hand, H3K79 methylation inhibits cell survival following treatment with the alkylating agent, methyl methanesulfonate, by inhibiting translesion synthesis, thereby preventing the bypass of DNA lesions.<sup>236,237</sup> Collectively, these observations support the conclusion that H3K79 methylation has a critical role in DNA damage responses; however, further investigation is necessary to elucidate the molecular details of the function of H3K79 methylation in these processes.<sup>238</sup>

### Transcription elongation

H3K79 methylation is a well-known histone modification that strongly correlates with active transcription. Numerous studies have shown that H3K79me2 and H3K79me3 are enriched in coding regions of actively transcribed genes in many organisms.<sup>39,239–242</sup> This preferential localization implicates H3K79 methylation in transcription elongation.<sup>241,243,244</sup> In addition, DOT1L is often associated with the transcription-elongation factor, ENL (eleven-nineteen leukemia), in some human cancer cell lines, and knockdown of ENL in HEK293 cells decreases H3K79 methylation and transcription-elongation efficiency.<sup>245</sup> Biochemical approaches in mammalian cells have further shown that DOT1L is present in a number of complexes that also contain transcription-elongation factors.<sup>246–248</sup> The presence of various DOT1L-containing complexes suggests that DOT1L may regulate transcription elongation in certain subset of genes through distinct mechanisms.

### DOT1L: a key player in MLL-rearranged leukemia

MLL-fusion proteins generated by chromosomal translocation are common causes of acute leukemia.<sup>249</sup> Interestingly, DOT1L-interacting proteins such as AF10, also known as MLLT10 (myeloid/lymphoid or mixed-lineage leukemia translocated to 10), and ENL are often found to be fused to MLL in leukemia, which delivers DOT1L to MLL-regulated genes.<sup>245,250</sup> For example, H3K79me2 is enriched at the MLL target gene *HoxA9* in MLL-AF10-transformed cells; as a result of this aberrant localization of DOT1L, expression of the *HoxA9* gene and leukemic transformation are highly upregulated.<sup>250</sup> Subsequent studies have demonstrated that DOT1L also causes CALM-AF10-, MLL-ENL-, MLL-AF4-, MLL-AF9- and MLL-AF10-mediated leukemogenesis through a similar mechanism.<sup>245,251–254</sup> Therefore, misregulation of H3K79 methylation is thought to be a crucial cue in MLL-rearranged leukemic cells. In this context, regulation of the enzymatic activity of DOT1L is considered a potential therapeutic target in the treatment of leukemia. Several chemicals that specifically disrupt the interaction between the methyl

donor S-adenosyl methionine and the hydrophobic cavity of DOT1L have been shown to inhibit tumor growth and increase animal survival rates.<sup>255–257</sup>

### Direct role of H3K79 methylation in transcription

Despite the strong correlation between H3K79 methylation and active transcription, whether H3K79 methylation directly stimulates transcription is an unanswered question. A recent study using *in vitro* transcription assays revealed that transcription was markedly enhanced using a nucleosome template with fully methylated H3K79 compared with an unmethylated nucleosome, suggesting a direct stimulatory effect of H3K79 methylation on transcription.<sup>258</sup> However, because the entire transcription unit, including the promoter region, was methylated in this *in vitro* study, the specific regulatory role of H3K79 methylation at each step of the transcription process needs to be further investigated. In addition, it would be interesting to test whether this stimulatory effect of H3K79 methylation is mediated by binding of as yet unidentified H3K79 methylation-specific reader proteins.

## H4K20 METHYLATION

### H4K20 methyltransferases

H4K20 methylation is catalyzed by several enzymes whose activities are restricted to specific methylation states. The first identified H4K20 methyltransferase, SET8/KMT5A (also known as PR-SET7), is a monomethylation-specific enzyme.<sup>259,260</sup> H4K20me1 can be further methylated to H4K20me2 and H4K20me3 by SUV4-20H1/KMT5B and SUV4-20H2/KMT5C.<sup>261–263</sup> From a structural perspective, an H4K20me1-containing peptide was shown to fit better into the SET domain of SUV4-20H2 compared with an unmethylated peptide.<sup>264</sup> On the other hand, *in vitro* peptide methyltransferase assays have shown that the enzymatic activity of recombinant SUV4-20H2 protein is restricted to H4K20me2, suggesting the presence of additional factors that enable SUV4-20H2 to trimethylate H4K20 *in vivo*.<sup>264</sup>

Interestingly, H4K20 methylation is also regulated by a histone *trans*-tail mechanism. The C-terminal region of SUV4-20H2 interacts with HP1 protein, which recognizes H3K9 methylation.<sup>261</sup> Thus, deletion of H3K9 methyltransferases (Suv39h1 and Suv39h2 in mouse; SU(VAR)3-9 in *D. melanogaster*) or HP1 causes decreased heterochromatic targeting of SUV4-20H2 and a global reduction in H4K20me3.<sup>261,263</sup> These results suggest that targeting of H4K20 methyltransferases to heterochromatin regions is modulated by H3K9 methylation.<sup>265</sup> Moreover, it was found that p300-dependent H4K16 acetylation decreases SET8-mediated H4K20me1.<sup>260</sup> Similarly, reduction of H4K20me3 by knockdown of SUV4-20H2 was shown to increase MOF1-dependent H4K16 acetylation and relieve promoter proximal pausing of RNA polymerase II.<sup>266</sup>

### H4K20 demethylases

Several distinct demethylases are involved in the removal of specific H4K20 methylation states. PHD8/KDM7B was first



identified as an H4K20me1-specific demethylase in a biochemical analysis using a nucleosomal substrate.<sup>267,268</sup> Intriguingly, the JmjC family protein, PHD8, also contains a PHD domain, enabling it to be recruited to target genes through interactions with H3K4me2 and H3K4me3. Another study found that LSD1n, an alternatively spliced form of LSD1/KDM1A that is exclusively expressed in neurons, exhibits demethylase activity towards H4K20me1 and H4K20me2 *in vitro*, and at least towards H4K20me1 *in vivo*.<sup>269</sup> In addition, it has been shown that PHF2 is recruited to target genes in an nuclear factor- $\kappa$ B-dependent manner and demethylates H4K20me3.<sup>270</sup>

### Genome stability

H4K20 methylation has important roles in genomic integrity.<sup>271</sup> Genomic deletion of *SET8* causes lethality in mice and *D. melanogaster*.<sup>259,272</sup> Knockdown experiments in cell lines have revealed critical roles of SET8 in cell-cycle progression, DNA replication and genome stability.<sup>273–275</sup> Perinatal lethality and cell cycle defects resulting from Suv4-20h1/h2 double-knockout mice also support the function of H4K20 methylation in ensuring genomic integrity.<sup>262</sup>

### DNA damage responses

A structural study has demonstrated a direct interaction between H4K20me2 and tandem tudor domains in TP53BP1.<sup>276</sup> A cell-based assay has further shown that a catalytically inactive SET8 mutant fails to restore TP53BP1 recruitment to DNA damage sites.<sup>277</sup> Moreover, formation of TP53BP1 foci following irradiation is reduced in Suv4-20h1/h2 double-knockout mice.<sup>262</sup> In addition, in fission yeast, recruitment of the TP53BP1 homolog, Crb2, to DSBs is also regulated by the H4K20 methyltransferase, Set9.<sup>278</sup> These studies suggest that H4K20 methylation is an evolutionarily conserved regulator of DNA-damage responses.

### Chromatin compaction

Another interesting H4K20 methylation-binding protein is L3MBTL1 (L(3)mbt-like 1), a transcriptional repressor that contains three MBT domains.<sup>279</sup> Using an electron microscopic analysis followed by sucrose gradient centrifugation, Reinberg and co-workers<sup>280</sup> showed that direct recruitment of L3MBTL1 by H4K20 methylation is sufficient for chromatin compaction *in vitro*. Consistent with this, RNA interference-mediated knockdown of SET8 in HEK293 cells was shown to result in the formation of aberrant nuclei and decondensation of chromatin.<sup>274</sup> Furthermore, recombinant nucleosome arrays containing H4K20me3 have provided direct evidence for H4K20 methylation-mediated chromatin condensation.<sup>281</sup>

### DNA replication

The BAH domain in ORC1 (origin recognition complex subunit 1) is known to be a specific reader of H4K20me2.<sup>282,283</sup> Moreover, the WD-repeat domain-containing protein ORCA, also known as LRWD1 (leucine-rich repeats and WD repeat domain-containing 1), has been shown to interact with H4K20me3.<sup>283</sup> These observations indicate that

H4K20 methylation is involved in recruitment of the ORC complex to the origin of replication. However, how H4K20 di- and trimethylation are regulated at the replication origin requires further investigation. Some studies have revealed that H4K20 monomethylation mediated by SET8 affects S-phase progression and assembly of the pre-RC complex during the DNA replication process.<sup>284,285</sup> However, the fact that deletion of SET8 causes more severe defects than deletion of other subunits in the ORC complex suggests that H4K20me1 may serve more pivotal and diverse functions in DNA replication.

### Nucleosome turnover during transcription

A recent study found that H4K20me1 correlates positively with transcription turnover, primarily at transcription start and termination sites.<sup>286</sup> Interestingly, another study showed that H4K20 methylation also marks low-turnover nucleosomes in coding DNA sequences.<sup>287</sup> This latter observation suggests that transcription-dependent nucleosome recycling allows time for progressive H4K20 methylation in coding DNA sequences. The accumulation of H4K20 methylation in old nucleosomes supports this hypothesis.<sup>288</sup> Whether higher levels of H4K20 methylation in old nucleosomes subsequently affect transcription-mediated nucleosome recycling by functioning as a binding platform for other chromatin readers or by affecting intrinsic chromatin compaction functions remains to be elucidated.

### H4K20 methylation and cancers

Several lines of evidence have implicated H4K20 methylation in cancer. The loss of H4K20me3 and H4K16 acetylation on repetitive DNA sequences and transposons in human cancer cell lines suggests that aberrant H4K20 methylation and the resulting misregulated transcription contribute to cancer development.<sup>289</sup> Subsequent cell line and animal studies have further reported that misregulation of H4K20 methylation is strongly correlated with various types of cancer.<sup>290–292</sup> However, the molecular basis for linkages between H4K20 methylation and tumorigenesis needs to be explored in greater detail.

### CONCLUDING REMARKS

Conserved histone lysine methylation, methyltransferases, demethylases and methyl-lysine-binding proteins are important in development, reprogramming and cancer development. Recent years have seen an explosion of reports on these important epigenetic regulators. Given the importance of histone lysine methylation in the precise regulation of gene expression and as a cause of various diseases, targeting histone lysine methylation regulators has been in the spotlight as a therapeutic strategy. Realizing this goal will require greater insight into structural aspects of histone lysine methylation-related proteins so as to obtain a more detailed understanding of the molecular mechanisms of actions of drugs. In addition to histone H3 and H4 lysine methylations described here are several as yet unstudied lysine methylations at the N-terminal tail of histone H2B and in the globular domains of histones.

Our mechanistic understanding of downstream effectors of these lysine methylations is also limited. In particular, lysine methylations in histone globular domains surrounded by DNA have so far been largely overlooked, despite the richness of their multiple modifications. The use of nucleosomes with homogeneously methylated lysine, generated using recently developed genetic and chemical engineering techniques,<sup>258</sup> will provide powerful tools for identifying and characterizing novel methyltransferases, demethylases and binding proteins targeting methyl-lysines located in the histone globular domain.

### CONFLICT OF INTEREST

The authors declare no conflict of interest.

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