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Research Article

Associations between Arsenic Exposure and Global Posttranslational Histone Modifications among Adults in Bangladesh

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Abstract

Background: Exposure to arsenic (As) is associated with an increased risk of several cancers as well as cardiovascular disease, and childhood neuro-developmental deficits. Arsenic compounds are weakly mutagenic, alter gene expression and posttranslational histone modifications (PTHMs) *in vitro*.

Methods: Water and urinary As concentrations as well as global levels of histone 3 lysine 9 di-methylation and acetylation (H3K9me2 and H3K9ac), histone 3 lysine 27 tri-methylation and acetylation (H3K27me3 and H3K27ac), histone 3 lysine 18 acetylation (H3K18ac), and histone 3 lysine 4 trimethylation (H3K4me3) were measured in peripheral blood mononuclear cells (PBMC) from a subset of participants ($N = 40$) of a folate clinical trial in Bangladesh (FACT study).

Results: Total urinary As (uAs) was positively correlated with H3K9me2 ($r = 0.36$, $P = 0.02$) and inversely with H3K9ac ($r = -0.47$, $P = 0.002$). The associations between As and other PTHMs differed in a gender-dependent manner. Water As (wAs) was positively correlated with H3K4me3 ($r = 0.45$, $P = 0.05$) and H3K27me3 ($r = 0.50$, $P = 0.03$) among females and negatively correlated among males (H3K4me3: $r = -0.44$, $P = 0.05$; H3K27me3: $r = -0.34$, $P = 0.14$). Conversely, wAs was inversely associated with H3K27ac among females ($r = -0.44$, $P = 0.05$) and positively associated among males ($r = 0.29$, $P = 0.21$). A similar pattern was observed for H3K18ac (females: $r = -0.22$, $P = 0.36$; males: $r = 0.27$, $P = 0.24$).

Conclusion: Exposure to As is associated with alterations of global PTHMs; gender-specific patterns of association were observed between As exposure and several histone marks.

Impact: These findings contribute to the growing body of evidence linking As exposure to epigenetic dysregulation, which may play a role in the pathogenesis of As toxicity. *Cancer Epidemiol Biomarkers Prev; 21(12); 2252–60. ©2012 AACR.*

Introduction

It is estimated that approximately 150 million people in at least 70 countries are exposed to naturally occurring arsenic (As) through contaminated drinking water (1). In Asia, an estimated 60 million people are chronically exposed, and roughly half reside in Bangladesh where exposure levels often exceed the permissible Environmental Protection Agency (EPA) levels (2, 3). In the United States, excess lifetime risk for lung and bladder cancers were shown to be elevated in the Western and New England regions of the United States, where there is As contamination of drinking water; excess fatality rates were 152 per million and 117 per million for domestic and public supplies in the Western region, and 125 per million for domestic supplies in New England (4).

Chronic exposure to As is known to cause skin, lung, and bladder cancers, and has been implicated in the development of liver and prostate cancers in several epidemiologic studies (5–9). Furthermore, As exposure has also been associated with cardiovascular disease, neurologic and childhood neuro-developmental deficits, and hypertension (10–14). However, although As exposure is associated with a diverse set of health

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outcomes, the mechanisms underlying the carcinogenic and noncarcinogenic effects of As are poorly understood. An emerging body of evidence suggests that As exposure may alter epigenetic marks, including DNA methylation and posttranslational histone modifications (PTHMs) (15, 16).

Posttranslational modifications of lysine (K) residues on histone (H) tails play a fundamental role in the regulation of chromatin structure, gene, and noncoding RNA transcription and nuclear architecture (17, 18). Enrichment in acetylation (ac) of histone tails in promoters is typically associated with transcriptional activation, whereas the functional consequences of methylation (me) depend on the number of methyl groups, the residue itself, and its location within the histone tail. For example, H3K4me2, H3K4me3, and H3K9ac are correlated with open chromatin and active gene expression, whereas H3K27me2, H3K27me3, H3K9me2, and H3K9me3 in gene promoters are associated with inactive chromatin and gene repression (19). In addition, some marks, such as H3K4me1 and H3K27ac are found in the enhancer elements of genes and can influence gene expression even at large distances from the gene (20). Moreover, alteration of epigenetic mechanisms, such as DNA methylation and histone modifications, has been reported in numerous diseases, including cancer, neurologic, and cardiovascular diseases (21–23).

A number of previous studies have shown that As exposure induces a myriad of global PTHMs *in vitro*, including reduction of acetylation in histone H3 and H4, loss of H4K16ac, increase in H3K14ac, increase in H3K9ac, increase in H3K4me2 and H3K4me3, loss of H3K27me3, loss or gain of H3K9me2, as well as increase in H3Ser10 and H2AX phosphorylation (24–34). Recent work has also shown that human peripheral blood mononuclear cells (PBMC) or white blood cells can be used to measure the association between metal exposure and PTHMs. Furthermore, previous work by our group showed that As exposure was associated with alterations in leukocyte DNA methylation and that global hypomethylation of leukocyte DNA seemed to increase the risk for As-induced premalignant skin lesions (24, 25, 35, 36). Importantly, PBMCs (or bone marrow progenitor cells) are a specific target for As toxicity. As an effective therapeutic drug for APL, As^{III} distributes to PBMC progenitor cells and influences their cellular function (37–39).

We conducted a pilot study to examine the influence of chronic As exposure on global levels of 6 posttranslational histone marks, including: H3K9me2 and H3K27me3, H3K4me3, H3K9ac, H3K18ac, and H3K27ac, using PBMC from an ongoing trial of folic acid and creatine supplementation [folate clinical trial in Bangladesh (FACT)] in Bangladesh. We found that environmental exposure to As is associated with alterations of all of the marks examined, and observed that 4 of the 6 marks, including: H3K4me3, H3K27me3, H3K18ac, and H3K27ac, were altered in a gender-specific manner.

Materials and Methods

Study site

The study site is a 25-km^2 region within Araihazar, approximately 30 km east of Dhaka, Bangladesh. The wide range of well water As (wAs) concentrations (0.1–960 μg/L) from more than 10,000 wells within this region presents a unique opportunity to study potential effects of As exposure. Informed consent was obtained by Bangladeshi field staff physicians. The study was approved by the Institutional Review Boards of Columbia University Medical Center (New York) and the Bangladesh Medical Research Council (Dhaka, Bangladesh) and is registered with ClinicalTrials.gov.

Eligibility criteria and study design

The Health Effects of Arsenic Longitudinal Study (HEALS) cohort study is part of Columbia University's Superfund Research Program that was launched in 2000, and currently includes roughly 30,000 participants. The present study uses samples from a subset of 600 HEALS participants who were recruited for enrollment into FACT study. This clinical trial, aimed primarily at lowering blood As concentrations through nutritional supplementation, enrolled a total of 600 study participants, and fieldwork was completed in June 2011. At the time of enrollment, all FACT study participants had wAs between 50 and 500 μg/L and were provided with a water filtration system that removed As. Women who were currently pregnant and/or planned to become pregnant, participants taking nutritional supplements, or having known renal or gastrointestinal disease were excluded from the study. To evaluate the effects of As exposure on histone modifications, PBMCs from 40 FACT study participants (20 from each gender) known to have a wide range of wAs exposure (50–500 μg/L As) were analyzed.

Sample collection and handling

Blood samples were obtained by venipuncture, and collected into heparin-containing vacutainer tubes, which were placed in IsoRack/IsoPack cool packs (Brinkmann Instruments). Within 4 hours, samples were transported in hand-carried coolers to the local laboratory, situated in our field clinic in Araihazar. Samples were centrifuged at 3,000 × *g* for 10 minutes at 4°C, and the plasma fraction was stored at −80°C. PBS was added to the remaining cells followed by a ficoll-hypaque gradient extraction of PBMCs using standard techniques. PBMCs were stored at −80°C. Blood and plasma samples were hand-carried frozen on dry ice to Columbia University.

Water arsenic

A survey of all wells in the study region assessed wAs concentration of tube wells at each participant's home between January and May 2000 (Van Geen and colleagues, 2002). Samples were analyzed at Columbia University's Lamont Doherty Earth Observatory by graphite furnace atomic absorption (GFAA), which has a detection limit of 5 μg/L (*AAnalyst 600*, PerkinElmer, Shelton, CT). Those

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samples found to have nondetectable As concentrations by GFAA were subsequently analyzed by inductively coupled mass spectrometry (ICP-MS), with a detection limit of 0.1 μg/L (Cheng and colleagues, 2004).

Urinary arsenic

Urine samples were collected in 50-mL acid-washed polypropylene tubes. These were kept in portable coolers, and within 4 hours were frozen at −20°C in Araihazar, and subsequently hand carried on dry ice to New York. Total urinary As (uAs) concentrations were measured by GFAA spec-trometry using an AAnalyst 600 graphite furnace system (PerkinElmer) in the Columbia University Trace Metals Core Lab, as described previously (Nixon and colleagues, 1991). This laboratory participates in a quality control program run by the Institut de Sante Publique du Quebec, Canada. Intraclass correlation coefficients (ICCs) between the Columbia laboratory's values and samples calibrated at the Quebec laboratory were 0.99. Urinary crea-tinine was analyzed using a method based on the Jaffe reaction and was used to correct for hydration status (40)

Histone extraction

Histones were extracted from the PBMCs as previously described (24, 41). Briefly, cells were washed with ice-cold PBS and lysed in ice-cold radioimmunoprecipitation assay (RIPA) buffer (50 mmol/L Tris–HCl, PH 7.4, 1% NP-40, 0.25% Na-deoxycholate, 150 mmol/L NaCl, 1 mmol/L EDTA, 1 mmol/L PMSF, supplemented with a protease inhibitor mixture (Roche Applied Sciences) for 10 minutes. The pellet was collected by centrifugation at 10,000 × *g* for 10 minutes. The pellet was washed once in 10 mmol/L Tris-Cl and 37 mmol/L EDTA (pH 7.4), and resuspended in 200 μL 0.4 N H_2SO_4. After an overnight incubation at 4°C, the supernatant was collected by centrifugation at 14,000 × *g* for 15 minutes, and mixed with 1.8 mL cold acetone and kept at −20°C overnight. Histones were collected by centrifugation at 14,000 × *g* for 15 minutes. After one wash with acetone, the histones were air dried and suspended in sterile deionized water. Total protein concentration in each sample was measured using the Bradford Assay according to the manufacturer's instructions (Bio-Rad Laboratories).

Histone modification analysis

The levels of each histone modification were determined using the sandwich ELISA, as previously described (24). Briefly, polystyrene 96-well microplates (Fisher Scientific) were coated with Histone H3 antibody (Abcam) and incubated overnight at 4°C. Plates were then blocked for 2 hours at room temperature with 5% milk in PBST (1× PBS, 0.05% TWEEN-20), washed with PBST, and the desired amount of standards (H3K9me2 and H3K4me3) recombinant proteins (Active Motif), or mixed calf histone proteins (Sigma) were added to each well, followed by the addition of histones diluted in water. The plates were then incubated at room temperature for 1.5 hours with agitation on an orbital shaker. After incuba-tion, the wells were washed, and primary antibody, such as H3 (Sigma), H3K9me2, H3K9ac, H3K18ac, H3K27ac (Abcam), or H3K4me3 (Millipore), was added to each well separately and incubated at room temperature for 1 hour with agitation. After another wash, secondary rabbit anti-goat IgG-HRP or mouse anti-goat IgG-HRP antibody (Santa Cruz Biotechnology) was added to each well and incubated at room tem-perature for 1 hour without agitation. Wells were then washed and TMB (3,3′, 5,5″-tetramethylbenzidine; Fisher Scientific) solution was added to each well and incubated at room temperature for 30 minutes in the dark. The reaction was stopped by adding 2 M H_2SO_4 to each well. All analyses were conducted in triplicate. The optical density was read at 450 nm using the SoftMax Pro software (version 5.2) and the SpectraMax 190 microplate reader (both from Molecular Devices). The percentages of each histone modification were derived from standard curves specific to each histone mark. The respective within- and between-assay coefficients of variation for each modification were: H3K9me2: 7.2% and 7.1%, H3K9ac: 5.1% and 10.9%, H3K4me3: 5.2% and 9.4%, H3K18ac: 3.9% and 13%, H3K27me3: 6.5% and 7.3%, and H3K27ac: 6.3% and 7.7%. To calculate the within-assay coefficient of variation, all samples were run in triplicate on the same plate on the same day. To calculate the between-assay coefficient of variation, multiple samples were run in triplicate for each modification on different days.

Statistical analysis

We calculated descriptive statistics for the total sample and by wAs category (high vs. low) for As exposure variables (wAs and urinary As) and covariates [age, sex, television ownership, cigarette smoking, use of betel nut, body mass index (BMI), total homocysteine, s-adenosyl methionine, and s-adenosyl homocysteine].

Bivariate associations between As exposure and the histone marks (H3K18ac, H3K27ac, H3K27me3, H3K4me3, H3K9ac, and H3K9me2) were evaluated using wAs as both a continuous and a categorical (high vs. low) variable and using uAs as a continuous variable. Scatterplots and Spearman correlation coefficients were used for uAs and when wAs was treated as a continuous variables. When wAs was treated as a binary variable, Wilcoxon rank-sum tests were used to determine whether there was a statistically significant difference in the histone marks by high versus low wAs category. Given previous observations that males and females in Bangladesh differ significantly in susceptibility to the effects of As exposure, Spearman correlations between water or uAs exposure and histone marks stratified by gender were used. In addition, median concentrations of the histone marks by wAs category and gender were calculated; a Kruskal–Wallis test was used to determine whether there was a statistically significant difference among the 4 groups and the Wilcoxon rank-sum test was used to compare specific groups. Correlations between the histone marks were evaluated using Spearman correlation coefficients.

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To evaluate potential confounding variables, associations between (i) covariates and wAs or uAs exposure and (ii) covariates and histone marks were examined. When both variables being examined were continuous, Spearman correlation coefficients were used. To examine associations between a categorical variable and a continuous variable *t* tests or the nonparametric Wilcoxon rank-sum test was used when appropriate. Multiple linear regression models were then used to further examine the associations between wAs or uAs exposure and the histone marks, after adjustment for age and land ownership, that is, covariates observed to be associated with both the exposure and outcome variables. Age was modeled as a continuous variable and land ownership was modeled as a binary (yes/no) variable. Variables with skewed distributions were natural log transformed before inclusion in linear regression models to (i) create approximately normal distributions for dependent variables, (ii) improve the linearity of the relationship between independent and dependent variables, or (iii) to reduce the impact of extreme values of an independent variable. Urinary As, age, H3K18ac, H3K27ac, H3K27me3, H3K4me3, and H3K9ac were log transformed. All analyses were conducted using SAS (version 9.2; SAS Institute Inc); all statistical tests were 2-sided with a significance level of 0.05.

Results

A total of 40 participants were selected for this pilot study; 50% were male, and the average age was 39. The characteristics of the participants are shown in Table 1 for the entire group by wAs exposure category (low vs. high). We selected 20 study participants with relatively low As exposure (low wAs group) and 20 with relatively high As exposure (high wAs group). The median wAs concentration for the low exposure group was 55 μg/L (range, 50–81 μg/L). For the high exposure group, the median wAs concentration was 216 μg/L and the range was wider (150–500 μg/L). Compared with those with high wAs exposure, participants in the low wAs group were more likely to own land (55% vs. 35%) or a television (65% vs. 55%), and were also more likely to have ever smoked (30% vs. 20%) or used betel nut (30% vs. 25%). Participants from the low wAs group also had lower total homocysteine (Hcys) concentrations (8.3 vs. 9.2 μmol/L).

Spearman correlation coefficients between As exposure (wAs and uAs) and the histone marks for the entire group and by gender are shown in Table 2. Both wAs and uAs were inversely correlated with H3K9Ac in the entire group [wAs: $r = -0.40$ ($P = 0.01$); uAs: $r = -0.47$ ($P = 0.002$)]. wAs and uAs were both positively correlated with H3K9me2, although the association with wAs did not reach statistical significance [wAs: $r = 0.27$ ($P = 0.10$); uAs: $r = 0.36$ ($P = 0.02$)]. The associations between As exposure and H3K9Ac or K3K9me2 did not differ significantly by gender (Table 2).

There were no statistically significant correlations between wAs or uAs exposure and H3K18Ac, H3K27ac, H3K27me3, or H3K4me3 in the entire group. However, the associations between As exposure and these 4 histone marks differed by gender (Table 2 and Fig. 1). wAs was significantly positively correlated with H3K4me3 ($r = 0.45$, $P = 0.05$) and H3K27me3 ($r = 0.50$, $P = 0.03$) among females and negatively correlated with H3K4me3 ($r = -0.44$, $P = 0.05$) and H3K27me3 ($r = -0.34$, $P = 0.14$) among males. The *P* value for the test of difference by

Table 1. General characteristics for the total study sample and by wAs group[a]

	Entire group ($n = 40$)	Low wAs group[b] ($n = 20$)	High wAs group[c] ($n = 20$)
Age, y	39 (13.5)	42.0 (12.5)	34.0 (12.5)
BMI, kg/m^2	19.5 (3.3)	20.5 (3.4)	18.5 (2.7)
wAs, μg/L	115.5 (161)	55.0 (4.9)	216.0 (71.0)
Urinary As, μg/L	91.5 (115.0)	69.0 (62.5)	165.0 (158.0)
Urinary creatinine, mg/dL	39.0 (35.8)	42.7 (37.8)	35.6 (34.8)
Urinary As/g creatinine	247.8 (376.3)	133.4 (75.6)	509.7 (221.6)
Total homocysteine, μmol/L	8.9 (5.5)	8.3 (6.9)	9.2 (5.4)
s-Adenosyl methionine, μmol/L	2.14 (0.95)	2.5 (1.2)	2.06 (0.64)
s-Adenosyl homocysteine, μmol/L	0.25 (0.17)	0.22 (0.15)	0.28 (0.17)
Female, %	50	50	50
Land ownership, %	45	55	35
Television ownership, %	60	65	55
Current cigarette smoking, %	25	30	20
Current betel nut use, %	27.5	30	25

[a]Median (interquartile range) unless otherwise noted.
[b]wAs 50 to 81 μg/L.
[c]wAs 150 to 500 μg/L

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Table 2. Spearman correlation coefficients (*P* value) between As exposure and histone marks by gender

	wAs				Urinary As[a]			
	Total	Females	Males	*P* value[b]	Total	Females	Males	*P* value[b]
H3K18ac	0.08 (0.62)	−0.22 (0.36)	0.27 (0.24)	0.14	0.11 (0.50)	−0.21 (0.37)	0.49 (0.03)	0.03
H3K27ac	0.07 (0.65)	−0.44 (0.05)	0.29 (0.21)	0.02	−0.009 (0.96)	−0.48 (0.03)	0.36 (0.12)	0.009
H3K27me3	0.06 (0.72)	0.50 (0.03)	−0.34 (0.14)	0.009	0.13 (0.44)	0.45 (0.04)	−0.42 (0.06)	0.007
H3K4me3	−0.04 (0.81)	0.45 (0.05)	−0.44 (0.05)	0.005	0.19 (0.23)	0.39 (0.09)	−0.18 (0.44)	0.08
H3K9ac	−0.40 (0.01)	−0.44 (0.05)	−0.40 (0.08)	0.89	−0.47 (0.002)	−0.63 (0.003)	−0.25 (0.28)	0.16
H3K9me2	0.27 (0.10)	0.17 (0.49)	0.27 (0.25)	0.76	0.36 (0.02)	0.12 (0.61)	0.52 (0.02)	0.18

[a]Urinary As adjusted for uCr using the residual method.
[b]*P* value for the test of difference by gender.

gender was 0.005 for H3K4me3 and 0.009 for H3K27me3. Similar associations were observed using uAs as the exposure.

wAs was inversely associated with the global levels of H3K27ac among females ($r = -0.44$) and positively associated among males ($r = 0.29$). Correlations between wAs and H3K18ac by gender also exhibited a similar pattern (females, $r = -0.22$; males $r = 0.27$). None of these correlations within gender reach statistical significance. The test of difference by gender was significant for H3K27ac ($P = 0.02$) but not for H3K18ac ($P = 0.14$). Findings for H3K27ac and H3K18ac were similar when uAs was used as the exposure variable (Table 2); however, when using uAs as the exposure the P value for the test of difference by gender was 0.03 for H3K18ac.

Table 3 shows the Spearman correlations between histone marks. H3K18ac was positively correlated with H3K27ac ($r = 0.44$, $P = 0.004$) and negatively correlated with H3K27me3 ($r = -0.47$, $P = 0.002$). H3K27ac, in turn, was positively correlated with H3K9me2 ($r = 0.35$, $P = 0.03$). H3K9ac was also inversely, but not significantly, correlated with H3K9me2 ($r = -0.27$, $P = 0.10$).

Overall, results from the linear regression models were similar to our main analyses. In addition, the results of

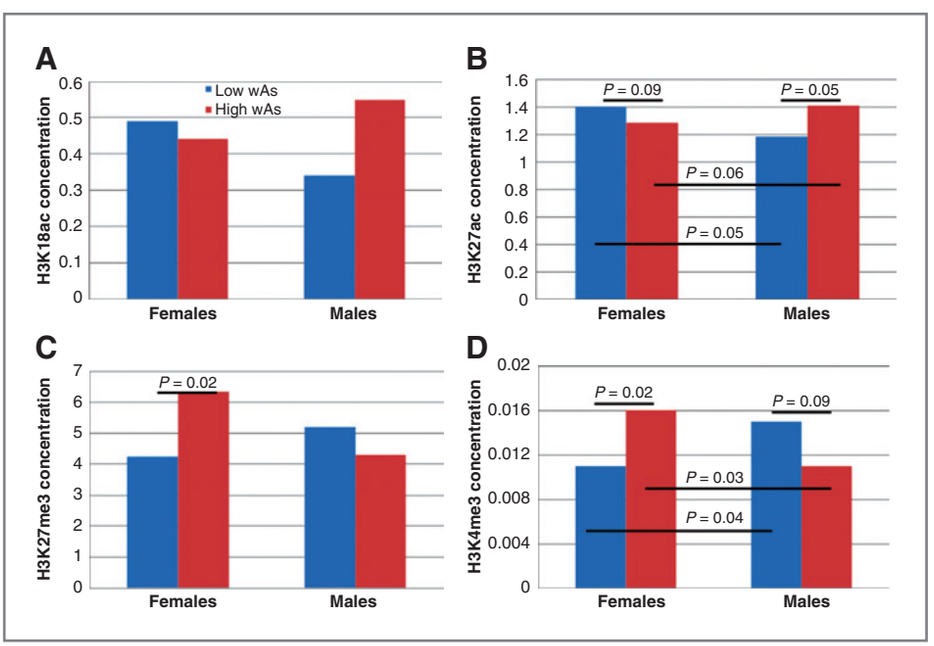

Figure 1. Median concentrations of histone marks by sex and wAs category[a] for (A) H3K18ac, (B) H3K27ac, (C) H3K27me3, and (D) H3K4me3[b]. A, low wAs range = 50 to 81 μg/L, high wAs range = 150 to 500 μg/L. B, on the basis of a Kruskal–Wallis test, there is a statistically significant overall difference among the 4 groups for H3K27Ac ($P = 0.049$), H3K27me3 ($P = 0.048$), and H3K4me3 ($P = 0.02$). Using Wilcoxon rank-sum tests, we also tested for (i) differences in histone marks by high/low wAs within gender and (ii) differences in histone marks by gender within wAs category (high/low)—*P* values less than 0.10 are indicated.

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Table 3. Spearman correlation coefficients (*P* value) between histone marks ($n = 40$)

	H3K18ac	H3K27ac	H3K27me3	H3K4me3	H3K9ac	H3K9me2
H3K18ac	1	0.44 (0.004)	−0.47 (0.002)	0.14 (0.39)	0.06 (0.73)	0.23 (0.16)
H3K27ac		1	0.04 (0.79)	−0.14 (0.38)	0.15 (0.36)	0.35 (0.03)
H3K27me3			1	0.04 (0.79)	−0.04 (0.81)	−0.05 (0.75)
H3K4me3				1	−0.16 (0.31)	0.18 (0.27)
H3K9ac					1	−0.27 (0.10)
H3K9me2						1

unadjusted models and those adjusted for age and land ownership were essentially the same (data not shown). The only notable difference between the linear regression results and those in Table 2 is that the inverse association between wAs and H3K27me3 in males presented in Table 2 was not observed in the regression models. There was also no statistically significant difference in the covariate-adjusted associations between wAs and H3K27me3 by sex.

Discussion

There is considerable interest among the scientific community in the field of epigenetics, with particular attention being paid to the study of PTHMs and their functional roles in gene expression dysregulation and carcinogenesis. Cancer cells exhibit both aberrant DNA methylation patterns and changes in the global levels of specific histone modifications, but the specific pattern of epigenetic modifications that precedes the onset of neoplasia is not well characterized (22). Given that As is a highly prevalent environmental contaminant worldwide and that some arsenicals (i.e., As_2O_3) are given to patients to treat disease, understanding the potential effects of As on the epigenome is of great importance.

This pilot study provides unique insights into the epigenetic effects of chronic As exposure in a generally healthy population in Bangladesh. Histone posttranslational modifications can change chromatin structure via an intricate set of interactions and influence both global and gene-specific DNA methylation, thereby regulating genomic stability and gene expression (19, 42, 43). The observed changes in the global levels of histone marks, such as an increase in H3K9me2, a mark of transcriptional repression, and a decrease in H3K9ac, a mark that is usually associated with relaxed and active chromatin, suggests that chronic As exposure may be associated with global transcriptional repression. An abundance of chromatin silencing marks may favor the silencing of tumor suppressor genes, which can predispose to cancer development. Moreover, H3K9 methylation and hypoacetylation play an important role in the establishment of DNA methylation (44).

Earlier work by our group has shown that chronic As exposure in Bangladesh was positively associated with genomic DNA methylation in a dose-dependent manner among folate-sufficient individuals (15). Recently, Christiani and colleagues have reported that exposure to higher levels of As in Bangladesh was positively associated with DNA methylation in LINE-1 repeated elements, in both maternal and fetal leukocytes (45). Although contradictory to the findings of some studies, the observed correlation between DNA hypermethylation and As exposure may potentially be explained by the findings reported here. H3K9me2 is a critical mark for cytosine methylation of DNA (46). A persistent increase of H3K9me2 following chronic As exposure could potentially trigger *de novo* DNA methylation, which would more permanently suppress gene expression and contribute to As-induced long-term silencing of tumor suppressor genes. Both *in vitro* and *in vivo* studies have shown that As exposure could lead to increased DNA methylation in the promoter region of tumor suppressor genes, such as p53 and p16 (47, 48). With respect to histone acetylation, a number of studies have linked both global and gene-specific DNA hypermethylation, with the loss of histone acetylation (30, 49, 50). Jensen and colleagues have shown that As-induced malignant transformation was accompanied by DNA hypermethylation and loss of histone 3 acetylation at gene promoters (30). Taken together, the As-associated increase in H3K9me2 and decrease in H3K9ac may provide some insight into the underlying mechanisms and physiologic implications of increased genomic DNA methylation observed in the earlier work.

The fact that As exposure seems to influence histone marks such as H3K27me3, H3K4me3, H3K18ac, and H3K27ac, in a gender-specific manner represents an interesting and significant finding. The gender differences occurred in both methylation and acetylation marks, however, the direction of the association with As by gender differed by the type of mark (i.e., H3K18ac and H3K27ac increased in males and decreased in females, whereas H3K27me3 and H3K4me3 increased in females and decreased in males). The effect modification by gender was unexpected. While it is possible that some of the statistically significant differences that were observed may have occurred by chance due to the small sample size, there is some evidence of estrogen-sensitive histone marks. For example, Bredfeldt and colleagues have shown that estrogen receptor signaling regulates a HMT

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enhancer, ultimately reducing levels of H3K27me3 in hormone-responsive cells (51). In addition, Hamilton and colleagues illustrated that As is an endocrine disruptor and influences ER-mediated gene expression (52). Interestingly, in the preliminary analyses of these same $n = 40$ FACT participants, *S*-adenosylhomocysteine (SAH), a strong inhibitor of most methylation reactions, including DNA and As methylation, also influenced histone marks in a gender-specific manner (53, 54). In the dataset, SAH was associated with significant decreases in 2 methylation marks: H3K9me2 in females and H3K27me3 among males (data not shown). Unfortunately, due to the small sample size and the fact that folate data are not yet available for these subjects, the analysis of this finding is limited, but will be investigated further in future work.

Another interesting finding was the correlations between the histone marks. H3K18ac was positively correlated with H3K27ac ($r = 0.44$, $P = 0.004$) and negatively correlated with H3K27me3 ($r = -0.47$, $P = 0.002$). H3K27ac, in turn, was positively correlated with H3K9me2 ($r = 0.35$, $P = 0.03$). As would be expected given the opposite direction of gene expression afforded by the presence of these 2 opposing marks, H3K9ac was also inversely, but not significantly, correlated with H3K9me2 ($r = -0.27$, $P = 0.10$). Contrary to an earlier hypothesis, however, a correlation between H3K4me3 and H3K9me2, which would be consistent with their reciprocal regulation (i.e., H3K4me3 is an activating mark and H3K9me2 is a repressive mark), was not observed. The inability to detect a correlation between these 2 marks might be due to the small sample size of this pilot study.

With respect to our findings, some potential mechanisms that may underlie the observed alterations in histone posttranslational modifications include: an increase in histone methyltransferases (HMT), such as G9a, which is responsible for the methylation of H3K9 and whose mRNA and protein expression increased following As exposure; induction of 2 H3K4 methyl "erasers," lysine-specific demethylase (LSD) 1 and 2, which were also required for global DNA methylation; and a very potent As-induced inhibition of pyruvate dehydrogenase, an enzyme that catalyzes the final step in acetyl CoA biosynthesis (32, 55–57). Acetyl CoA is a requisite substrate for histone acetylation; inhibition of acetyl CoA biosynthesis would decrease histone acetylation by depletion of substrate leading to chromatin condensation and increased DNA methylation.

In conclusion, H3K9ac and H3K9me2 were found to be associated with As exposure similarly in males and females, whereas H3K4me3, H3K18ac, H3K27ac, and H3K27me3 were associated with As exposure in a gender-specific manner. Future studies will be directed at examining the proposed mechanisms underlying the observed alterations in histone posttranslational modifications and further investigating the gender effects. In addition, exploring the genomic location of the altered histone marks will be of importance in understanding whether they impact mostly gene expression by producing changes in gene promoters or whether they affect other genomic regulatory components such as noncoding RNA. Finally, additional work is warranted to evaluate the potential impact of these histone modifications on various As-induced health outcomes.

Disclosure of Potential Conflicts of Interest

No potential conflicts of interest were disclosed.

Authors' Contributions

Conception and design: Y. Chervona, A. Arita, M.V. Gamble, M. Costa
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Analysis and interpretation of data (e.g., statistical analysis, biostatistics, computational analysis): Y. Chervona, M.N. Hall, E. Ali, X. Liu, M.V. Gamble
Writing, review, and/or revision of the manuscript: Y. Chervona, M.N. Hall, H. Sun, M.A. Zoroddu, M.V. Gamble, M. Costa
Acquisition of data (provided animals, acquired and managed patients, provided facilities, etc.): H.C. Tseng, E. Ali, M.V. Gamble
Study supervision: M.V. Gamble, M. Costa
Other: Generated data, Y. Chervona; Biological sample processing, M.N. Uddin

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References

1. Ravenscroft P, Brammer H, Richards K. Arsenic pollution: a global synthesis. UK: Wiley-Blackwell; 2009.
2. Kinniburgh PLS. Arsenic contamination of groundwater in Bangladesh. Keyworth, UK: British Geological Survey; 2001.
3. Bank TW. Towards a more effective operational response; 2005.
4. Kumar A, Adak P, Gurian PL, Lockwood JR. Arsenic exposure in US public and domestic drinking water supplies: a comparative risk assessment. J Expo Sci Environ Epidemiol. 2010;20:245–54.
5. IARC Monographs on the Evaluation of Carcinogenic Risks to Humans. Some drinking-water disinfectants and contaminants, including Arsenic. Lyon, France: IARC; 2004.
6. Schuhmacher-Wolz U, Dieter H, Klein D, Schneider K. Oral exposure to inorganic arsenic: evaluation of its carcinogenic and non-carcinogenic effects. Crit Rev Toxicol 2009;39:271–98.
7. Chiu H, Ho S, Wang L, Wu T, Yang C. Does arsenic exposure increase the risk for liver cancer? J Toxicol Environ Health A 2004; 67:1491–500.
8. Benbrahim-Tallaa L, Waalkes M. Inorganic arsenic and human prostate cancer. Environ Health Perspect 2008;116:158–64.
9. Rahman M, Ng J, Naidu R. Chronic exposure of arsenic via drinking water and its adverse health impacts on humans. Environ Geochem Health 2009;31(Suppl 1):189–200.

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Published OnlineFirst October 12, 2012; DOI: 10.1158/1055-9965.EPI-12-0833

10. Wasserman GA, Liu X, Parvez F, Ahsan H, Factor-Litvak P, Kline J, et al. Water arsenic exposure and intellectual function in 6-year-old children in Araihazar, Bangladesh. Environ Health Perspect 2007; 115:285–9.
11. Chen Y, Parvez F, Gamble M, Islam T, Ahmed A, Argos M, et al. Arsenic exposure at low-to-moderate levels and skin lesions, arsenic metabolism, neurological functions, and biomarkers for respiratory and cardiovascular diseases: review of recent findings from the Health Effects of Arsenic Longitudinal Study (HEALS) in Bangladesh. Toxicol Appl Pharmacol 2009;239:184–92.
12. Tseng CH, Chong CK, Tseng CP, Hsueh YM, Chiou HY, Tseng CC, et al. Long-term arsenic exposure and ischemic heart disease in arseniasis-hyperendemic villages in Taiwan. Toxicol Lett 2003;137: 15–21.
13. Wasserman GA, Liu X, Parvez F, Ahsan H, Factor-Litvak P, van Geen A, et al. Water arsenic exposure and children's intellectual function in Araihazar, Bangladesh. Environ Health Perspect 2004; 112:1329–33.
14. Chen CJ, Hsueh YM, Lai MS, Shyu MP, Chen SY, Wu MM, et al. Increased prevalence of hypertension and long-term arsenic exposure. Hypertension 1995;25:53–60.
15. Pilsner JR, Liu X, Ahsan H, Ilievski V, Slavkovich V, Levy D, et al. Genomic methylation of peripheral blood leukocyte DNA: influences of arsenic and folate in Bangladeshi adults. Am J Clin Nutr 2007; 86:1179–86.
16. Ren X, McHale CM, Skibola CF, Smith AH, Smith MT, Zhang L. An emerging role for epigenetic dysregulation in arsenic toxicity and carcinogenesis. Environ Health Perspect 2011;119:11–9.
17. Berger SL. The complex language of chromatin regulation during transcription. Nature 2007;447:407–12.
18. Esteller M. Cancer epigenomics: DNA methylomes and histone-modification maps. Nat Rev Genet 2007;8:286–98.
19. Schneider R, Grosschedl R. Dynamics and interplay of nuclear architecture, genome organization, and gene expression. Genes Dev 2007;21:3027–43.
20. Creyghton MP, Cheng AW, Welstead GG, Kooistra T, Carey BW, Steine EJ, et al. Histone H3K27ac separates active from poised enhancers and predicts developmental state. Proc Natl Acad Sci U S A 2010;107:21931–6.
21. Lorenzen JM, Martino F, Thum T. Epigenetic modifications in cardiovascular disease. Basic Res Cardiol. 2012;107:245.
22. Kurdistani SK. Histone modifications in cancer biology and prognosis. Prog Drug Res 2011;67:91–106.
23. Jakovcevski M, Akbarian S. Epigenetic mechanisms in neurological disease. Nat Med 2012;18:1194–204.
24. Arita A, Niu J, Qu Q, Zhao N, Ruan Y, Nádas A, et al. Global levels of histone modifications in peripheral blood mononuclear cells of subjects with exposure to nickel. Environ Health Perspect 2012; 120:198–203.
25. Cantone L, Nordio F, Hou L, Apostoli P, Bonzini M, Tarantini L, et al. Inhalable metal-rich air particles and histone H3K4 dimethylation and H3K9 acetylation in a cross-sectional study of steel workers. Environ Health Perspect 2011;119:964–9.
26. Zhou X, Li Q, Arita A, Sun H, Costa M. Effects of nickel, chromate, and arsenite on histone 3 lysine methylation. Toxicol Appl Pharmacol 2009;236:78–84.
27. Ramirez T, Brocher J, Stopper H, Hock R. Sodium arsenite modulates histone acetylation, histone deacetylase activity and HMGN protein dynamics in human cells. Chromosoma 2008;117: 147–57.
28. Jensen TJ, Wozniak RJ, Eblin KE, Wnek SM, Gandolfi AJ, Futscher BW. Epigenetic mediated transcriptional activation of WNT5A participates in arsenical-associated malignant transformation. Toxicol Appl Pharmacol 2009;235:39–46.
29. Arrigo AP. Acetylation and methylation patterns of core histones are modified after heat or arsenite treatment of *Drosophila* tissue culture cells. Nucleic Acids Res 1983;11:1389–404.
30. Jensen TJ, Novak P, Eblin KE, Gandolfi AJ, Futscher BW. Epigenetic remodeling during arsenical-induced malignant transformation. Carcinogenesis 2008;29:1500–8.
31. Jo W, Ren X, Chu F, Aleshin M, Wintz H, Burlingame A, et al. Acetylated H4K16 by MYST1 protects UROtsa cells from arsenic toxicity and is decreased following chronic arsenic exposure. Toxicol Appl Pharmacol 2009;241:294–302.
32. Zhou X, Sun H, Ellen T, Chen H, Costa M. Arsenite alters global histone H3 methylation. Carcinogenesis 2008;29:1831–6.
33. Li J, Chen P, Sinogeeva N, Gorospe M, Wersto RP, Chrest FJ, et al. Arsenic trioxide promotes histone H3 phosphoacetylation at the chromatin of CASPASE-10 in acute promyelocytic leukemia cells. J Biol Chem 2002;277:49504–10.
34. Li J, Gorospe M, Barnes J, Liu Y. Tumor promoter arsenite stimulates histone H3 phosphoacetylation of proto-oncogenes c-fos and c-jun chromatin in human diploid fibroblasts. J Biol Chem 2003;278: 13183–91.
35. Pilsner J, Liu X, Ahsan H, Ilievski V, Slavkovich V, Levy D, et al. Genomic methylation of peripheral blood leukocyte DNA: influences of arsenic and folate in Bangladeshi adults. Am J Clin Nutr 2007; 86:1179–86.
36. Pilsner JR, Liu X, Ahsan H, Ilievski V, Slavkovich V, Levy D, et al. Folate deficiency, hyperhomocysteinemia, low urinary creatinine, and hypomethylation of leukocyte DNA are risk factors for arsenic-induced skin lesions. Environ Health Perspect 2009;117:254–60.
37. Geoffroy MC, Jaffray EG, Walker KJ, Hay RT. Arsenic-induced SUMO-dependent recruitment of RNF4 into PML nuclear bodies. Mol Biol Cell 2010;21:4227–39.
38. Zhu J, Chen Z, Lallemand-Breitenbach V, de Thé H. How acute promyelocytic leukaemia revived arsenic. Nat Rev Cancer 2002;2: 705–13.
39. Platanias L. Biological responses to arsenic compounds. J Biol Chem 2009;284:18583–7.
40. Slot C. The significance of systemic arteriovenous difference in creatinine clearence determinations. Scand J Clin Lab Invest 1965;17: 201–8.
41. Chen H, Ke Q, Kluz T, Yan Y, Costa M. Nickel ions increase histone H3 lysine 9 dimethylation and induce transgene silencing. Mol Cell Biol 2006;26:3728–37.
42. Latham JA, Dent SY. Cross-regulation of histone modifications. Nat Struct Mol Biol 2007;14:1017–24.
43. Strahl BD, Allis CD. The language of covalent histone modifications. Nature 2000;403:41–5.
44. Cedar H, Bergman Y. Linking DNA methylation and histone modification: patterns and paradigms. Nat Rev Genet 2009;10:295–304.
45. Kile ML, Baccarelli A, Hoffman E, Tarantini L, Quamruzzaman Q, Rahman M, et al. Prenatal arsenic exposure and DNA methylation in maternal and umbilical cord blood leukocytes. Environ Health Perspect 2012;120:1061–6.
46. Jackson JP, Johnson L, Jasencakova Z, Zhang X, PerezBurgos L, Singh PB, et al. Dimethylation of histone H3 lysine 9 is a critical mark for DNA methylation and gene silencing in Arabidopsis thaliana. Chromosoma 2004;112:308–15.
47. Chanda S, Dasgupta UB, Guhamazumder D, Gupta M, Chaudhuri U, Lahiri S, et al. DNA hypermethylation of promoter of gene p53 and p16 in arsenic-exposed people with and without malignancy. Toxicol Sci 2006;89:431–7.
48. Mass MJ, Wang L. Arsenic alters cytosine methylation patterns of the promoter of the tumor suppressor gene p53 in human lung cells: a model for a mechanism of carcinogenesis. Mutat Res 1997;386: 263–77.
49. Minardi D, Lucarini G, Filosa A, Milanese G, Zizzi A, Di Primio R, et al. Prognostic role of global DNA-methylation and histone acetylation in pT1a clear cell renal carcinoma in partial nephrectomy specimens. J Cell Mol Med 2009;13:2115–21.
50. Agrawal-Singh S, Isken F, Agelopoulos K, Klein HU, Thoennissen NH, Koehler G, et al. Genome-wide analysis of histone H3 acetylation patterns in AML identifies PRDX2 as an epigenetically silenced tumor suppressor gene. Blood 2012;119:2346–57.
51. Bredfeldt TG, Greathouse KL, Safe SH, Hung MC, Bedford MT, Walker CL. Xenoestrogen-induced regulation of EZH2 and histone methylation via estrogen receptor signaling to PI3K/AKT. Mol Endocrinol 2010;24:993–1006.

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52. Davey JC, Bodwell JE, Gosse JA, Hamilton JW. Arsenic as an endocrine disruptor: effects of arsenic on estrogen receptor-mediated gene expression *in vivo* and in cell culture. Toxicol Sci 2007;98:75–86.
53. Lee WJ, Shim JY, Zhu BT. Mechanisms for the inhibition of DNA methyltransferases by tea catechins and bioflavonoids. Mol Pharmacol 2005;68:1018–30.
54. De Kimpe J, Cornelis R, Vanholder R. *In vitro* methylation of arsenite by rabbit liver cytosol: effect of metal ions, metal chelating agents, methyltransferase inhibitors and uremic toxins. Drug Chem Toxicol 1999;22:613–28.
55. Cheng X, Blumenthal RM. Coordinated chromatin control: structural and functional linkage of DNA and histone methylation. Biochemistry 2010;49:2999–3008.
56. Voet D VJ. Biochemistry. New York: John Wiley & Sons; 1990.
57. Arsenic exposure and health effects. 5th ed. Amsterdam: Elsevier; 2003.

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