EZH2: Not EZHY (Easy) to Deal
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Abstract
Seminal discoveries have established that epigenetic modifications are important for driving tumor progression. Polycomb group (PcG) proteins are highly conserved epigenetic effectors that maintain, by posttranslational modification of histones, the silenced state of genes involved in critical biologic processes, including cellular development, stem cell plasticity, and tumor progression. PcG proteins are found in two multimeric protein complexes called Polycomb repressive complexes: PRC1 and PRC2. Enhancer of zeste homolog 2 (EZH2), catalytic core subunit of PRC2, epigenetically silences several tumor-suppressor genes by catalyzing the trimethylation of histone H3 at lysine 27, which serves as a docking site for DNA methyltransferases and histone deacetylases. Evidence suggests that overexpression of EZH2 is strongly associated with cancer progression and poor outcome in disparate cancers, including hematologic and epithelial malignancies. The regulatory circuit and molecular cues causing EZH2 deregulation vary in different cancer types. Therefore, this review provides a comprehensive overview on the oncogenic role of EZH2 during tumorigenesis and highlights the multifaceted role of EZH2, as either a transcriptional activator or repressor depending on the cellular context. Additional insight is provided on the recent understanding of the causes and consequences of EZH2 overexpression in specific cancer types. Finally, evidence is discussed on how EZH2 has emerged as a promising target in anticancer therapy and the prospects for targeting EZH2 without affecting global methylation status. Thus, a better understanding of the complex epigenetic regulatory network controlling EZH2 expression and target genes facilitates the design of novel therapeutic interventions. Mol Cancer Res; 12(5); 1–15. ©2014 AACR.

Introduction
More than five decades ago, C.H. Waddington defined “Epigenetics” as a discipline, which aims to describe changes in the development of organisms that could not be explained by the changes in DNA sequence. Local chromatin configuration at the gene promoter determines the accessibility of transcription machinery and associated proteins to bind to the specific DNA sequences. They either directly interact with the nucleosome components or modulate the degree of compaction of nucleosome complexes into higher structures. DNA methylation at CpG islands in the promoter region and covalent chemical modification of less structured, protruding N-terminal tails of core histones by methylation, acetylation, ubiquitylation, and phosphorylation at certain amino acid residues have emerged as two integral mechanisms of epigenetic regulation that principally modulate local chromatin structure (for a review see ref. 1). These epigenetic alterations in DNA, which do not alter the nucleotide sequence, are inheritable and potentially reversible, unlike genetic changes. The transcription state of any gene may be predicted by deciphering the histone modification pattern at the promoter, which is often referred to as “Histone Code” (for a review see ref. 2).

The Polycomb group (PcG) of proteins and their counterparts, the Trithorax group (TrxG) of proteins, have long been found to be associated with the establishment of heritable gene transcription patterns. The antagonistic activities of the PcG proteins that act as epigenetic repressors and TrxG families of proteins function as epigenetic activators, resulting in the maintenance of the spatial patterns of homeotic gene expression in Drosophila, throughout development and adulthood (3, 4). PcG proteins represent evolutionarily conserved multiprotein complexes that include the Polycomb repressive complexes, PRC1 and PRC2. Histone H3 lysine 27 trimethylation (H3K27me3) is a distinct histone modification catalyzed by a histone methyltransferase (HMTase) enhancer of zeste homolog 2 (EZH2), a catalytic component of PRC2, involved in the regulation of homeotic (Hox) gene expression and in the early steps of X-chromosome inactivation in women (5, 6). Given the essential role of PcG proteins in establishing the repressed state of several genes during development and maintenance of embryonic stem cell (ESC) identity and pluripotency, recent studies imply that PcG proteins are often deregulated in various cancer types, and their overexpression is closely associated with carcinogenesis (reviewed in refs. 7–9).
In this review, we comprehensively discuss the role of one of the most important component of the PRC2 complex, viz., EZH2, in the tumorigenesis of different cancer types. After evaluating the role of EZH2 in the mammalian PRC2 complex, we systematically discuss its function and interaction with other epigenetic modifiers and elaborate in detail the causes and consequences of EZH2 overexpression, focusing on each cancer type. Recent literature focused on studying the molecular circuit guiding EZH2 expression and function in normal cells, and its deregulation in tumor cells is also highlighted. Finally, owing to the pivotal "oncogenic" role of EZH2 in the development and progression of several cancer types, recent literature highlighting the potential of EZH2 as a promising cancer target is discussed.

**EZH2 and its role in the PRC2 complex**

The composition of the PRC2 complex is dynamic, consisting of some core subunits responsible for catalyzing H3K27me3 and several accessory regulatory subunits controlling the enzymatic activity and function of the holoezyme (10, 11). The core components of the mammalian PRC2 complex include EZH1/2, suppressor of zeste 12 (SUZ12), embryonic ectoderm development (EED), and retinoblastoma (Rb)-associated protein 46/48 (RbAp46/48). Other accessory units that regulate PRC2 enzymatic activity and function include AEBP2, PCLs, and JARID2 (Fig. 1).

EZH2 is the catalytic core of the PRC2 complex that catalyzes the H3K27me3 repressive chromatin mark. Both genetic and biochemical evidence suggests that EED...
physically associates with EZH2 and histone H3, and thus functions as a scaffold protein. Molecular analysis of the EZH2–EED interaction by X-ray crystallographic studies revealed that the EED-binding domain of EZH2 (EBD) binds to the bottom of the Trp–Asp (WD) repeat domain of EED (12). SUZ12 is required for the nucleosome recognition, activity, and stability of the PRC2 complex in both in vivo and in vitro conditions (13, 14). In addition, other PRC2 members, such as RbAp46/48, are involved in histone binding, and AEBP2, a zinc-finger protein, enhances the enzymatic activity of the PRC2 complex (11, 15).

Human EZH2 is a 746 amino acid protein belonging to the histone–lysine methyltransferase family, all having a conserved SET (Su(var)3–9 enhancer of zeste trithorax) domain. In addition to the SET domain at the C-terminus, EZH2 contains several other functional domains, such as CXC (cysteine-rich domain) and ncRBD (noncoding RNA– and DNA-binding domain), required for its interaction with other PRC2 members and regulatory proteins (11, 15–17). Structural and biochemical analysis of SET domains in various HMTases has unraveled the molecular mechanism of histone methylation. Such studies highlighted the presence of a conserved catalytic triad—the Asp–His–Ser (NHS) motif—responsible for recognition of the amino acid sequence of the histone peptide tail and for the binding of S-adenosyl-methionine (SAM; refs. 18, 19). Mutation of any of these residues in the active site of EZH2 abolishes its HMTase activity. Focusing on highly evolutionarily conserved Tyr641 of EZH2, Yap and colleagues demonstrated that EZH2 Y641–mutant protein containing PRC2 complexes display enhanced H3K27me3 activity on dimethylated peptides (and not on unmethylated histone peptides) as compared with wild-type containing PRC2 complexes, which ultimately shifts the steady state of H3K27 in favor of trimethylation in vivo (20). The presence of the wild-type EZH2–PRC2 complex was found to be mandatory for the Y641 EZH2 mutant to act, so that previously methylated histone substrates remain available for trimethylation. Several posttranslational modifications (PTM) of the EZH2 protein have also been reported to alter its H3K27me3 activity. For example, phosphorylation of EZH2 by Akt1 at serine 21 reduces H3K27me3 activity, whereas phosphorylation of Thr 345 by CDK1 and CDK2 is required for the maintenance of H3K27me3 repressive marks at target gene promoters (21, 22).

Notably, besides few exceptions, most invertebrates have only single copy of PcG genes; however, in vertebrates, multiple copies of PcG genes have been reported. Among PRC2 components, mammalian homologs EZH1 and EZH2 have been reported to be paralogs that remain an integral part of the PRC2 complex, but are generally associated with contrasting H3K27me2/3 repressive roles (23). Although EZH1 was the first Ez homolog to be cloned, it is not as well characterized as its mammalian homolog EZH2 or its counterpart Drosophila Ez. Shen and colleagues demonstrated that EZH2 conditional knockout allele containing ESCs (EZH2 

\[ \text{EZH2} \rightarrow \text{EZH2}^\text{mut}\] sustains H3K27me3 at some developmental genes and displays H3K27me1, despite the global loss of di- and trimethylation on H3K27, indicating the presence of another HMTase catalyzing methylation on H3K27 (24). They reported EZH1 to be an HMTase that is physically present in a noncanonical PRC2 complex, both in vivo and in vitro, and prevents derepression of PRC2 target genes. Margueron and colleagues investigated the cellular role of EZH1 in comparison with EZH2 and showed that EZH1 is ubiquitously expressed, whereas the expression of EZH2 is found in proliferating tissues (23). Also, as part of similar PRC2 complexes, they control an overlapping set of PRC2 target genes. Surprisingly, the functional roles of EZH1 and EZH2 were distinctly different; PRC2–EZH1 exhibit low histone–lysine methyltransferase activity as compared with PRC2–EZH2, which may be attributed to their differential expression patterns and subfunctionalization of Ez during evolution (23). This indicates that PRC2–EZH2 function in establishing the cellular H3K27me3 repressive marks on PRC2 target genes, while PRC2–EZH1 may help restore the repressive methylation pattern (H3K27me2/me3) of histones after demethylase activity or histone exchange that might cause the loss of their methylation mark.

**EZH2- and PRC2-dependent H3K27 trimethylation**

The unstructured histone tails protruding from the nucleosome assembly are subjected to various PTMs, including lysine methylation, which alter the physical state of chromatin and thus modulate gene expression. Lysine residues in the histone tail may be present in the unmethylated form or covalently modified by HMTases into mono-, di-, and trimethylated lysine (H3K27me1, H3K27me2, and H3K27me3), each form functionally different from the other. Methylation of histone H3 lysine 27 by the SET domain of EZH2 (as part of the PRC2 complex) has been reported to be a processive event in which H3K27me3 results from monomethylation of H3K27me2 (25). Di- and trimethylated forms of histone H3 lysine 27 are associated with a facultative heterochromatin region, whereas the monomethylated form is associated with stably silent constitutive heterochromatin (26, 27). In ESCs, 50% of the H3 histone was reported to be dimethylated, 15% trimethylated, and 15% monomethylated, which add up to a total of 80% methylated histone H3 (28). H3K27me3 is a stable repressive chromatin mark catalyzed by PRC2 complexes containing either EZH1 or EZH2. H3K27me2, which is also catalyzed by PRC2, represents an intermediary product that not only serves as a substrate for subsequent H3K27me3 but might also inhibit acetylation of H3K27, which is reported to be antagonistic to PRC2-mediated gene repression (29, 30). In plants, two monomethyltransferases, namely Arabidopsis trithorax–related protein 5 (ATXR5) and ATXR6, which are not orthologous to Ez, are involved in generating H3K27me1 mark; but in mammals the appearance of H3K27me1 is still controversial (31). Some reports speculate that, in mammals, H3K27me1 might be catalyzed by an enzymatic activity distinct from PRC2, and its presence in actively transcribed genes may result from H3K27me2/3 demethylation by the demethylases UTX or OPT3.
JMJD3 (32). In contrast, few reports suggest that in Droso-
phila, the generation of the H3K27me1 mark is dependent
on Ez, while in mammals the PRC2 complex containing
either EZH1 or EZH2 function redundantly controls the
global H3K27me1 levels. EED was also shown to be
required for the H3 lysine monomethylation (24, 33).
Further experimental studies in mammals are needed to
characterize PRC2-type complexes capable of HMTase
activity, so that the origin and function of H3K27me1 mark
could be comprehensively understood.

Supported by various experimental studies in the past
several years, it is a well-established fact that H3K27me3
enrichment is associated with gene silencing (34). Probing
into the molecular mechanism reveals that this chromatin
mark may serve as a docking site and facilitate the binding
of the PRC1 complex that catalyze the monoubiquitylation
of histone 2A at lysine 119 (H2AK119ub), and thus main-
repressed state of the target gene (Fig. 1). Also, the
H3K27me3 mark might indirectly regulate transcription by
posing a steric hindrance to the binding of transcription
machinery to the promoter region of the target gene. The
presence of RNA polymerase II (RNA Pol II) phosphory-
lated at serine 5 of its C-terminal tail in a wide fraction
of H3K27me3-enriched promoters and low transcript levels
suggests that RNA Pol II might be paused at PcG-targeted
genes causing transcriptional repression (35). Studies reveal
that the RNA Pol II transcription complex that is recruited
to the PcG target genes gets involved in early transcription but
fails to proceed to the elongation stage. Kanhere and col-
leagues demonstrated that short RNAs that are transcribed
from the 5 prime end of polycomb target genes marked by the
transcription initiation marker H3K4me3 form a stem-loop
structure resembling the PRC2-binding site that could recrui
t and interact with the PRC2 complex (36).

EZH2- and PRC2-independent function

Apart from the canonical role of EZH2 as a transcriptional
repressor, recent literature reports highlight its less-known
function as a transcriptional activator. In our previous
review, we have comprehensively discussed the mechanism
of action of EZH2 as a transcriptional inducer, where it
functions independently (not as part of the PRC2 complex),
in endocrine-related cancers of the breast and prostate
(reviewed in ref. 37). Depending on the estrogen receptor
(ER) status of the breast cancer cells, the EZH2-mediated
target gene activation mechanism varies. In ER-positive,
linumal-like MCF-7 cells, it was demonstrated that EZH2
physically links β-catenin and T-cell factor (TCF; ER-α and
Wnt signaling components) on the target gene promoters of
cyclin B1 and c-Myc. The domain II of EZH2 interacts with
the mediator complex and induces transcription (38). How-
ever, in ER-negative MDA-MB-231 cells, EZH2 activates
the transcription of NF-κB target genes TNF and interleu-
kin (IL)-6 by forming a ternary complex with RelA and RelB
(39). In castration-resistant prostate cancer (CRPC), meth-
ylation of androgen receptor (AR) or AR-associated proteins
has emerged as a potential mechanism for EZH2-mediated
transcriptional induction (40). EZH2 is phosphorylated by
Akt1 at serine 21, which allows its association with AR.
Furthermore, it was demonstrated that depletion of EZH2
causes a decrease in AR-associated lysine methylation at
lysine 630 and 632, but the AR levels remain unchanged.

The noncanonical role of EZH2 independent of its
HMTase activity was also observed in a highly aggressive
lymphoid malignancy called natural killer/T-cell lymphoma
(NKTL). Interestingly, EZH2 overexpression in NKTL was
found not to be associated with H3K27 trimethylation (41).
Also, in NKTL cell lines, ectopic expression of EZH2
mutant lacking HMTase activity was found to confer growth
advantage and prevent growth inhibition upon endogenous
EZH2 depletion (41). Jacob and colleagues showed that in
differentiated Th cells, binding of polycomb proteins YY1,
Mel-18, Ring1A, Ezh2, and Eed to the Il4 and Ifng gene loci
exhibited a differential pattern and induced transcription
(42). In summary, recent findings support the hypothesis
that EZH2 functions as a dual-faced molecule, which may
function both as a transcriptional repressor or activator
depending on its association with other members of the
PRC2 complex and cellular context.

EZH2 and its interaction with other epigenetic modifiers

Early evidence in Drosohila and Caenorhabditis elegans
showed that polycomb-mediated H3K27me3 was deployed
in transcriptional silencing, but DNA methylation was
absent in their chromatin, emphasizing the notion that
polycomb-based silencing was independent from DNA
methylation (43). However, recent studies have completely
changed this outlook, and it has now become apparent that
there exists a cross-talk between various epigenetic modifiers,
such as DNA methylation and histone modification path-
ways, which are mediated at the molecular level by bio-
chemical interactions between DNA methyltransferases
(DNMT) and SET domain containing HMTase, respec-
tively (Fig. 1). A key study by Vire and colleagues first
described that PRC2-dependent EZH2-mediated silencing and
DNA methylation systems are mechanistically linked
(44). Using glutathione S-transferase (GST) pull-down
assays, they demonstrated that all three DNMTs (*in vitro*
translated 35S-labeled DNMT1, DNMT3A, and
DNMT3B) can interact and bind to full-length GST–
EZH2. Furthermore, they showed that PRC2 members
EZH2 and EED coimmunoprecipitated with all three
DNMTs in HeLa nuclear extracts. The physical interaction
between EZH2 and DNMTs facilitated the binding of the
DNMTs to EZH2 target genes, such as MYT1 and WNT11,
and was essential for CpG methylation of the target pro-
moters. Interestingly, the EZH2–DNMT interaction was
reported to be dispensable for EZH2 binding to the target
gene promoter, suggesting that EZH2 acts upstream in the
silencing pathway and serves as a recruiting platform for
DNMTs. On the contrary, McGarvey and colleagues pro-
duced a dominant role for CpG DNA methylation in gene
silencing and maintenance of heritable repressive states of
target gene promoters by demonstrating that EZH2 deple-
tion neither affected the methylation status nor induced the
hypermethylated genes such as p16INK4a in U2OS cells.
EZH2-mediated methylation of function in deacetylation of the K27 side chains and allow both are mutually exclusive (29, 30). Possibly, HDACs may antagonistically to H3K27me3-mediated silencing and not the core subunits of the PRC2 complex, but they are susceptible to subsequent DNA methylation and silencing during cellular transformation. On the basis of the methylated CpG island microarray (MCAM) analysis of H3K27me3-modified CpG islands in PC-3 and MCF-7 cell lines, Kondo and colleagues proposed that DNA methylation and H3K27me3-based silencing may be independent mechanisms, and overlapping genes targeted by both pathways are relatively rare (48). In conclusion, the current opinion supported by various experimental studies emphasizes that DNA methylation and polycomb-mediated silencing may act together in the epigenetic repression of some genes depending on the cellular context. However, there are discrepancies among studies suggesting a direct mechanistic link between these silencing pathways.

In human cells, the PRC2 complex containing EZH2 has been shown to physically interact with histone deacetylases (HDAC) such as HDAC1 and HDAC2 (49, 50). On the basis of the available biochemical data, HDACs are not the core subunits of the PRC2 complex, but they function in synergy during transient interactions in gene silencing. H3K27 acetylation has been shown to be functionally antagonistic to H3K27me3-mediated silencing and both are mutually exclusive (29, 30). Possibly, HDACs may function in deacetylation of the K27 side chains and allow PRC2-mediated methylation of e-amino groups. Also, HDACs may alter the chromatin configuration by modulating local histone code favorable to polycomb-mediated silencing by deacetylation of other histone lysines such as H3-K9, H3-K14, or H4-K8. In addition, H3K4me3 and H3K36me2, which mark actively transcribing genes, have been shown to antagonize EZH2-mediated H3K27me3 silencing (51, 52). Although current literature reports advocate the fact that EZH2-mediated gene silencing has evolved to sense the surrounding epigenetic landscape and is linked to other epigenetic silencing mechanisms, further experimental studies are needed to address the direct mechanistic and functional link among them in driving oncogenesis.

Role of EZH2 in Cancer Progression

Accumulated evidence reveals that EZH2 deregulation and overexpression are frequently observed in a variety of cancer types, including solid tumors and hematologic malignancies. EZH2 levels have been reported to increase steadily as the tumor progresses, and elevated EZH2 levels often are directly correlated with advanced metastatic stages of cancer progression and poor prognosis. Studies suggest that EZH2 overexpression may be caused by a variety of signals or pathways, some of them are universal for all cancer types, while others are more specific and limited to particular malignancies. The causes and consequences of EZH2 deregulation in different cancer types are discussed.

EZH2 and hematologic malignancies

Overexpression of PcG proteins, particularly EZH2, has been linked to the pathogenesis of complex and heterogeneous hematologic malignancies such as myelodysplastic syndromes and acute myeloid leukemia (AML; ref. 53). It is well established that deregulated epigenetic factors coupled to genetic mutations contribute to their pathogenesis by causing abnormal silencing of critical tumor-suppressor genes (TSG). A study by Xu and colleagues demonstrated that in comparison with the patients with nonclonal cytopenia diseases, patients with myelodysplastic syndromes/AML have overexpression of EZH2, RING1, and BMI1 genes, leading to poor prognostic scoring (53). Elevated levels of DNMTs and hypermethylation of TSGs, such as p15, DAPK, and SOCS-1, are frequently observed in patients with myelodysplastic syndromes. In patients with p15NK4b methylation, EZH2 levels were found to be high as compared with patients without methylation. In a study using high-resolution chromatin immunoprecipitation (ChIP-on-chip), Paul and colleagues demonstrated that as compared with unmethylated p15INK4b samples, there was lower enrichment of the p15INK4b locus with active chromatin mark H3K4me3 in AML cells with p15INK4b DNA methylation (54). However, the repressive chromatin mark H3K27me3 catalyzed by EZH2 was found at p15INK4b as well as in neighboring TSGs p14ARF and p16INK4a, in both samples with and without p15INK4b DNA methylation. Therefore, it was concluded that the p15INK4b locus was enriched by bivalent histone marks H3K27me3/H3K4me3 in AML cells without DNA methylation. They further reported that epigenetic therapies could restore the loss of H3K4me3 and reactivate p15INK4b expression, but the H3K27me3 mark is retained, which ultimately causes the return of the p15INK4b locus to a bivalent state.

The genomic organization and revised mapping of the EZH2 gene by Cardoso and colleagues revealed that it is located on 7q35, a critical region associated with malignant myeloid disorders (55). Recent findings suggest that there are multiple mechanisms causing EZH2 deregulation in myeloid malignancies. Mutations in the EZH2 gene have been described in myelodysplasia–myeloproliferative neoplasms (MPNs) (10%–13%), myelofibrosis (13%), and various subtypes of myelodysplastic syndromes (9, 56–58). In myeloid neoplasms, EZH2 mutations were found to be inactivating/hypomorphic and distributed throughout the gene, which includes missense, nonsense, and premature stop codons (9). HMTase activity was predicted to be lost in all EZH2 missense and nonsense mutants, as the SET domain responsible for catalyzing H3K27 trimethylation was located in the C-terminal domain of the EZH2 protein (56, 57). Assessment of mutational status in 469 cases of myeloid malignancy revealed that EZH2 mutations were present in 8% cases.
while EED/SUZ12 mutations were reported in 3.3% cases. In addition to EZH2 mutation, decreased EZH2 expression was found to be associated with hemizygous deletion (−7/ del7q) involving EZH2 locus (78% of cases), diploid chromosome 7 (41% of cases), and spicisomal U2AF1/SRSF2 mutations (63% of cases). EZH2 mutation was associated with reduced H3K27me3 methylation and derepression of EZH2 target genes, which may contribute to leukemogenesis. HOXA9, one of the major downstream genes involved in stem cell renewal, was found to be elevated in cases with reduced EZH2 expression. Unlike myeloid neoplasms, in follicular lymphomas and diffused B-cell lymphomas, a heterozygous missense somatic mutation at tyrosine 641 (Y641) in the EZH2–SET domain causes a gain-of-function leading to increased H3K27me3 (59). The complex role of EZH2 in tumorigenesis is reflected by the fact that both activating and inactivating mutations in the EZH2 gene contribute to oncogenesis and malignancy.

**EZH2 and prostate cancer**

Prostate cancer is one of most common noncutaneous malignancies responsible for the majority of cancer-related deaths among men in the United States. Like other cancer types, the interplay between genetic and epigenetic factors has been demonstrated to play a major role in the pathogenesis and progression of prostate cancer. Epigenetic alterations, such as aberrant DNA methylation (hypo- or hypermethylation), changes in chromatin remodeling patterns due to dysfunction in histone-modifying enzymes, and microRNA (miRNA, miR) deregulation have been reported to be the major players in prostate carcinogenesis (reviewed in ref. 60). Focusing on aberrant histone PTMs, evidence indicates that critical histone-modifying enzymes, particularly HDACs and HMTase, are deregulated in prostate tumors.

In recent years, the lack of success in defining useful molecular markers to evaluate disease progression and clinical outcome had led to the application of high-throughput genomic approaches, such as microarray expression analysis, to predict differences in the gene expression profiles of normal versus tumor samples at the molecular level. Using cDNA microarray analysis, Varambally and colleagues reported that increased expression of the PcG protein EZH2 in metastatic prostate tumor samples distinguished them from organ-confined localized tumors (61). EZH2 has been found to promote prostate carcinogenesis by PRC2-mediated silencing of critical TSGs such as \( DAB2IP, SLIT2, TIMP-3, \) and \( MSMB \) (reviewed in ref. 37). However, a recent study by Xu and colleagues highlighted that the oncogenic role of EZH2 in CRPC cells is independent of its transcriptional repressor function (40). Using an androgen-dependent LNCaP cell line and its androgen-independent derivative LNCaP-abl as models to study prostate cancer progression, they have shown that EZH2 levels were higher in abl cells than in LNCaP cells. Also, unlike androgen-dependent growth of LNCaP cells, EZH2 silencing has been demonstrated to have a more profound effect in androgen-independent growth, both in vitro (abl cells) and in vivo (mouse xenograft CRPC model using CWR22Rv1 cells). The study further investigated the factors causing EZH2 to switch to a gene activation function in CRPC. EZH2 phosphorylation at serine 21 by the phosphoinositide 3-kinase (PI3K)–Akt pathway was demonstrated to be crucial for EZH2-mediated androgen-independent growth, gene activation, and association with AR-containing complexes.

Recent reports indicate that androgens and the AR signaling pathway play a critical role in regulating EZH2 levels, suggesting a potential reason for increased EZH2 levels after androgen deprivation therapy (ADT) in metastatic and hormone-refractory prostate cancer. Androgens have shown to repress EZH2 expression (62). Rh- and p130-dependent pathways mediate EZH2 repression in the presence of functional AR. Using coimmunoprecipitation, Xu and colleagues reported that EZH2 and AR physically interact in androgen-independent abl cells, and the interaction was lost in EZH2 deletion mutants either in domain I (N-terminal protein–protein interaction domain) or in the C-terminal SET domain, emphasizing the importance of these two domains for the interaction (40). They have also shown that the AR mRNA or protein levels did not change upon EZH2 depletion, but there was decrease in AR-associated lysine methylation. It was further demonstrated that through their cooperative recruitment or binding, EZH2 and AR activate a set of target genes. Another study, by Zhao and colleagues, has shown that EZH2 and AR collaborate with each other in repressing developmental regulators involved in nonprostatic pathways (63). The AR-dependent transcriptional silencing is mediated by EZH2 in an androgen-deprived environment.

In prostate cancer, various molecular mechanisms have been proposed to be responsible for EZH2 overexpression, which includes EZH2 gene amplification, miR-101 deletion, and transcriptional regulation by MYC and ETS gene family members (reviewed in ref. 37). Using the FISH technique, Saramaki and colleagues determined the copy number of the EZH2 gene in prostate cancer cell lines LNCaP, DU145, PC-3, 22Rv1, xenografts, and clinical tumors (64). The data showed increased EZH2 copy number in all the cell lines. Unlike early prostate cancer, in late-stage tumor samples, EZH2 gene amplification was associated with its overexpression. Also, quantitative real-time reverse transcriptase (RT)-PCR analysis indicated that EZH2 expression was elevated in hormone-refractory prostate cancer as compared with benign prostate hyperplasia or untreated prostate cancer. In another study, Varambally and colleagues proposed that miR-101 negatively regulates EZH2 expression, and somatic loss of one or both miR-101 genomic loci elevates EZH2 levels, causing deregulation of various epigenetic pathways in prostate cancer (65). Their study revealed that there was a negative correlation between miR-101 and EZH2 levels during prostate cancer progression. An increase in EZH2 levels paralleled a concomitant decrease in miR-101 levels in human prostate cancer samples. In addition, some studies reported that the ETS transcriptional network consisting of ERG and
epithelial-specific ETS factor, ESE3, are important molecular players with opposing effects regulating EZH2 expression in prostate cancer cells (66). ESE3 have been demonstrated to suppress EZH2 expression, whereas ERG competes with ESE3 for promoter occupancy and opposes its effects. Although prior studies have proposed various molecular mechanisms for EZH2 upregulation in prostate cancer cells, they were insufficient in explaining the reason for elevated EZH2 levels in primary prostate cancer and high-grade prostatic intraepithelial neoplasia (PIN). Interestingly, a study by Koh and colleagues proposed two additional, yet complementary, Myc-regulated molecular mechanisms responsible for EZH2 upregulation in prostate carcinogenesis (67). Because both Myc and EZH2 are frequently overexpressed in human PIN and primary carcinoma lesions, the study demonstrates that there exists a molecular link between them. In prostate cancer, elevated Myc induces EZH2 expression by directly binding to the E-box containing promoter region of EZH2 and activating transcription. Similar findings were also reported by Salvatori and colleagues in AML (68). Interestingly, Myc is also known to regulate miRNAs. In LNCaP and PC-3 cell lines, promoter regions of CTDSPL, CTDSP2, and CTDSP1 genes (miR-26a and miR-26b primary transcripts are embedded in the intron region) were found to be enriched by Myc, which results in transcriptional repression (67). When Myc levels are low, miR-26a/miR-26b are actively transcribed and incorporated into the RISC complex. It is then targeted to the 3′-untranslated region (3′-UTR) of EZH2, which destabilizes EZH2 mRNA, ultimately repressing its translation. Repression of miR-26a/miR-26b by elevated Myc levels contributes to EZH2 overexpression by increasing the stability of EZH2 mRNA due to the less availability of the miR-26a/miR-26b–RISC complex binding to EZH2–3′-UTR. In conclusion, elevated Myc levels enforce EZH2 overexpression by altering both transcriptional and posttranscriptional regulatory mechanisms controlling EZH2 expression in prostate cancer cells.

**EZH2 and breast cancer**

Recent experimental advances in breast cancer research have established EZH2 as a promising novel biomarker indicating cancer progression and disease aggressiveness. EZH2 levels have been found to increase steadily as the disease progresses from a benign tumor to clinically evident metastasis (69, 70). Highest EZH2 levels are associated with the ER-negative basal-like phenotype of breast cancer cells that represents the most aggressive form of breast carcinoma characterized by nuclear polymorphism, lack of ER, and BRCA1 protein (71). Using a high-density tissue microarray, Kleer and colleagues showed that as compared with normal or patients with atypical hyperplasia, EZH2 levels were significantly higher in patients with invasive breast carcinoma (69). Interestingly, Ding and Kleer reported that in breast tissue samples that seemed to be histologically normal, but at a high risk of developing cancer, showed increased EZH2 expression, and hence identified EZH2 as a potential in vivo biomarker that may detect a precancerous state in otherwise morphologically normal breast epithelial cells (72). Both in vitro and in vivo genetic knockout studies targeting EZH2 demonstrated that a decrease in EZH2 levels results in decreased breast cancer cell proliferation, delayed G2–M cell-cycle transition, reduced breast xenograft growth, and improved survival. Upregulation of EZH2 levels caused H3K27me3-mediated aberrant silencing of various essential TSGs such as FOXC1, CDKN1C (p57KIP2), RUNX3, RKIP, CIITA, IL-6, and IL-8 (for a review see ref. 37).

Over the years, several molecular mechanisms have been proposed to address the causes and consequences of EZH2 overexpression in breast cancer cells. Bracken and colleagues reported that the expression of two PRC2 complex components, viz., EZH2 and EED, is regulated by E2F transcription factors (73). It is well established that defects in the pRb–E2F pathway are a mandatory event in the pathogenesis of almost all human malignancies. E2F transcription factors are known for regulating genes, such as CyclinE1, CyclinA2, CDC6, DHFR, and TK1, that control entry into S-phase and DNA replication, which are well-studied targets of the pRb pathway. Upon pRb phosphorylation, E2F dissociates from the pRb–E2F complex, and the activated E2F directly binds to the promoters of EZH2 or EED containing putative E2F-binding sites and transactivates their transcription. The study further confirmed that, although the abrogation of EZH2 or EED expression could significantly decrease positive regulators of cell proliferation, such as cyclin D1 (CCND1), cyclin E1 (CCNE1), cyclin A2 (CCNA2), and cyclin B1 (CCNB1), there was no increase in the expression of negative regulators of the cell cycle, viz., p14ARF. This study provides a direct link between the pRb–E2F pathway–mediated growth control and PcG-regulated essential chromatin modifications.

In another study, Fujii and colleagues reported that the MEK–ERK–Elk-1 pathway, which is commonly upregulated in various cancer types, is linked to EZH2 overexpression in triple-negative and ERBB2-overexpressing breast cancer cells (74). Computational analysis revealed that the EZH2 promoter harbors three Elk-1–binding motifs and other sequence elements for NF-kB, c-Myb, STAT1, and SRF (serum response factor) recruitment. Treatment with MAP–ERK inhibitor, U0126, decreased EZH2 levels in triple-negative breast cancer type MDA-MB-231 cells and ERBB2-overexpressing SKBr3 cells. Also, siRNA-mediated knockdown of Elk-1 caused a significant decrease in EZH2 mRNA expression, which was similar to the decrease caused by U0126 treatment. Furthermore, they demonstrated that MEK inhibitor treatment significantly decreased the association of phospho-Elk-1 with the EZH2 promoter in breast cancer cells. In conclusion, the study suggests that the MEK–ERK pathway activated via KRAS mutation, EGFR receptor (EGFR) amplification, and ERBB2 amplification in triple-negative and ERBB2-overexpressing cells causes EZH2 overexpression.

Under cancer-predisposed hypoxic conditions in breast tumor–initiating cells (BTIC), EZH2 expression was
reported to be regulated by hypoxia-inducible factor-1α (HIF-1α). Chang and colleagues identified a consensus sequence for HIF response element (HRE) by promoter analysis of the EZH2 promoter (75). They further demonstrated that a hypoxic microenvironment induces HIF-1α binding to the HRE and transactivates EZH2 expression. Increased EZH2 expression downregulates double-strand break repair protein RAD51 expression, which ultimately results in impaired DNA repair and accumulation of genomic abnormalities. Furthermore, they demonstrated that EZH2-mediated downregulation of RAD51 causes expansion of self-renewing BTIC population and RAF1 amplification, which further activates downstream p-ERK–β-catenin signaling. EZH2-mediated RAF1–ERK signaling promotes BTIC expansion and aggravates breast cancer condition.

Recent evidence indicates that PTMs also play a crucial role in regulating EZH2 levels in breast cancer cells. Studies by Cha and colleagues have shown that Akt-mediated phosphorylation of EZH2 at a highly conserved serine 21 residue inhibited its H3K27 methyltransferase activity (21). Although EZH2 phosphorylation had no impact on the integrity of the PRC2 complex, there was a marked decline in the affinity of EZH2 for histone H3, which ultimately results in decreased H3K27me3. Interestingly, in another study, Gonzalez and colleagues reported that elevated EZH2 in breast cancer cells induces the PI3K–Akt pathway by specifically activating Akt isoform 1 (76). Increased EZH2 levels positively correlated with elevated phospho-Akt1 (Ser473) and decreased nuclear localization of phospho-BRCA1 (Ser1423). The role of EZH2 in nuclear shuttling of BRCA1 may be regarded as one of the non–PRC2-dependent EZH2 functions, as discussed in the previous sections. The accumulation of the BRCA1 protein in the nucleus promotes tumorigenesis by causing aberrant mitosis, aneuploidy, and genomic instability. The multifaceted role of EZH2 in promoting breast tumorigenesis, where it may act as a transcriptional activator or repressor depending on the cellular context, has been highlighted in the previous section on non–PRC2-dependent EZH2 function.

**EZH2 and lung cancer**

Lung cancer is a leading cause of cancer-related mortality among both men and women worldwide, accounting for almost 1.4 million deaths each year (77). Small cell lung cancer (SCLC) is a highly aggressive neuroendocrine carcinoma and represents a histologic subtype that is distinct from other lung cancer types called non–small cell lung cancers (NSCLC). SCLC has been found to be strongly correlated to cigarette smoking and accounts for approximately 15% of all lung cancer cases. Like other cancer types, the accumulation of several genetic and epigenetic aberrations has been implicated in the initiation and progression of lung cancer. Focusing on the role of HMTase EZH2 in the pathogenesis of lung cancer, recent evidence suggests that EZH2 overexpression and polycomb-mediated H3K27me3 promote malignancy in various lung cancer types, including SCLC and NSCLCs, which is commonly associated with poor prognosis (78–80). In a recent study, Coe and colleagues found a strong correlation between deregulation of the E2F–Rb pathway in 96% SCLC samples and EZH2 overexpression (81). Their study revealed that genomic loss of the E2F–Rb pathway by loss of either Rb1 or E2F amplification leads to increased EZH2 expression. Generation of a “stem cell–like” hypermethylator profile in SCLC tumors due to aberrant methylation of PRC2 target genes was found to be associated with elevated EZH2 levels. In addition, the finding that lentivirus-mediated knockdown of EZH2 in two SCLC cell lines caused a significant decrease in growth as compared with empty-vector controls emphasized the proliferative and oncogenic role of EZH2 in SCLC. Using microarray analysis on a genome-wide scale, Satoh and colleagues revealed that the expression levels of EZH2 and other PRC2 members, such as SUZ12 and EED, were significantly higher in SCLC samples than in normal tissues, including the lung (78). They also demonstrated that H3K27me3-mediated repression of PRC2 target genes, such as JUB, in both SCLC cell lines and clinical samples correlated with poor prognosis. Findings by Hubaux and colleagues highlighted the implication of EZH2 in cell death and cell-cycle regulation by demonstrating that short hairpin RNA (shRNA)–mediated knockdown of EZH2 in SCLC cells induced apoptosis by elevating proapoptotic factors Puma and Bad, increased p21 protein levels, and decreased the fraction of cells in S or G2–M cell-cycle phases.

NSCLCs, including squamous cell carcinoma (SCC), adenocarcinoma, large cell carcinoma, and several other types that occur less frequently, account for more than 85% of all lung cancer cases and are associated with poor prognosis mainly due to late diagnosis, with an overall 5-year survival rate of approximately 11%. Immunohistochemical analysis of 157 surgically resected NSCL samples by Kikuchi and colleagues revealed a strong correlation between elevated EZH2 protein levels with advanced pathologic tumor stage, moderate or poor differentiation, nonadenocarcinoma histology, and high Ki-67 and cyclin E levels (79). Corroborating with the previous findings, Huqun and colleagues reported that there was a significant association of increased EZH2 expression with larger tumor size and shorter overall survival in NSCLC (82). These studies highlighted EZH2 protein levels as a negative prognostic indicator in NSCLC.

In recent years, studies focusing on the identification of molecular mechanisms causing lung carcinogenesis have revealed that deregulation of several miRNAs, such as miR-126, miR-21, miR-200c, miR-145, and miR-107, miR-185, and miR-101, contributes to tumor cell growth, invasion, and apoptosis. Interestingly, Zhang and colleagues demonstrated EZH2 to be a direct functional target of miR-138 in NSCLC and highlighted its therapeutic importance in NSCLC treatment strategy (83). They showed that miR-138 expression was downregulated in NSCLC tissues and A549, SPC-A1, SK-MES-1, and H460 cell lines as compared with the matched normal tissue samples from the same patients and normal bronchial epithelial cell line 16HBE, respectively. Lentivirus-mediated overexpression of miR-138 caused decreased viability, G0–G1 arrest, and apoptosis
in A549 and H460 cell lines. Furthermore, using bioinformatics analysis, EZH2 3′-UTR was found to harbor a highly conserved miR-138–binding site. Transfection of miR-138 overexpressing A549 and H460 cells with the wild-type 3′-UTR EZH2 luciferase reporter construct resulted in decreased luciferase activity as compared with cells transfected with the 3′-UTR EZH2-mutant plasmid construct. Also, miR-138 overexpression caused significant decrease in EZH2 mRNA and protein levels in both cell lines. In addition, ectopic expression of EZH2 was shown to rescue miR-138–induced growth inhibition, cell-cycle arrest, and apoptosis in the lung cancer cells. In another study, Cho and colleagues demonstrated an inverse correlation between miR-101 and EZH2 expression levels in lung cancer tissue samples (84). miR-101 was shown to inhibit lung cancer cell invasion by regulating EZH2 and H3K27me3 levels. In conclusion, miRNA deregulation has emerged as a major cause of EZH2 overexpression in lung carcinomas, and novel therapeutic strategies should consider targeting specific miRNAs, such as miR-138, miR-101, and miR-26a, in lung cancer treatment.

EZH2 and bladder cancer

Bladder cancer is one of the most common malignancies in the United States, and based on National Cancer Institute’s (Bethesda, Maryland, USA) statistics, it accounted for approximately 72,570 new cases and 15,210 deaths in 2013. On the basis of the site of origin, bladder cancer may be categorized into various types, which include transitional cell carcinomas (TCC; cancer develops in the inner cells lining the bladder), SCC (cancer originates in thin, flat cells), and adenocarcinoma (cancer begins in cells that produce and secrete mucus and other fluids). TCCs, which account for >90% of bladder cancer, are associated with superficial, non–muscle-invasive tumors, which may be treated by local transurethral resection. However, the risk of recurrence is high, and the noninvasive lesions may progress to more lethal and metastatic carcinoma. Although epigenetic molecular alterations involved in bladder cancer initiation and progression are not as comprehensively studied as genetic abnormalities of TSGs or oncoproteins, recent studies correlate elevated EZH2 levels to high-grade lesions and invasive bladder carcinomas (85–87). Raman and colleagues demonstrated increased EZH2 mRNA and protein expression in TCC compared with adjacent nontumorous tissue (88). Takawa and colleagues analyzed EZH2 mRNA and protein levels in clinical bladder cancer samples by quantitative real-time PCR and immunohistochemistry (89). Their findings were in line with previous studies showing significant upregulation of EZH2 levels in tumor cells as compared with normal cells. Zhang and colleagues showed that inhibition of EZH2 expression by RNA interference resulted in decreased cell proliferation and G1 arrest in bladder cancer EJ cells (90). Interestingly, some studies have highlighted overexpression of E2F transcription factors, including E2F3, and deregulation of the pRb–E2F pathway, which directly regulate EZH2 expression, as one of the fundamental factors driving human bladder tumorigenesis (91, 92). Collectively, these findings suggest that aberration in the pRb–E2F pathway may cause elevated EZH2 levels at successive stages of bladder carcinogenesis. In another study, Tang and colleagues revealed a novel link between p53 TSG and EZH2 by demonstrating that activated p53 suppresses EZH2 gene expression by binding to its promoter (93). This raises an interesting question of whether alterations in p53 may lead to increased EZH2 expression in bladder cancer. In fact, Yamada and colleagues showed that in SCC of the esophagus (SCCE), elevated EZH2 expression was associated with p53 alteration and activated p53 reduced EZH2 mRNA levels in SCCE cell lines (94). Furthermore, EZH2 was found to be a miR-144 target gene, and miR-144 downregulation in bladder cancer cells was demonstrated to restore EZH2 expression, which further resulted in the activation of the Wnt/β-catenin pathway and subsequent cell proliferation (95).

EZH2 and ovarian cancer

Ovarian cancer develops in tissues of the ovary and can be categorized into two major types based on the tissue of origin—ovarian epithelial carcinomas (cancer forms in the cells on the surface of the ovary) or malignant germ cell tumors (cancer develops in egg cells). Epithelial ovarian cancer (EOC) accounts for the majority of gynecologic cancer–related deaths in the United States. Accumulated evidence indicates that EZH2 overexpression plays a major role in the etiology and pathogenesis of EOC. Li and colleagues demonstrated that, although elevated EZH2 levels were positively correlated with cell proliferation markers such as Ki-67 and tumour grade, there was no association of EZH2 expression with tumor stage and overall or disease-free survival in patients with high-grade serous histotype EOC (96). Interestingly, knockdown of EZH2 expression in both in vitro and in vivo xenograft models resulted in decreased H3K27me3 levels, induced apoptosis, suppressed growth, and invasion of human EOC cells. Rao and colleagues reported that EZH2 overexpression was absent in normal ovaries, while high EZH2 expression in the ovarian carcinomas (50% cases) was positively associated with increasing histologic tumor grade and advanced stage of the disease (97). Furthermore, this study underscores the potential role of EZH2 in regulating cell proliferation, migration, or invasion via modulation of TGF-β1 expression and demonstrated a positive correlation between high EZH2 and TGF-β1 levels in ovarian carcinoma tissues. EZH2 knockdown was shown to reduce expression of TGF-β1 and increase E-cadherin expression either at the transcript or protein levels. Together, recent findings suggest that elevated EZH2 levels in EOC promote carcinogenesis by H3K27me3-mediated silencing of target genes, which ultimately induce cell proliferation, invasiveness, and suppress apoptosis.

Notably, Hu and colleagues found that EZH2 was overexpressed in cisplatin-resistant ovarian cancer cell line A2780/DDP as compared with cisplatin-sensitive A2780 cell line (98). siRNA-mediated knockdown of EZH2 resulted in resensitization of A2780 cells to cisplatin and...
also decreased H3K27me3 levels. Similarly, Rizzo and colleagues reported EZH2 overexpression in ovarian tumor–derived side population (SP) cells, which are stem cell–like cells enriched by chemotherapy, and demonstrated that siRNA knockdown of EZH2 caused loss of SP and reduced anchorage-independent growth in ovarian tumor models (99). This evidence suggests that EZH2 regulates stem cell–like attributes of ovarian cancer cells, which may contribute to chemoresistance in EOCs.

In a recent study, Garipov and colleagues examined the molecular mechanism underlying EZH2 overexpression in EOCs (100). Their study highlighted the role of NF-YA, the regulatory subunit of CCAAT-binding transcription factor NF-Y, in regulating EZH2 transcription by associating with two CCAAT boxes in the proximal EZH2 promoter in EOC cells. They also showed that there is a positive correlation between EZH2 and NF-YA expression levels in EOC, and elevated NF-YA levels predict shorter overall survival in patients with EOC. Furthermore, NY-YA knockdown downregulated EZH2 expression as well as H3K27me3 levels, induced apoptosis, and reduced both in vitro and in vivo growth of human EOC cells. Consequently, ectopic EZH2 expression rescued NF-YA–induced apoptosis in EOC cells. In another study, Guo and colleagues emphasized the oncogenic role of EZH2 in ovarian cancer by possible downregulation of anti-oncogene p57 and showed that there is an inverse correlation between EZH2 and p57 mRNA expression levels in ovarian tissue samples (101). Lu and colleagues showed that EZH2 is an important regulator of tumor angiogenesis (102). EZH2 overexpression in EOC-associated endothelial cells was demonstrated to be a direct result of paracrine circuit involving VEGF stimulation. EZH2 was shown to promote angiogenesis by silencing vasoohibin1. Furthermore, siRNA-mediated EZH2 silencing caused significant growth inhibition in tumor-associated endothelial cells and reduced angiogenesis. Together, accumulated evidence proposes EZH2 to be a promising novel target in antiangiogenesis therapy.

**EZH2 and skin cancer**

As per the latest National Cancer Institute’s statistics, skin cancer remains as one of the most common cancers in the United States, with nearly more than 2 million people treated for nonmelanoma (basal cell or SCC) and 76,690 new melanoma cases each year. Melanoma is a type of cancer that develops in the melanocytes in the skin and represents a genetically and epigenetically complex group of malignancy characterized by deregulation of multiple tumor-suppressor and oncogenic pathways, including \(BRAF\), \(NRAS\), \(PTEN\), and \(CDKN2A\) (103–105). Like several other human cancers, EZH2 overexpression has been implicated in the progression of benign nevi to invasive or metastatic melanoma (70, 106). Athanassiadou and colleagues investigated EZH2 expression in SCC and actinic keratosis (107). In this study, weak EZH2 immunostaining was reported in actinic keratosis cases (62.8%), whereas moderate expression was found in SCCs (42.1%) and 77.8% EZH2 expression levels in ”mixed” SCC/actinic keratosis cases.

A key oncogenic event reported in the majority of melanoma cases is the \(BRAF^{1799A}\) mutation that results in the constitutively activated \(BRAF^{V600E}\) kinase. The epigenetic mechanism of action of \(BRAF^{V600E}\), which is well known to play an important role in melanoma progression, was recently studied as one of the potential mechanisms for \(BRAF^{V600E}\)-mediated gene hypermethylation via upregulation of DNMT1 and EZH2 in melanoma cells (108). During tumor initiation, oncogenic stimuli in melanocytes exacerbate an oncogene-induced senescence, known as melanocytic nevus, which is a benign precursor of melanoma. Cells overexpressing EZH2 escape this senescence through the inhibition of p21. In contrast, EZH2 depletion results in p21 activation and senescence induction in human melanoma cells (109). The PRCC2 complex inhibits the expression of several tumor-suppressor miRNAs in various cancer types. Luo and colleagues demonstrated that overexpression of miR-101 inhibited melanoma cell invasion and proliferation via downregulation of microphthalmia-associated transcription factor (MITF) and EZH2 protein levels (110). Similarly, miR-137 was also demonstrated to have a tumor-suppressive role, and c-Met, YB1, MITF, and EZH2 were identified as direct targets in malignant melanoma (111). Downregulation of miR-31 is a common event in melanoma, which is associated with genomic loss in a subset of samples. Decreased miR-31 gene expression was found to be a result of epigenetic silencing by DNA methylation and via EZH2-mediated histone methylation (112). Importantly, miR-31 has emerged as a complex player in a number of cancers, and evidence suggests that miR-31 can act either as an oncomiR or a tumor-suppressive miR in a tumor type-specific manner (113). Another critical TSG Rap1GAP, which is downregulated in multiple aggressive tumors, including melanoma, pancreatic, and thyroid cancer, was demonstrated to be epigenetically silenced by promoter hypermethylation in melanoma cells (114), whereas EZH2-mediated Rap1GAP transcriptional repression by H3K27 trimethylation was reported in SCC of head and neck (115).

**Role of EZH2 in cancer stem cells**

Cancer stem cells (CSC) are responsible for the initiation and proliferation of a tumor mass, and their recent in vivo validation in certain solid tumors has attracted considerable scientific attention mainly because of their potential clinical significance (116). CSCs were first identified in AML and later on found to be present in various solid tumors (117). A modern CSC model postulates that there exists a subset of tumor cells with stem cell–like properties, including self-renewal as well as multi-lineage differentiation capability. CSCs are characterized by their ability to seed tumor in vivo, self-renewal property and to spawn differentiated non-CSC progeny lacking tumor-initiating capabilities (118).

With the emergence of the CSC model, it was obvious to analyze the shared features of normal stem cells with CSCs. PcG proteins play their important role in stem cell maintenance by reversibly repressing the genes encoding transcription factors required for differentiation (119). This
feature of normal stem cells was also generalized for CSCs and it hypothesizes that the acquisition of promoter DNA methylation at these repressed genes could lock in a stem cell phenotype to initiate abnormal clonal expansion to develop cancer (120). In various cancers, including breast, prostate, ovary, pancreas, lung, and liver, the isolated CSC populations have been reported to overexpress EZH2, which is proposed to be essential for the maintenance of an intact CSC population (121). In a limited number of studies, the epigenetic mechanism of gene silencing by EZH2 has been linked to CSC-associated features such as invasion and chemoresistance. The role of EZH2 in cancer could be related to the interesting mechanism of silencing through the repression of differentiating and antimitotic genes. CSCs maintain their pool by suppressing cell-differentiating genes, such as p16 and p19, and show other characteristics such as decrease of E-cadherin expression to make them metastatic (121). EZH2 mediates p16, p19, and E-cadherin silencing through histone H3K27 trimethylation. Furthermore, EZH2 has been shown to repress the Forkhead box transcription factor C1, thereby enhancing the invasive potential of breast cancer cells (122). EZH2 is also a key mediator of DNA damage response in tumor cells and contributes to CSC chemoresistance, suggesting its additional role in therapeutic resistance, apart from tumorigenesis (123). Altogether, EZH2 has emerged as an important molecular component required for the onset of the CSC phenotype in tumor cells as well as maintaining its associated features.

**EZH2 as a Therapeutic Target**

Emerging experimental evidence clearly demonstrates that EZH2 plays critical roles in driving carcinogenesis, from tumor initiation to clinically evident metastasis in various cancer types. Like other epigenetic enzymes, such as DNMTs and HDACs, EZH2 has emerged as a potential anticancer target in present epigenetic strategies. In recent years, the search for novel small-molecule EZH2 inhibitors has yielded some promising results. One of the best known and widely used EZH2 inhibitors, 3-deazaadenosine-A (DZNep), was identified by Tan and colleagues through library-based drug screening. DZNep has demonstrated a significant antitumor activity in various cancer types, including breast, prostate, lung, liver, and brain cancer cells (124). Notably, treatment with DZNep depletes EZH2 levels and reactivates PRC2 target genes. DZNep targets S-adenosyl-l-homocysteine (SAH) hydrolase and causes SAH to increase, which further inhibits SAH cofactor dependent methyltransferases such as EZH2 by a feed back inhibitory mechanism. Although DZNep has exhibited some promising results in *in vitro* and *in vivo* studies, there are concerns about its specificity as a potential therapeutic compound, as it may also affect other SAM-dependent processes. Also, questions on its short plasma half-life, effect on global methylation status, and toxicity profile in animal models remain open. More recently, the quest for more specific EZH2 inhibitors has identified some molecules that are highly selective over EZH1 and other histone methyl transferases and directly inhibit EZH2 by binding to the active site through competitive inhibition with methyl group donor SAM. EPZ005687 displayed considerable specificity and selectivity when tested on tyrosine 641 or alanine 677 mutation harboring lymphoma cells (125).

Another EZH2 inhibitor El1, which also acts in a SAM-competitive manner, has been developed by Qi and colleagues (126). El1 has demonstrated remarkable selectivity across an HMT panel and decreased H3K27me3 levels without altering other histone H3 methylation marks. They also showed that El1-mediated selective inhibition of EZH2 caused reduced proliferation, cell cycle arrest and apoptosis in DLBCL cells harbouring Y641 mutation and other EZH2 overexpressing cancer cell lines. Interestingly, Kim and colleagues reported an inhibition strategy of targeting EZH2 that is distinct compared with other small-molecule inhibitors that target the EZH2 catalytic site (127). They reported the dose-dependent disruption of the EZH2–EED complex by stabilized α-helix of EZH2 (SAH–EZH2) peptides, which inhibited H3K27me3 and reduced EZH2 protein levels. Furthermore, upon treatment with SAH–EZH2, PRC2-dependent MLL-AF9 leukemic cells were demonstrated to undergo growth arrest, monocyte-macrophage differentiation, and changes in PRC2-regulated lineage-specific marker genes.

Recent studies highlighted some natural chemopreventive phytochemicals, such as green tea polyphenols and curcumin, as potential EZH2 inhibitors that can reactivate PRC2-silenced target genes in various cancer types. Choudhury and colleagues showed that epigallocatechin-3-gallate (EGCG), a major constituent of green tea and DZNep, alone or in combination, reduced PcG protein levels, including EZH2, by increased ubiquitylation and proteasomal-associated degradation (128). Consistently, there were decreased H3K27me3 levels and upregulation of TSG expression. Hua and colleagues demonstrated that curcumin, a natural phytochemical present in turmeric, downregulates EZH2 levels by modulating the mitogen-activated protein kinase (MAPK) pathway in MDA-MB-435 breast cancer cells (129). Curcumin treatment showed antiproliferative effect and induced G1 arrest in MDA-MB-435 cells. Dietary omega-3(−3) polyunsaturated fatty acids (PUFA) were also shown to downregulate EZH2 expression by enhancing its proteasomal degradation, which resulted in the re-activation of EZH2-regulated TSGs such as E-cadherin and insulin-like growth factor–binding protein (130).

Because EZH2 plays key roles in the normal functioning of the cells by establishing the repressive state of genes that function as developmental regulators and maintain stem cell pluripotency, alternative inhibition strategies are needed that focus on the regulatory network, causing EZH2 deregulation in a specific cancer type. Direct EZH2 inhibition by small molecules targeting the enzyme active site may have detrimental effects on global methylation patterns in normal cells. For example, a recent study proposed that inhibition of CDK1/2-mediated Thr 350 phosphorylation of EZH2 may emerge as an alternative therapeutic option to diminish...
EZH2 activity in cancer cells without affecting the global EZH2-mediated gene silencing (22). Further experimental studies may also focus on the development of “combined treatment strategies” targeting the epigenetic regulatory network involving EZH2 in tumor cells.

Conclusion and Future Perspectives

On the basis of a large body of in vivo and in vitro experimental evidence, it is now well established that EZH2 functions as a key mediator of tumorigenesis, and its overexpression is associated with invasive growth, tumor aggressiveness, and poor clinical outcomes in hematologic as well as epithelial cancers. Traditionally, the oncogenic role of EZH2 depends on its ability to act as a “transcriptional repressor,” which causes H3K27me3-based silencing of critical TSGs and contributes to tumorigenesis. However, recent studies in hormone-refractory breast cancer and CRPC demonstrated that EZH2 is a multifaceted molecule that could switch to “transcriptional activator” function and act independent of the PRC2 complex on nonhistone substrates. As discussed in previously, EZH2 can be regulated through multiple mechanisms, depending on cellular context and cancer type. Together, this evidence warrants the need for the identification of EZH2 target genes, which are either activated or repressed, in specific cancer type, so that effective therapeutic strategies could be developed. There is a scope for the development of more specific EZH2 inhibitors that are highly selective and exhibit less toxicity in normal cells. As suggested by Chang and colleagues HIF inhibitors, which showed marked decrease in tumor growth and have been used in clinical trials, may prove effective in EZH2 inhibition because HIF-1α regulates EZH2 expression in BTICs (75). Also, the development of CDK1/2, which controls EZH2 phosphorylation, may emerge as an alternative treatment strategy. Notably, administration of EZH2 inhibitors by a cancer cell or tumor-specific delivery mechanism may also reduce the unwanted side effects and toxicity to the normal or stem cells. In conclusion, understanding the complex epigenetic regulatory network controlling EZH2 expression and target genes in tumor cells may help design better therapeutic intervention strategies.

Disclosure of Potential Conflicts of Interest

No potential conflicts of interest were disclosed.

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