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Molecular Mechanisms of Arsenic-Induced Disruption of DNA Repair

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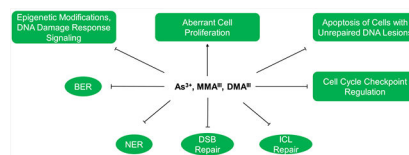
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Abstract

Exposure to arsenic in contaminated drinking water is an emerging public health problem that impacts more than 200 million people worldwide. Accumulating lines of evidence from epidemiological studies revealed that chronic exposure to arsenic can result in various human diseases including cancer, type 2 diabetes, and neurodegenerative disorders. Arsenic is also classified as a Group I human carcinogen. In this review, we survey extensively different modes of action for arsenic-induced carcinogenesis, with focus being placed on arsenic-mediated impairment of DNA repair pathways. Inorganic arsenic can be bioactivated by methylation, and the ensuing products are highly genotoxic. Bioactivation of arsenicals also elicits the production of reactive oxygen and nitrogen species (ROS and RNS), which can directly damage DNA and modify cysteine residues in proteins. Results from recent studies suggest zinc finger proteins as crucial molecular targets for direct binding to As^{3+} or for modifications by arsenic-induced ROS/RNS, which may constitute a common mechanism underlying arsenic-induced perturbations of DNA repair.

Graphical Abstract



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1. INTRODUCTION

Being the 20th most abundant element in the Earth's crust, arsenic (As) is widely distributed in the environment.¹ Arsenic pollution incidents have been documented around the world, including the United States, influencing approximately 200 million people in over 70 countries primarily through contaminated drinking water.² For instance, the levels of arsenic in groundwater in most regions in Bangladesh exceed the level set by the U.S. EPA (i.e., 10 ppb).^{3,4} Arsenic has been one of the most widely studied metals/metalloids in the last 20 years, and it has been placed on the top of the hazardous substance priority list by the U.S. Agency for Toxic Substances and Disease Registry (ATSDR) for over 15 years.

Aquatic arsenic is the most significant source of arsenic contamination in groundwater due to its solubility.⁵ Inorganic arsenite (As^{3+}) and arsenate (As^{5+}) are the predominant forms of arsenic in water,⁶ and they also confer higher toxicity and display higher mobility in the environment when compared to organic forms of arsenic.⁷ Naturally occurring inorganic arsenic (iAs) is present mainly in its sulfide form within complex minerals containing silver, lead, copper, nickel, antimony, cobalt, and iron.¹ Arsenic can be mobilized by a variety of natural and anthropogenic activities, where natural occurrences, such as volcano eruptions and weathering of rocks and soils, are only secondary mobilizers in comparison to anthropogenic activities.¹ Mining, smelting of nonferrous metals, burning of fossil fuels, and agricultural irrigation using contaminated groundwater are the primary routes through which arsenic species are released into the environment, though historically the application of arsenic-containing pesticides also released a significant amount of arsenic to agricultural soil.¹

Arsenic is classified as a Group I human carcinogen by the International Agency for Research on Cancer.^{1,8} Over the last few decades, an increasing body of evidence from numerous epidemiological and animal studies has documented a strong association between arsenic exposure and tumor progression in skin, lung, bladder, kidney, and liver.^{1,4,9–16}

Carcinogenesis is a multistep process encompassing cancer initiation, promotion, and malignant progression.^{17,18} Cancer can arise after accumulation of mutations in cellular DNA, which could emanate from impaired capacity in DNA repair. Metabolic and other endogenous cellular processes constantly generate ROS and reactive metabolites, which can result in DNA damage.¹⁹ The ensuing DNA adducts need to be efficiently removed by the DNA repair machinery; otherwise, they may elicit nucleotide misincorporation during DNA replication, thereby inducing mutations in DNA.²⁰ A mutated proto-oncogene could be activated, whereas a mutated tumor suppressor gene may not function properly, both scenarios favoring carcinogenesis.

There are a number of proposed mechanisms for arsenic-elicited carcinogenesis, including, but not limited to, elevated oxidative stress, diminished DNA repair, dysregulated cell proliferation and apoptosis, and aberrant DNA methylation and histone post-translational modifications.²¹ In the following sections, we review briefly the biotransformation of arsenic species and discuss these different modes of action of arsenic carcinogenesis, with

the focus being placed on the molecular mechanisms through which arsenic exposure leads to compromised DNA repair.

2. BIOTRANSFORMATION OF INORGANIC ARSENIC

Toxicity of inorganic arsenic (As^{3+} and As^{5+}) in humans depends largely on their metabolism. Approximately 90% of ingested inorganic arsenic (As^{3+} or As^{5+}) is absorbed by the gastrointestinal tract.²² Inorganic As^{5+} subsequently undergoes a sequential process, that is, glutathione (GSH)-mediated two-electron reduction to As^{3+} , and oxidative methylation of As^{3+} by arsenite methyltransferase ($\text{As}3\text{MT}$) to pentavalent organic arsenic species (e.g., MMA^{V} and DMA^{V}) in the liver (Figure 1).^{21,23} DMA^{V} was previously shown to be a teratogen, a nephrotoxin, a tumor promoter, and a complete carcinogen in mammals.^{24–27} In this biotransformation process, iAs can also be methylated to yield trivalent arsenic compounds such as MMA^{III} and DMA^{III} (Figure 1), which exhibit higher potency in being cytotoxic/genotoxic agents and enzyme inhibitors over iAs^{3+} .²³ Therefore, it is important to consider both inorganic arsenic and their trivalent methylated arsenic species when discussing arsenic toxicity.^{28–30}

3. ARSENIC EXPOSURE AND OXIDATIVE STRESS

Arsenic-induced oxidative stress has been widely studied and may constitute a major factor contributing to arsenic carcinogenesis (Figure 2). Inorganic and methylated trivalent arsenic species have been shown to induce the generation of reactive oxygen species (ROS) and oxidative stress in mammalian cells.^{31–33}

Apart from direct generation of ROS from arsenic and its metabolites, arsenic exposure can result in antioxidant imbalance, mitochondrial dysfunction, and impairment of ROS-scavenging enzymes, which together result in arsenic-induced oxidative stress, as noted previously.³⁴ Because glutathione (GSH) serves as an electron donor in arsenic metabolism,^{21,23} the intracellular GSH pool is heavily depleted upon chronic arsenic exposure and becomes unavailable for scavenging ROS as a cellular defense mechanism against oxidative stress. In addition, arsenic-mediated disruption of the mitochondrial electron transport chain exacerbates oxidative stress, because mitochondrion constitutes a major source of intracellular ROS.^{35–37} Moreover, arsenic-induced oxidative stress emanates from impaired activities of ROS-scavenging enzymes such as superoxide dismutase, catalase, glutathione peroxidase, glutathione *S*-transferase, and glutathione reductase.^{34,38}

Arsenic carcinogenesis may arise, in part, from the genotoxicity of ROS and RNS. Along this line, increasing lines of evidence demonstrated that iAs and its methylated metabolites damage DNA indirectly through the induction of free radicals.^{33,39–42} For instance, hydroxyl radicals generated from arsenite exposure are believed to react with nucleobases in DNA to yield DNA lesions, for example, 8-oxo-7,8-dihydroguanine, 5-hydroxycytosine, and 5-hydroxyuracil.⁴³ In addition, arsenite-induced ROS and RNS can elicit cross-links between DNA and proteins or other molecules in cells.⁴⁴ Moreover, *in vitro* studies with cultured human cells indicated that arsenite-induced oxidative stress causes persistent telomere

attrition, DNA strand breaks, chromosomal aberrations, and sister chromatid exchanges.
45–48

Aside from oxidative DNA damage, arsenite-induced ROS may perturb the cellular functions of ROS as secondary messengers.^{33,34} Last but not least, ROS/RNS generated from arsenite exposure can directly impair important cysteine-containing proteins involved in DNA repair and DNA damage response (DDR) signaling. For example, inhibition of PARP1 by peroxynitrite through *S*-nitrosylation of its zinc finger cysteines was shown to compromise DNA repair.^{49,50}

4. INHIBITION OF DNA REPAIR

Arsenite alone is a weak mutagenic agent, but it is known to enhance the mutagenicity of other carcinogens. For instance, arsenite was found to enhance the mutagenicity of X-rays, UV light, methylmethanesulfonate (MMS), and diepoxybutane in mammalian cells.^{51–53} Arsenic's role in augmenting the mutagenicity of other carcinogens perhaps can be attributed to its ability in inhibiting the repair of DNA lesions induced by these carcinogens. In this section, we review the previous work regarding the perturbation of various cellular DNA repair and DDR pathways after exposure to iAs (Figure 3).

4.1. Excision Repair.

A number of studies revealed that arsenite can target several key molecular players in base excision repair (BER) and nucleotide excision repair (NER) pathways through perturbing the expression levels of DNA repair genes or catalytic activities of DNA repair proteins.

4.1.1. BER.—BER is a crucial DNA repair pathway mainly responsible for the removal of oxidatively generated and alkylated nucleobase lesions, apurinic/aprimidinic (AP) sites, and strand breaks.⁵⁴ For instance, 8-oxoG is one of the most abundant oxidatively generated DNA lesions,^{55–57} and 8-oxoguanine DNA glycosylase-1 (OGG1) is the main glycosylase responsible for the excision of 8-oxoG from DNA in mammals.^{57–59} A previous study revealed a dose-dependent decline in mRNA level and enzymatic activity of OGG1 in A549 human lung epithelial cells after exposure to micromolar concentrations of arsenite and its metabolites.⁶⁰

Aside from OGG1, AP endonuclease 1 (APE1), the major endonuclease responsible for the excision of apurinic/aprimidinic (AP) sites in eukaryotic cells, was shown to be diminished at the mRNA and protein levels after exposure to As³⁺.⁶¹ Additionally, DNA polymerase β , an important enzyme for DNA repair synthesis during BER,⁶² exhibited decreased expression at both the mRNA and protein levels after exposure to As³⁺ at concentrations that are 5 μ M.⁶¹ Moreover, Osmond et al.⁶³ observed a dose-dependent decrease in mRNA levels of APE1, DNA ligase I (LIG1), OGG1, PARP1, and DNA polymerase β (DNA Pol β) in 24-week old mice subchronically (2 weeks) exposed to arsenite-contaminated drinking water, further substantiating that arsenic exposure can impair the BER pathway.

4.1.2. NER.—NER is a critical and versatile DNA repair pathway for the removal of bulky DNA adducts and helix-distorting lesions induced by environmental carcinogens (e.g.,

UV-induced dimeric DNA photoproducts and adducts generated from metabolites of polycyclic aromatic hydro-carbons).⁶⁴

A number of prior studies revealed that arsenic mainly interferes with NER by disrupting the gene expression levels and activities of crucial NER players. For instance, exposure to arsenic in drinking water was found to be correlated with reductions in mRNA levels of *ERCC1*, *XPB*, and *XPF* genes in lymphocytes,⁶⁵ and the mRNA and protein expression levels of *ERCC1* were also shown to be diminished upon arsenic exposure in a follow-up study.⁶⁶ Additionally, a dose-dependent decline in mRNA levels of *ERCC1* gene was observed in human cardiomyocytes following a 72-h exposure to arsenite.⁶⁷

An earlier large-scale microarray analysis revealed that the mRNA expression levels of a number of DNA repair genes, encompassing *XPC*, *DDB2*, and *TP53*, were significantly down-regulated in human epidermal keratinocytes after exposure to submicromolar concentrations of arsenite.⁶⁸ Another microarray study showed that the mRNA expression levels of *XPD*, *PCNA*, *APE1*, *RFC*, *XPC*, and DNA ligase I were reduced by at least 1.5-fold following a 4-h exposure to 5 μ M arsenite.⁶⁹ Moreover, treatment of human skin fibroblast cells with arsenite and MMA^{III} lowered, in a dose-dependent manner, the mRNA levels of *XPC* and *DDB2* as well as the protein level of *XPC*.⁷⁰ Furthermore, treatment of IMR-90 human lung fibroblasts with arsenite reduced the protein level of *XPC*, partially through proteasomal degradation, as well as reducing the mRNA levels of several NER genes, including *XPA*, *XPC*, and *DDB2*.⁷¹ A recent Bru-seq study showed that a 1-h acute exposure to 5 μ M arsenite led to diminished transcription of *RAD23B* and *DDB2* genes.⁷² Impairment of NER by arsenic was also observed for DNA lesions induced by cisplatin, a clinically used chemotherapeutic agent for treating human cancers through the generation of Pt-d(GpG) intrastrand cross-link lesions in DNA.⁷³ In particular, exposure to arsenite prevented the induction of *XPC* after treatment of mice with cisplatin.⁷⁴

Interestingly, arsenic exposure has been shown not to affect the protein level of *XPA*,⁷¹ which is essential for recognition of damaged DNA and subsequent recruitment of other NER components, especially *RPA70* and *TFIIH*.^{75,76} The *XPA* protein contains a Cys_4 (C_4)-type zinc finger that is involved in binding with damaged DNA and *RPA70*. Biochemical studies indicated that mutations in any of the four zinc-coordinating cysteines result in an unfolded protein.⁷⁷ Arsenite has been demonstrated to interact with zinc finger proteins by substituting for the zinc ion,^{78,79} and several zinc finger proteins involved in DNA repair, for example, *XPA* and poly(ADP-ribose) polymerase 1 (*PARP-1*), have been shown to be direct molecular targets for binding with iAs^{3+} and MMA^{III} .^{80–83}

Lastly, arsenite exposure has been proposed to interfere with and inhibit NER activity through NO-mediated nitrosylation of DNA repair proteins.^{49,50,84,85} All the above studies together support that arsenite and its trivalent metabolites may perturb NER by perturbing the central NER players at both transcript and protein levels.

4.2. DNA Ligation.

DNA ligases assume important roles in various DNA metabolic processes including DNA replication, repair, and recombination, and arsenite has been shown to inhibit the DNA

ligation process. It was reported that the levels of mRNA, protein and enzymatic activities of DNA ligase I and DNA ligase III are significantly diminished in mammalian cells after exposure to iAs^{3+} and MMA^{III} .^{61,86} It was also shown that arsenite inhibits DNA ligation by interacting with the vicinal cysteines in DNA ligase III, thereby retarding DNA break rejoining in MMS-treated hamster cells.⁸⁷ In addition, XRCC1 plays an indispensable role in recruiting and stabilizing ligase III α in the DNA ligation step of excision repair by acting as a scaffolding protein,^{88–91} where down-regulation of the XRCC1 protein by iAs exposure also contributes to the impairment of the DNA ligation step of the excision repair pathways.⁹² Because the inhibition of DNA ligation by arsenic exposure prevents the completion of DNA repair, it may lead to accumulation of damaged intermediates including single- and double-strand breaks, ultimately contributing to genome instability.

4.3. Fanconi Anemia (FA)/BRCA Pathway for DNA Interstrand Cross-Link and DNA-Protein Cross-Link Repair.

DNA interstrand cross-links (ICLs) can arise from endogenous metabolism or from exposure to therapeutic cross-linking agents such as mitomycin C (MMC).⁹³ ICLs are extremely cytotoxic because covalent linkage of the two complementary strands of DNA blocks essential DNA metabolic processes including replication and transcription.⁹³ FA/BRCA pathway, which encompasses three stages of DNA repair processes, that is, nucleolytic incision, translesion synthesis (TLS) and homologous recombination (HR), is indispensable for the repair of DNA ICLs.^{93,94} As^{3+} was shown to disrupt the FA/BRCA pathway-mediated repair of DNA ICLs.⁹⁵

In the FA/BRCA pathway, monoubiquitination of FANCD2 is essential for the recruitment of SLX4/FANCP, an endonuclease protein complex required for unhooking the DNA cross-link and for the downstream TLS and HR steps of the ICL repair pathway, to DNA damage sites.^{93,96} Monoubiquitination of FANCD2, catalyzed by the E3 ubiquitin ligase FANCL,^{97,98} is also necessary for the relocalization of the Fanconi-associated nuclease 1 into nuclear DNA repair foci for recovery of stalled replication forks during ICL repair.⁹⁹ Recently, arsenite was shown to inhibit the repair of DNA ICLs induced by MMC through diminishing monoubiquitination and compromising the access of FANCD2 to DNA damage sites in chromatin in cultured human cells.¹⁰⁰ This occurs through inhibition of the E3 ubiquitin ligase activity of FANCL via direct binding of arsenite to its RING finger domain.¹⁰⁰ We reason that, apart from FANCL, arsenite may also bind to RING finger-containing SUMO E3 ligases PIAS1 and RNF4, which may inhibit the SUMOylation, polyubiquitination, and degradation of FANCA, thereby perturbing FA/BRCA pathway.¹⁰¹

Unhooking of an ICL by XPF-ERCC1 is necessary for the stable localization of FANCD2 onto chromatin and its subsequent HR-mediated repair of DNA DSBs, as manifested by the failure to repair ICL-induced DSBs in XPF-ERCC1-deficient human cells.^{102–104} Decreases in the mRNA levels of XPF and ERCC1,⁶⁵ and in the protein level of ERCC1,⁶⁶ in individuals exposed to arsenite in drinking water suggest that arsenite may impair ICL repair through suppressing mRNA and protein expression and disrupting the proper functions of the XPF-ERCC1 complex.

BRCA1 has been proposed to be crucial for homologous recombination-independent repair of DNA ICLs by promoting the recruitment of FANCD2 to DNA damage sites.^{105,106} In particular, BRCA1 was shown to antagonize the inhibitory effect of the Ku70-Ku80 heterodimer on FANCD2 foci formation¹⁰⁵ and promote the unloading of the CMG helicase from stalled replication forks during ICL repair.¹⁰⁷ Additionally, BRCA1 is believed to amplify the FA/BRCA pathway by regulating FANCD2's interaction with other proteins.¹⁰⁸ It has been hypothesized that BRCA1 is involved in homology-based DNA repair through its E3 ubiquitin ligase activity; the RING domain of the ligase is indispensable for its interaction with BRCA1-associated RING domain (BARD1) protein, forming a heterodimeric complex to modulate the stability and enzymatic activity of BRCA1.^{107,109} Exposure to arsenite was recently found to diminish the recruitment of BRCA1 to DNA DSB sites,¹¹⁰ suggesting that arsenite might also interfere with ICL repair through binding and inhibiting the E3 ubiquitin ligase activity of the BRCA1-BARD1 complex.

4.4. DNA Double-Strand Break Repair.

Double-strand breaks (DSBs) are among the most deleterious types of DNA lesions, which can lead to mutations, loss of heterozygosity, and chromosomal rearrangement; if not properly repaired, they can lead to cell death and cancer.^{111,112} In mammalian cells, DSB repair proceeds through two different pathways, namely HR and nonhomologous end-joining (NHEJ).¹¹³ Exposure to arsenic was shown to induce DSBs and ultimately lead to chromosomal aberrations and sister chromatid exchanges.^{114,115} Exposure to arsenic was also found to inhibit DNA DSB repair and influence the DNA DSB repair pathway choice by favoring error-prone NHEJ repair while inhibiting the error-free HR pathway, leading to mis-repair of DSBs and genome instability.¹¹⁶

Since DSB repair occurs on DNA substrates that are localized in chromatin, the efficiency in DSB repair depends mainly on how accessible the site of damage is, which is largely determined by the compactness of the local chromatin.¹¹⁷ Generation of open chromatin involves the actions of multisubunit chromatin-remodeling complexes and post-translational modifications of core histone proteins. In the latter regard, acetylation of lysine 16 in histone H4 (H4K16Ac) and monoubiquitination of lysine 120 in histone H2B (H2BK120ub) represent those histone epigenetic marks that promote the formation of biochemically accessible chromatin at or near DNA DSB sites.^{110,118,119} Recently, it was reported that arsenite inhibits H4K16Ac by binding to the zinc finger motif of two MYST family histone acetyltransferases TIP60 and hMOF,^{120,121} and arsenite was also shown to inhibit H2BK120ub catalyzed by RNF20-RNF40 histone E3 ubiquitin ligase in a similar fashion, thereby diminishing the recruitment of BRCA1 and RAD51 to DSB sites for repair.¹¹⁰ Therefore, arsenite could disrupt DSB repair by inhibiting histone epigenetic modifications, which leads to compact chromatin structures unfavorable for DNA DSB repair.

In addition to the aforementioned histone modifications that regulate the accessibility of DNA lesions in chromatin, a myriad of zinc finger proteins are involved in post-translational modifications (PTMs) of proteins that control DDR and transcription of DNA repair genes. For instance, the RING finger E3 ubiquitin ligases RNF8 and RNF168 are essential for DDR in response to DSB formation through ubiquitination of H2A/H2AX surrounding DNA DSB

sites,¹²² where RNF168 interacts with PALB2-containing protein complex to DSB-induced H2A ubiquitination, thereby promoting DSB repair.¹²³ In addition, DNA DSB repair pathway choice is modulated by deubiquitinating enzymes (DUBs) and other E3 ubiquitin ligases (e.g., RNF169 and RNF126).^{124–127} In this vein, being a negative regulator of the ubiquitin-dependent DDR signaling, RNF169 directly recognizes RNF168-mediated ubiquitination near DNA DSB sites and competes with other ligases for nonproteolytic ubiquitination at DSB sites to limit the deposition of 53BP1 and RAP80, thereby fine-tuning the DSB repair pathway choice.^{125,126,128} Moreover, after being recruited to DSB sites in a RNF8-dependent manner, RNF126 directly interacts with and ubiquitinates RNF168 to negatively regulate the RNF168-mediated H2AX ubiquitination and favor the HR-mediated repair of DSBs.¹²⁷

Within seconds after DSB induction, poly(ADP-ribose) polymerases, including PARP-1, sense, recognize, and bind to DSBs to catalyze global protein poly(ADP-ribosylation) (PARylation).^{129–131} Global PARylation around DSB sites serves as a docking platform for rapid recruitment of various DNA repair factors including MRE11, NBS1, BARD1, CHFR, and RNF146 to chromatin.^{130,132} Meanwhile, PARP-1 can PARylate different proteins globally, including BRCA1, DNA-dependent protein kinase catalytic subunit (DNA-PKcs), and core histones, to promote DNA DSB repair.^{132–134} In addition, arsenite was shown to interfere with DNA damage-elicited global PARylation in human cells by inhibiting PARP1 activity through displacement of zinc ions from its zinc finger motifs.^{80,135–137}

PARP1 perhaps can be viewed as a typical paradigm among DNA repair proteins, many of which contain redox-sensitive cysteine residues within zinc finger domains.^{34,138,139} Given that arsenic exposure can stimulate the generation of ROS/RNS,^{33,49,140} arsenite-induced oxidative stress can result in modification of thiol groups on the cysteine residues in zinc finger motifs of these DNA repair proteins, leading to the loss of their enzymatic functions.^{82,85,141,142} This has been demonstrated for PARP1, which could be inhibited by peroxyxynitrite-mediated *S*-nitrosation of its zinc finger cysteine(s).^{49,50,80} Global PARylation, a PTM predominantly mediated by PARP1 and critical for immediate initiation of DDR to maintain genomic stability, was shown to be markedly inhibited upon an 18-h exposure to 0.01 μ M arsenite.¹⁴³ Therefore, apart from direct As³⁺ binding, arsenic-induced oxidative stress also contributes, in part, to diminished DNA repair arising from arsenic exposure (Figure 4).^{84,144}

Recently, CTCF, a versatile 11-zinc finger transcription regulator with well-established roles in three-dimensional genome organization and transcriptional regulation, was found to facilitate DNA DSB repair by enhancing HR.^{145,146} CTCF is recruited to DSB sites through its zinc finger domains independently of PARylation.¹⁴⁵ Therefore, substitution of zinc ions within those 11 zinc finger domains of CTCF by iAs³⁺ can diminish its DNA binding capability. Additionally, a recent study demonstrated that CTCF binds to MRE11 and CtIP through its zinc finger domains, which enables robust CtIP recruitment for 5'-end DNA resection, thereby promoting HR while suppressing NHEJ pathway of DNA DSB repair.¹⁴⁷ Hence, the binding of iAs³⁺ with CTCF might explain, in part, how arsenite disrupts the outcome of this DSB repair pathway.

4.5. Disruption of DNA Damage Response Signaling.

Arsenite exposure has been shown to impair DDR signaling, especially through dysregulation of protein PARylation, ubiquitination, and SUMOylation,^{148,149} as reviewed recently.⁷² DDR is a tightly regulated temporal- and spatial-sensitive chromatin-associated process important for sensing DNA damage, recruiting DNA repair machinery to damage sites, and intertwining DNA repair with other DNA-transacting activities.¹⁵⁰ For example, H2AX phosphorylation, PARylation, and histone acetylation mediated by ATM, PARP1, and TIP60, respectively, are among the earliest events in DNA damage response; they are activated by DNA damage and involve early and rapid detection of DNA lesions and chromatin decompaction, thereby providing better accessibility for DNA repair machinery to DNA damage sites.¹⁵⁰ Reversible ubiquitination and SUMOylation of DDR proteins are crucial for effective DDR signaling and repair of DNA DSBs,¹⁵¹ where zinc finger-containing ubiquitin ligases and SUMO-conjugating enzymes can be disrupted by arsenic exposure, with examples of RAD18, MORC2, RNF4, and RNF111 being briefly discussed below.⁷²

During replication stress, the E3 ubiquitin ligase RAD18 induces monoubiquitination of PCNA, which is in turn recognized and bound by Spartan for its subsequent recruitment of Pol η (i.e., a TLS polymerase important for bypassing UV-induced DNA lesions).^{152–154} The monoubiquitinated PCNA also promotes efficient monoubiquitination and chromatin localization of FANCD2,^{155,156} and this ubiquitination is indispensable for recruiting SNM1A to DNA repair complexes assembled at MMC- and UV-induced DNA lesions to promote ICL repair.¹⁵⁷

PARylation is also important in DDR. To achieve DNA damage-induced PARylation and PAR-dependent recruitment of DNA repair proteins to DNA damage sites, PARP1 recruits chromatin remodeling enzyme MORC2 to DNA damage sites and catalyzes PARylation of its CW-type zinc finger domain, thereby activating its ATPase and chromatin remodeling activities. Meanwhile, PARylated MORC2 stabilizes PARP1 through enhancing the NAT10-mediated acetylation of lysine 949 in PARP1, which is no longer subjected to CHFR ubiquitination and the subsequent proteasomal degradation.^{132,158} This illustrates that the crosstalk between different DNA repair enzymes is important for the dynamic PARylation in DDR.

SUMOylation and ubiquitination are also necessary for robust DDR. To favor DDR with coordinated SUMOylation and ubiquitination, the SUMO E3 ligases PIAS1 and PIAS4 are recruited to DSB sites and lead to accumulation of SUMO1/2/3 at DSB sites, which leads to the recruitment of RNF4 to DNA damage sites.^{159,160} RNF4 subsequently ubiquitinates and facilitates the degradation of polySUMOylated MDC1 and RPA, thus promoting efficient DSB repair.^{148,161–164}

Similar to RNF4, RNF111 promotes nonproteolytic ubiquitination of SUMOylated XPC, which is in turn recruited to UV-damaged DNA.¹⁶⁵ Given the extensive involvement of zinc finger-harboring ubiquitin and SUMO E3 ligases in DDR signaling (e.g., RAD18, RNF4), arsenite exposure may hamper ubiquitination or SUMOylation through direct binding or

inducing oxidative modifications of cysteine residues in their zinc finger motifs, thereby disrupting DDR.

5. DISRUPTION OF CELL CYCLE CHECKPOINTS, PROMOTION OF CELL PROLIFERATION, AND SUPPRESSION OF APOPTOSIS

In arsenic-induced carcinogenesis, iAs has been shown to interfere with cell cycle regulation, promote cell proliferation, and suppress apoptosis, which indirectly inhibit DNA repair (i.e., by not providing enough time) and allow cells with DNA damage to propagate^{166–168}

Cell cycle checkpoints, including DNA damage checkpoints at the G1/S and G2/M boundaries as well as in the S phase, tightly regulate cell cycle progression by accurately assessing mitogenic signals and properly repairing DNA damage while avoiding further propagation of damaged genomes through promoting apoptosis of the severely damaged cells.^{169–172} This regulation is executed by checkpoint proteins, which comprise cyclins, cell cycle-dependent kinases, and phosphatases.^{170,171}

A recent study demonstrated that a 48-h exposure of acute promyelocytic leukemia (APL) cells to 2 μM iAs³⁺ increased the mRNA expression of several cell cycle-associated genes, including *CCND1* (encodes for cyclin D1 protein), *CCNE1* (cyclin E1 protein), and *GADD45A*, but reduced those of *CCNF* (cyclin F) and *CDKN1A* (p21), resulting in a transition of cell populations from G1/S phases to G2/M phases and arresting cell cycle progression. This result suggests that acute exposure to iAs³⁺ disturbs cell cycle checkpoints, leading to uncontrolled cell cycle progression and proliferation of APL cells.¹⁶⁸ Notably, the DNA damage checkpoint at the G1/S boundary was bypassed by iAs³⁺-mediated alterations in expression of checkpoint proteins, especially cyclin D1.^{173–175}

Another recent study demonstrated that a 1-month exposure of human BEAS-2B cells and keratinocytes to 0.5 μM arsenite delayed the transition from mitosis by compromising mitotic checkpoint through the attenuation of anaphase promoting complex-mediated cyclin B1 degradation.¹⁶⁷ In this vein, long-term arsenite exposure up-regulates Polo-like kinase 1 via acting on Akt in the PI3K/Akt pathway, thereby potentiating mitotic catastrophe and genetic instability.^{167,176}

Arsenite-elicited up-regulation of p53 protein expression and abrogation of p53-dependent increase in p21 expression together unleash the checkpoint restraints at the G1/S and G2/M boundaries as well as in the S phase.^{174,177,178} Chronic low-dose (e.g., 14 days, 0.1 μM) and acute noncytotoxic-level (e.g., 24 h, 1 μM) of arsenite exposure, as well as acute low-level (e.g., 24 h, 1 μM) of MMA^{III} exposure, were found to induce p53 protein expression in normal human fibroblast cells.^{70,174,177} In addition, arsenite-elicited up-regulation of Hdm2 and the ensuing ubiquitination of p53 promote nuclear export of p53, thereby disrupting its ability to transcriptionally activate its target genes, including p21 and NER genes.^{179–181} These may give rise to unimpeded cell cycle progression and accrual of mutations from unrepaired DNA lesions.^{178,181}

Arsenite has been reported to promote the proliferation of human cells.^{33,68,182–187} Arsenite is thought to achieve this through stimulating pathways for cell proliferation and survival (e.g., Erk, EGFR, MAPK pathways) while inhibiting pathways involved in cell death (e.g., JNK signaling) via modulation of a myriad of transcription factors (e.g., AP-1 and NF- κ B).¹⁸⁷ Exposure to 5 μ M arsenite was found to increase the proliferation of SH-SY5Y human neuroblastoma cells via activation of ERK in VEGF signaling, which might favor tumor progression.¹⁸⁴ Arsenite-induced cell proliferation was shown to arise from elevated levels of epidermal growth factor receptor (EGFR) ligand, heparin-binding EGF, and its subsequent activation of EGFR phosphorylation that induces pERK and cyclin D1 expression in human cells.¹⁸⁸ Arsenite-elicited ERK signaling is required for arsenic-induced transactivation of NF- κ B,¹⁸⁹ which might be mediated by arsenic-stimulated oxidative stress.^{190–192} Additionally, low-dose arsenite treatment has been documented to activate ERK, as well as transcription factors E2F1 and Activating Protein 1 (AP-1), enhance the DNA binding activities of AP-1 and NF- κ B, and elevate the expression of a number of positive cell growth-related genes including *FOS*, *JUN*, *MYC*, and *EGR-1*.^{185,190,193–197}

The major cell growth and ROS-mediated pathways are regulated by protein tyrosine phosphorylation, which itself is controlled by tyrosine kinases and protein tyrosine phosphatases. Therefore, arsenite exposure is believed to inactivate protein tyrosine phosphatases by ROS/RNS-induced modifications of redox-sensitive cysteines at their active sites, thereby augmenting the total cellular tyrosine phosphorylation.^{34,198–203} Combined, arsenite and arsenite-induced ROS/RNS can stimulate a phosphorylated state of EGFR, and activate ERK, transcription factor AP-1 complex, and its downstream target genes *JUN*, *FOS*, and *MYC*, thereby increasing cyclin D1 expression.^{190,204} Together with arsenite-activated E2F transcription factors and their modulation of cyclin E levels, arsenite exposure elicits unchecked cell cycle progression and uncontrolled cell proliferation.^{194,204–206}

Chronic exposure to arsenic has been shown to increase cell survival and elevate levels of DNA damage in cultured human cells.⁴² PARP1 inhibition by low concentrations of arsenic has been proposed to enhance the survival of cells with unrepaired DNA lesions including a population of “initiated carcinogenic cells” that represents the first step of the multistage carcinogenesis process.¹⁸ Chronic arsenic exposure was also shown to decrease p53 at the post-translational level via arsenic-induced PARylation as well as the mRNA expression level of Bax.⁴² This arsenite-elicited inhibition of apoptotic mediators was also found to impair the XPC-mediated global-genome NER, resulting in mutation accrual and neoplastic transformation of DNA damage-containing cells.⁴²

Together, arsenite-induced positive cell proliferation and suppression of apoptosis confer insufficient time for efficient DNA repair before replication of damaged DNA and/or allow cells with damaged DNA to propagate, which may give rise to mutations and genome instability.

6. EPIGENETIC DYSREGULATION ASSOCIATED WITH ARSENIC-INDUCED CARCINOGENESIS

Arsenic-elicited carcinogenesis is believed to stem, in part, from its disruption of epigenetic signaling by alterations of histone PTMs and DNA methylation patterns (Figure 5). Histone PTMs and DNA methylation tightly regulate the chromatin dynamics to modulate the inheritable expression patterns of different genes.²⁰⁷ Therefore, arsenic can induce carcinogenesis by epigenetic silencing of tumor suppressor genes or activation of oncogenes. Here, we review the current evidence about the role of arsenic exposure in modulating the epigenetic pathway of gene regulation.

6.1. Alterations of Histone PTMs.

In the nucleus, DNA is packaged into chromatin, where the nucleosome core consists of stretches of DNA (~147 bp) wrapping around a histone octamer consisting of two copies each of core histones H2A, H2B, H3, and H4.²⁰⁸ Hence, nucleosomes form linear 11 nm beads-on-a-string structures that further compact into 30 nm fibers and other higher-order chromatin states.²⁰⁹ The N-terminal histone tails extending from nucleosomes are subjected to a range of PTMs, including methylation, acetylation, phosphorylation, ubiquitination, SUMOylation, ADP ribosylation, deimination, and proline isomerization,²¹⁰ which in turn modify the chromatin compaction and recruitment of nonhistone proteins, including gene regulatory factors and DNA repair enzymes, to chromatin. The formation of open, relaxed chromatin conformation is required for DNA repair machinery to gain access to the spatially confined region surrounding DNA damage sites, as described in the “access-repair-restore” model.^{211,212}

Inorganic arsenic and its metabolites have been documented to disrupt histone PTMs, including but not limited to H2AX phosphorylation, H2AX ubiquitination, H2B ubiquitination, H3 methylation, and H4K16 acetylation,^{110,120,121,213,214} which were reviewed elsewhere.^{207,215,216} Here, we focus on the effect of arsenic exposure on those histone PTMs that are closely associated with DNA repair and genomic stability.

A number of previous *in vitro* studies have demonstrated that arsenic exposure elicits alterations in a variety of global histone PTMs, which include loss of H4K16Ac, H3K27me3, and ubiquitination of H2B, as well as gain of H3K4me2, H3K4me3, H3K9me2, H3K9Ac, H3K14Ac, and phosphorylation of H3S10 and H2AX (γ H2AX).^{118,217–222} For example, the PBMC from the participants of the folic acid and creatine supplementation trial (FACT) study exposed to 50–500 μ g/L arsenite in drinking water exhibited a decrease in H3K9me3 and H3K9ac, and a gain in H3K9me2.^{217,220} In addition, A549 human lung carcinoma cells displayed a global loss of H3K4me1 and a global gain of H3K4me2 and H3K4me3 following a 24-h exposure to 1 μ M arsenite, where H3K4me3 remained elevated even at 1 week after arsenite withdrawal.²¹⁹ In another study, a 24-h exposure of A549 cells to arsenite led to elevated levels of gene-silencing marks, H3K9me2 and H3K27me3, while also augmenting the global level of H3K4me3, a gene-activating mark.²¹⁸

In contrast to transcriptional activators, elevated levels of H3K9me2 mediated by increased mRNA and protein levels of histone methyltransferase G9a are correlated with transcriptional repression,^{218,223} which has been shown to be involved in the silencing of tumor suppressor genes in cultured cancer cells.^{224,225} H3K27me3 is frequently accompanied by inactive promoters and gene silencing, and it labels chromatin by polycomb repressive complex 1 (PRC1) via H2AK119 ubiquitination to facilitate chromatin compaction.²²⁶ Exposure of human cells to 0.5 μM arsenic trioxide (ATO) induces the expression of components PRC2 protein complex, consisting of SUZ12, EZH2, and BMI1, resulting in elevated H3K27me3 and the ensuing diminished expression of tumor suppressors p16^{INK4a} and p14^{ARF}.²²⁷ Arsenite-induced H3K27me3 in chromatin silences tumor suppressor genes, for example, *HOXB7* and *CDKN2A*, which are involved in DNA repair.^{228–230} Therefore, histone H3 PTMs are among the targets of arsenic exposure and aid in the subsequent disruption of DNA repair.

As briefly discussed above, histone H2BK120ub and histone H4K16Ac also play a significant role in the generation of relaxed chromatin environment that is conducive for the access of DNA repair enzymes. Histone H2BK120ub is crucial for decompacting the 30 nm chromatin fiber,²³¹ while H4K16Ac also decondenses chromatin,²³² thereby facilitating DSB repair by increasing the accessibility of chromatin to DNA repair machinery.^{233–235} H2BK120ub is mediated by the E3 ubiquitin ligase composed of the RNF20-RNF40 heterodimer,²³³ whereas H4K16Ac is modulated by both hMOF and TIP60 MYST-family of histone acetyltransferases.²³⁶ In UROtsa human bladder epithelial cells, global H4K16Ac levels were reduced in a dose- and time-dependent manner upon exposure to As³⁺ and MMA^{III}.¹¹⁸ Arsenite exposure was also documented to diminish H2BK120ub and H4K16Ac by inhibiting the above-mentioned zinc finger-containing proteins.^{110,120,121} Moreover, the PARylation of lysine residues of the core histone tails mediated by PARP1, including H2AK13, H2BK30, H3K27, H3K37, and H4K16, can result in a rapid decondensation of chromatin around DNA damage sites and facilitate DNA repair.^{133,134,237} Therefore, arsenic exposure could result in a compact chromatin structure by interfering with these histone-modifying enzymes and by diminishing the chromatin-decompacting histone PTMs, limiting the access of DNA repair proteins to chromatin.

Finally, phosphorylation of H2AX, which is mediated by ATM and DNA-PKcs following DNA damage,²³⁸ contributes to the initiation of DNA damage response.^{214,239} Phosphorylation of H2AX at different sites triggers distinct downstream cellular processes. For instance, phosphorylation of Tyr142 in H2AX stimulates XPD-dependent apoptosis and enhances DDR.²⁴⁰ Recently, it was reported that a 24-h exposure to 4 μM ATO significantly stimulated levels of phosphorylated H2AX in mouse embryonic fibroblasts (MEFs), possibly via inhibition of *de novo* dTMP biosynthesis through inducing SUMOylation, ubiquitination, and subsequent degradation of MTHFD1.²¹³ Since iAs has been documented to elicit ATR and DNA-PKcs *in vivo* and *in vitro*,^{241–243} this increase in H2AX phosphorylation is thought to originate from the activation of ATR and DNA-PKcs and might also be modulated by TOPK.²⁴⁴

Studies have suggested that arsenic-induced phosphorylation of histone H3 might be responsible for the up-regulation of caspase 10, a proto-apoptotic factor,²²² and the proto-

oncogenes *FOS* and *JUN*,²⁴⁵ which can lead to transformation of human fibroblast cells and the induction of tumors in animals.²⁴⁶ Additionally, since arsenite could induce *FOS* and *JUN* via activation of JNKs and p38/MAPK2 kinases, and promote H3S10 phosphorylation,^{221,247} therefore, the impact of the arsenic-induced H3 phosphorylation on DNA repair may be regulated by JNK/MAPK pathway, which was recently shown to be linked to DNA damage response.²⁴⁸

6.2. DNA Methylation.

DNA methylation constitutes another important epigenetic mechanism of gene regulation. Depending on the type of regulatory elements where the methylation occurs, the effect of DNA methylation on gene expression varies. Under normal circumstances, DNA methylation events in the promoter and gene body are associated with gene repression and activation, respectively.²⁴⁹ Alterations in DNA methylation are known to play roles in carcinogenesis partly through inactivation of tumor suppressor genes or activation of oncogenes.²⁵⁰

Several potential mechanisms have been proposed to account for the arsenite-induced alterations in DNA methylation including SAM deficiency, diminished expression of DNMT genes, inhibition of Tet proteins, and aberrant occupancy of CTCF binding on promoters of *DNMT* and *TET* genes (Figure 6). As noted above, biotransformation of inorganic arsenic depletes SAM, which is also utilized in DNA methylation catalyzed by DNA cytosine-5-methyltransferases (DNMTs).²⁵¹ In addition, arsenic exposure was found to repress, in a dose-dependent manner, the mRNA expression levels and activities of DNA methyltransferases DNMT1, DNMT3A, and DNMT3B, thereby resulting in a loss of global DNA methylation.^{251–253} Interestingly, arsenic exposure was shown to reduce CTCF expression and inhibit the binding of CTCF to DNA, which diminishes the occupancy of CTCF in the promoters of DNMT1, DNMT3A, and DNMT3B genes; this may explain the observation of arsenite-induced diminished expressions of DNMT genes.²⁵⁴

Arsenic exposure has been documented to result in global DNA hypomethylation,^{175,255–257} which is a hallmark of various human cancers.^{258–260} It was reported that chronic exposure of cultured rat liver cells to a low dose (0.5 μM) of arsenite resulted in global DNA hypomethylation.²⁵⁷ DNA hypomethylation was also observed in leukocytes of human populations who were exposed to arsenic and developed skin cancers.²⁶¹ Chronic exposure of mice to 45 ppm arsenite for 48 weeks induced hepatic global DNA hypomethylation as well as promoter hypomethylation of the *ESR1* gene, which encodes for estrogen receptor α .¹⁷⁵ Promoter hypomethylation is believed to stimulate the expression of *ESR1* gene, which in turn can induce cell cycle-dependent DSBs and contribute to initiation of breast cancer.^{262,263} Arsenic-induced promoter hypomethylation of the *ESR1* gene is consistent with the observation of frequent mutations of DDR and DNA repair proteins in estrogen-dependent breast cancers, suggesting that ER signaling converges to inhibit effective DNA repair and apoptosis, thereby favoring proliferation.^{175,263}

Although arsenic exposure causes global DNA hypomethylation, it also leads to promoter hypermethylation and repression of specific tumor suppressor genes. For instance, the DNA repair gene *MLH1* displays significant promoter hypermethylation in whole blood obtained

from humans chronically exposed to arsenic.²⁶⁴ Additionally, significant promoter hypermethylation of NER genes (*ERCC2*, *RPA1*, *POLD3*, *POLE2*) was observed in human hepatocytes exposed to 0.2 μM ATO for 3 months.²⁶⁵ Recently, hypermethylation of NER genes *ERCC1* and *ERCC2*, and suppression of their expression in human cells, was also correlated with chronic arsenic exposure.²⁶⁶

5-Methylcytosine (5-mC) in DNA can be oxidized by the ten-eleven translocation (Tet) family enzymes to 5-hydroxymethylcytosine (5-hmC), which may convey regulatory epigenetic functions by binding to specific proteins to confer active gene transcription.^{267–270} In addition, diminished levels of 5-hmC in DNA are hallmarks of human cancers.²⁶⁸ Tet enzymes were found to prevent DNA damage-induced chromosome mis-segregation, indicating that 5-hmC was pivotal in promoting DNA repair and maintenance of genome integrity.^{271,272} Arsenite was shown to bind directly with the zinc finger motifs of Tet proteins and inhibit the Tet-mediated oxidation of 5-mC to 5-hmC in HEK293T cells with ectopic expression of Tet proteins and in mouse embryonic stem cells following an acute 24-h exposure to 2–5 μM arsenite.²⁶⁷ On the other hand, global hyper-hydroxymethylation of cytosine was observed in arsenite-transformed BEAS-2B cells (after a 8-week exposure to 0.5 μM arsenite),²⁷³ which was accompanied by elevated expression of Tet enzymes and was attributed to arsenic-elicited selective inhibition of CTCF binding on the proximal, weaker CTCF binding sites in the promoters of *TET* genes.²⁷³ The differences in these observations are likely attributed to the uses of different cell lines and exposure conditions, where long-term exposure to arsenite may induce adaptive response in cells. Future studies in laboratory animals and human subjects are needed to determine how arsenic exposure affects the levels of 5-hmC *in vivo*.

Combined together, chromatin compaction around damaged DNA and disturbed methylation pattern in DNA upon arsenite exposure perturb the sophisticated epigenetic network of DNA repair machinery, which may compromise genome stability and result in arsenic-elicited carcinogenesis.

7. CONCLUSIONS AND PERSPECTIVES

In this review, distinct modes of action for arsenic-induced impairment of DNA repair pathways are extensively discussed. Unlike conventional carcinogens (e.g., alkylating agents, UV light), which can damage DNA directly, arsenic's role in carcinogenesis perhaps resides on its ability to compromise the repair of DNA lesions induced by DNA damaging agents that are formed from endogenous metabolism or arise from other environmental exposure. Multiple mechanisms are likely at play, and they encompass diminished expression of DNA repair genes, functional disruption of DNA repair proteins, induction of a chromatin environment that is not conducive for DNA repair, and aberrant cell cycle regulation. Hence, chronic arsenic exposure can result in a progressive decline in DNA repair capacity, which may represent a crucial pathway through which arsenic contributes to carcinogenesis. In addition, elevated production of ROS/RNS from arsenic exposure and ensuing accumulation of DNA lesions from these species may also contribute, in part, to arsenic carcinogenesis.

The findings cited in this review also suggest that zinc finger proteins, which are encoded by genes constituting approximately 10% of the human genome and play significant roles in DNA repair as well as epigenetic regulation, constitute important molecular targets for arsenic binding (Figure 7).²⁷⁴ iAs exposure induces ROS/RNS, which can target the redox-active nucleophilic sulfhydryl group on cysteine residues located within the zinc finger motifs of these proteins. The resulting modification products, especially S-nitrosylation, disturb the native Zn²⁺ coordination sphere of the zinc finger proteins and alter their structure and functions.^{49,50,275–279} Thus, direct iAs³⁺ binding, perhaps in conjunction with oxidation and nitrosylation of cysteine sulfhydryl groups of zinc finger motifs of proteins involved in DNA repair and epigenetic regulation of gene expression, may represent important molecular mechanisms underlying the modes of action for the exacerbated DNA repair capacity in arsenic-induced carcinogenesis.

It is important to note that, while substantial progress has been made in this area of research, much remains to be done to further illustrate the above-mentioned mechanisms. First, most of the previously published studies were conducted with the use of cell-based systems. It will be important to examine whether the findings made from the cell-based assays can be extended to laboratory animals and human subjects exposed to environmentally relevant levels of arsenic species.

Second, RING finger proteins make up a large family of E3 ubiquitin ligases,²⁸⁰ and it will be important to systematically investigate, at the proteome-wide scale, how exposure to arsenite modulates the ubiquitination of proteins, especially those that are involved in DNA repair and DNA damage response signaling.

Third, the C3H-type zinc-finger proteins represent the second largest group of RNA-binding proteins in mammals.²⁸¹ It remains unclear how arsenic exposure affects the functions of these RNA-binding proteins and influences the metabolisms of RNA (i.e., stability, translation efficiency, and alternative splicing of RNA), especially those mRNA species that encode DNA repair proteins and epigenetic modifiers or those noncoding RNAs that modulate chromatin structure.

Lastly, if diminished DNA repair and elevated oxidative DNA damage constitute the major mechanisms of arsenic carcinogenesis, we would expect to observe elevated rates of mutations in arsenic-exposed laboratory animals and human subjects. In this vein, Hei et al.²⁸² demonstrated, by employing A_L cell assay, that arsenite could induce, in a dose-dependent manner, mutations (mostly large deletions) in mammalian cells. They also observed that the mutagenicity of arsenite could be diminished markedly by cotreating cells with a radical scavenger, dimethyl sulfoxide.²⁸² It will be important to unveil the degree to which arsenic exposure leads to mutagenesis. Recent advances in next-generation sequencing, especially exome sequencing,²⁸³ render it possible to unveil how arsenic exposure leads to mutagenesis in laboratory animals or human subjects.

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Nathan Price obtained his Ph.D. degree in Chemical Biology from the University of Missouri Columbia in 2014, where he worked with Prof. Kent S. Gates on chemistry of abasic site-derived interstrand cross-link lesions. He subsequently joined the laboratory of Yinsheng Wang at the University of California Riverside, and his main research projects involve the development and application of shuttle vector methods for studying how structurally defined DNA lesions affect DNA replication in human cells. He also developed a strong interest in scientific and medical writing.

Yinsheng Wang is currently a Distinguished Professor in the Chemistry Department and the Environmental Toxicology graduate program at the University of California Riverside. His research interest encompasses DNA damage and mutagenesis, proteomics, and epigenetics. In recent years, he also developed a strong interest in understanding the molecular mechanisms of arsenic toxicity and carcinogenicity. His group members employ a multidisciplinary approach, including mass spectrometry-based bioanalytical chemistry, synthetic organic chemistry, molecular biology, genetics, and genomics, to tackle their research projects.

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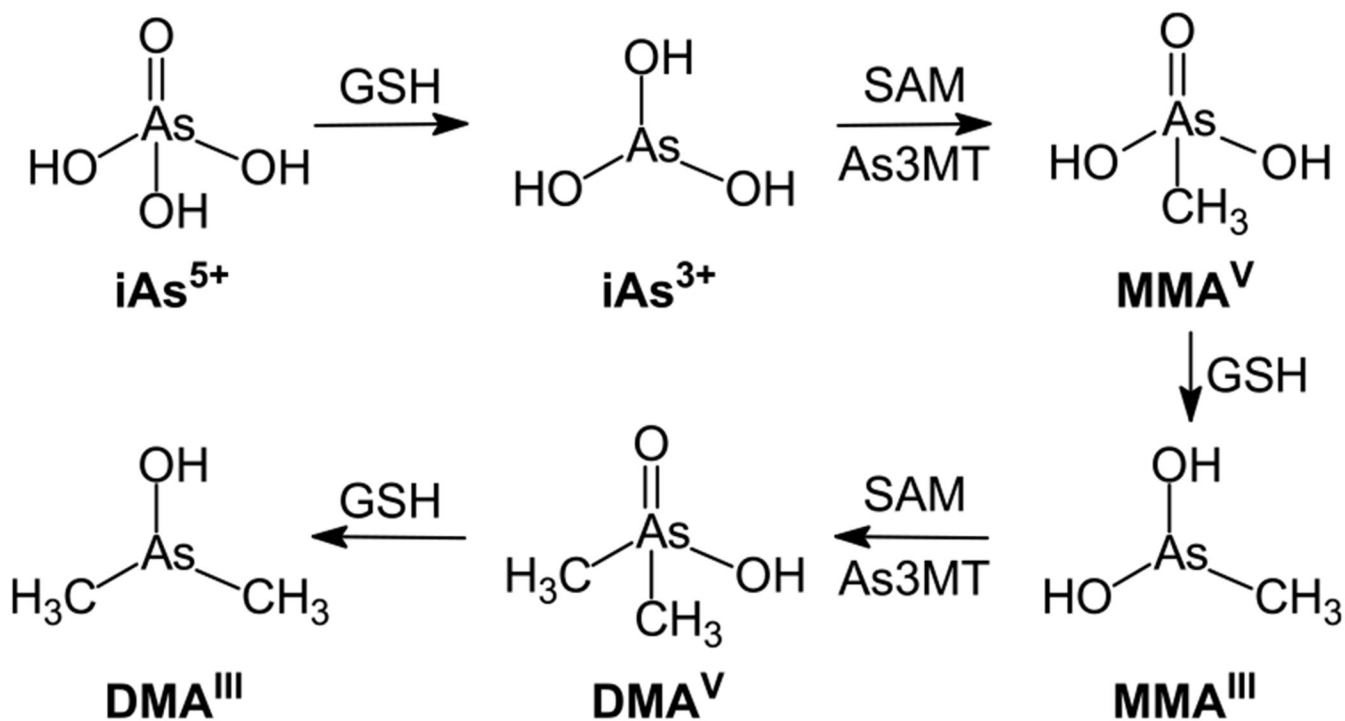


Figure 1.

Inorganic arsenic and its metabolism. In liver, absorbed As⁵⁺ is reduced to As³⁺ by GSH as an electron donor, and As³⁺ undergoes sequential methylation and reduction with SAM and GSH as the donors of methyl group and electron, respectively, to generate MMA^V, MMA^{III}, DMA^V, and DMA^{III}.

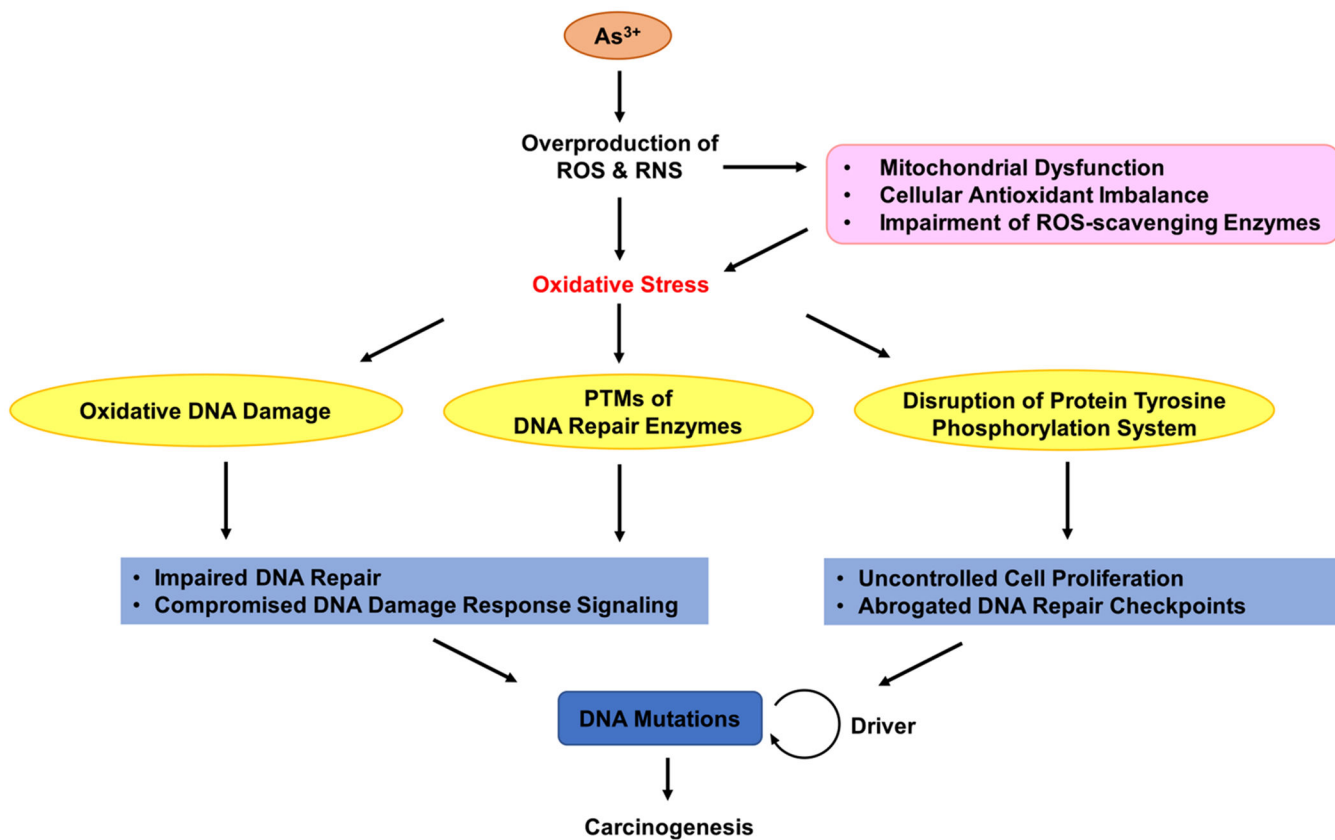


Figure 2. iAs-elicited oxidative stress enhances carcinogenesis through impairing DNA repair pathway to induce mutations in DNA. As³⁺ can induce the overproduction of ROS and RNS through mitochondria dysfunction, cellular antioxidant imbalance, and impairment of ROS-scavenging enzymes. Hence, iAs-elicited oxidative stress induces oxidative DNA damage, disturbs PTMs of DNA repair enzymes, and disrupts protein tyrosine phosphorylation, thereby enhancing DNA mutations to promote carcinogenesis.

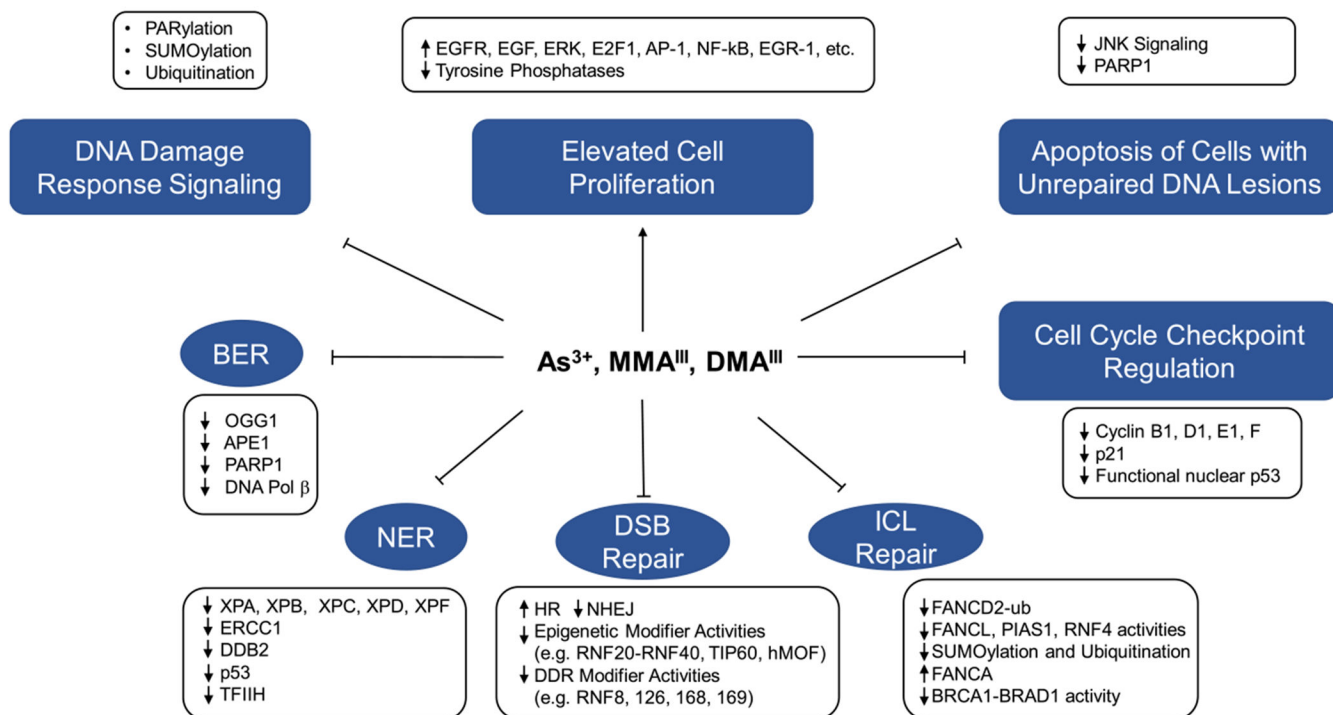


Figure 3. Major events governing the disruption of DNA repair pathways by iAs and its trivalent metabolites. Arsenite and its metabolites induce cell proliferation while inhibiting BER, NER, DSB repair, ICL repair, DDR signaling, cell cycle checkpoint regulation, and apoptosis of damaged cells. These together diminish the capacity of DNA repair and impair genetic integrity.

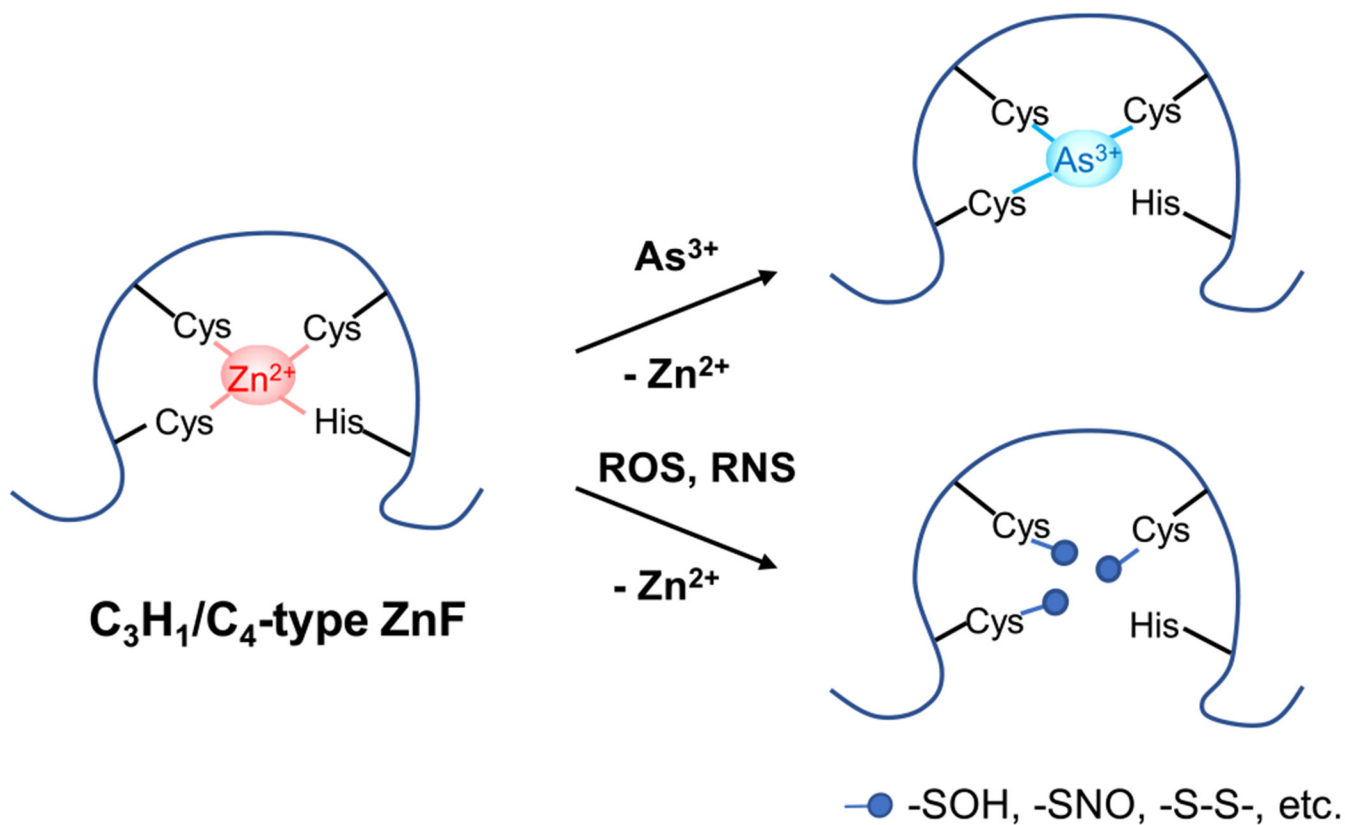


Figure 4.

Modes of action of inorganic arsenic and iAs-induced ROS/RNS in impairing the enzymatic activity of zinc finger (ZnF) proteins. iAs and ROS/RNS can target vicinal cysteines within the zinc coordination spheres of zinc finger proteins: (i) As^{3+} directly binds to these cysteines more strongly than Zn^{2+} ; (ii) ROS oxidizes these cysteines to form a series of oxidation products, such as $-\text{SOH}$ and $-\text{S}-\text{S}-$; (iii) RNS, especially peroxynitrite, can S-nitrosylate these cysteines. In all these cases, Zn^{2+} bound within zinc finger motifs is released through its displacement by As^{3+} , which alters the conformation of zinc finger proteins and hence their enzymatic activities.

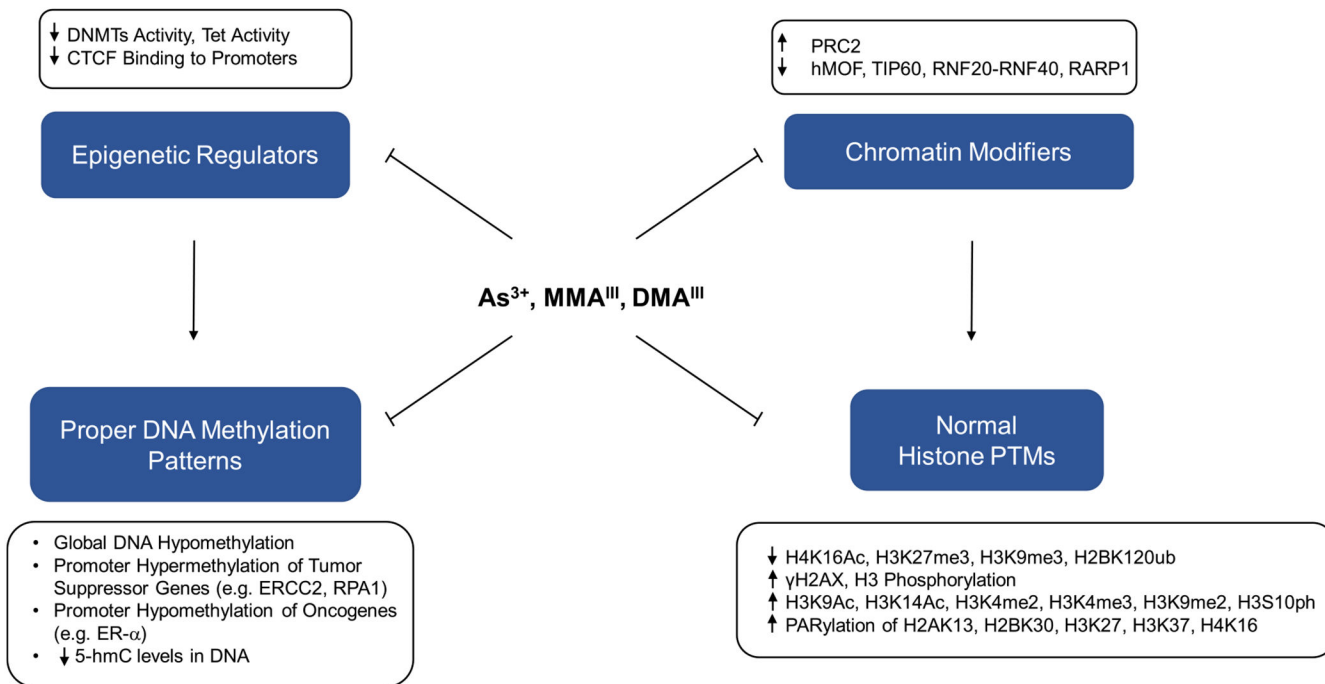


Figure 5. Major events through which inorganic arsenite and its trivalent metabolites disrupt epigenetic integrity via inhibition of epigenetic regulators and chromatin modifiers. As^{3+} , MMA^{III} , and DMA^{III} can impair the enzymatic activities of DNA epigenetic regulators (e.g., DNMTs, Tet, and CTCF) and chromatin-modifying enzymes (e.g., hMOF, TIP60, and PARP1), which subsequently perturb DNA methylation and histone PTMs, respectively, thereby disrupting epigenetic integrity.

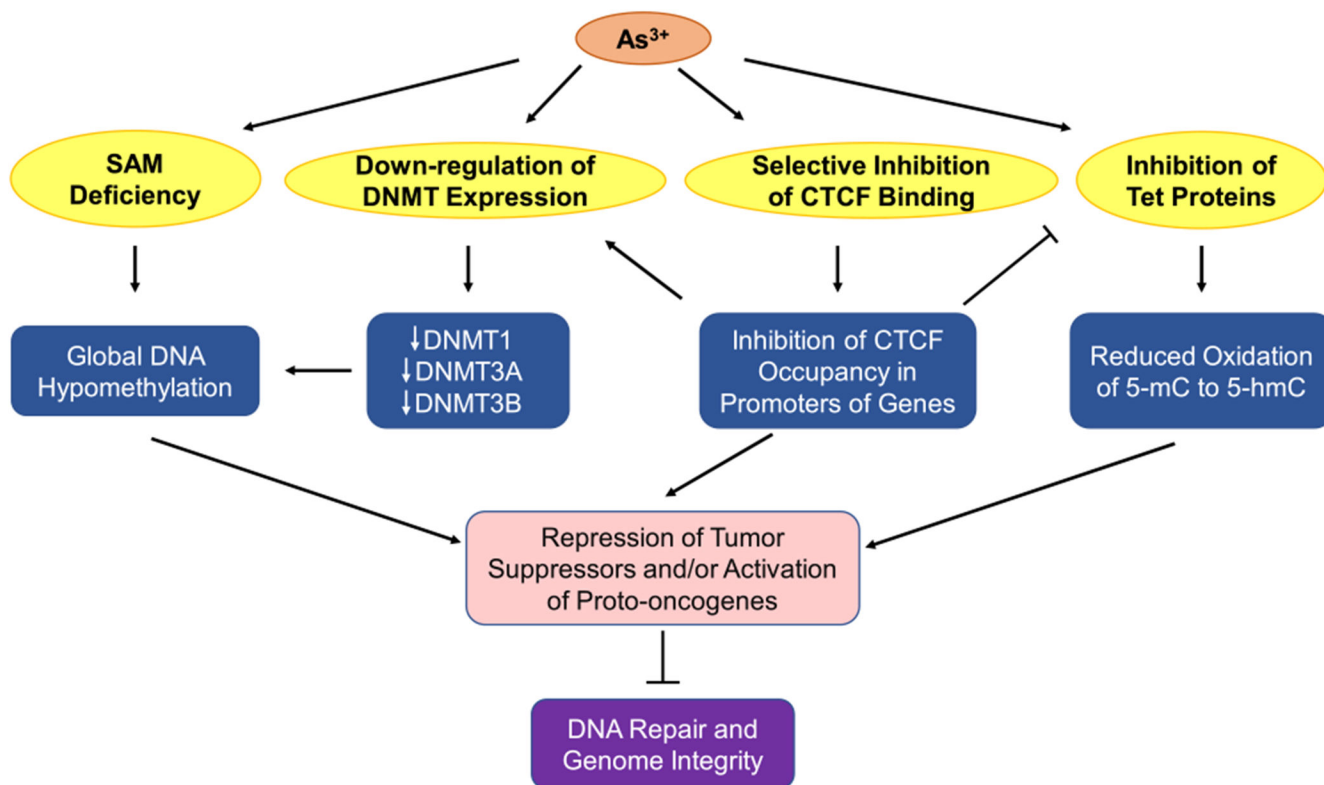


Figure 6. Arsenite disrupts DNA methylation. Methylation events in promoters repress gene expression, whereas those in gene bodies activate gene expression. Metabolism of iAs induces SAM deficiency, which results in global DNA hypomethylation. iAs exposure leads to decreased expressions of DNMT1, DNMT3A, DNMT3B, thus diminishing global DNA methylation. Additionally, iAs selectively inhibits the binding of CTCF to promoters of genes (e.g., DNMTs), leading to repression of tumor suppressor genes. Meanwhile, iAs inhibits Tet proteins, thus reducing the level of 5-hmC, which can be inhibited by weakened occupancy of CTCF in the promoters of *TET* genes. Combined together, iAs can repress tumor suppressors and activate proto-oncogenes, thereby impairing DNA repair and genome integrity.

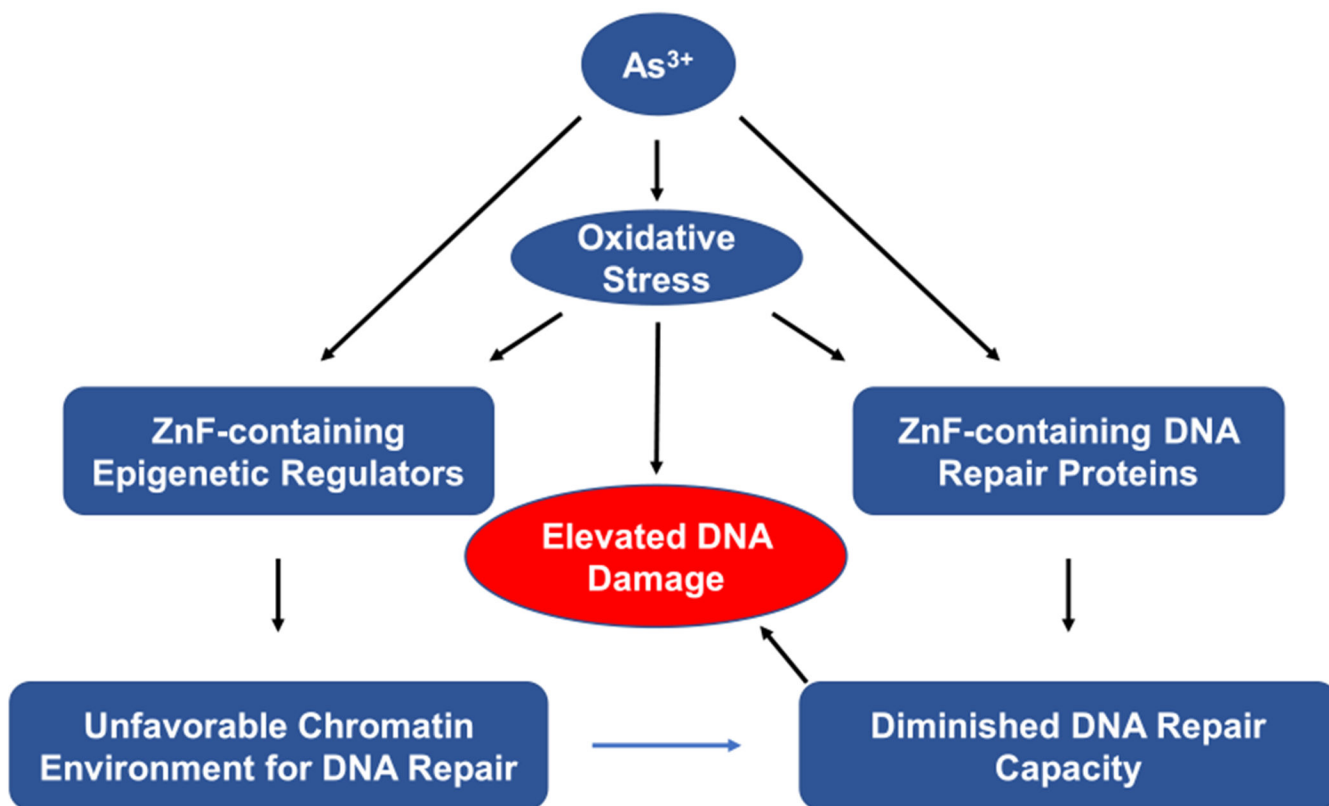


Figure 7. Arsenite and iAs-induced oxidative stress enhance DNA damage through disrupting the functions of zinc finger proteins. iAs-induced oxidative stress and As³⁺ itself can disrupt the zinc finger-containing epigenetic regulators and DNA repair enzymes, thereby impairing DNA repair. Simultaneously, oxidative stress generates oxidative DNA damage. These together may result in tumorigenesis.