EPIGENETIC EFFECTS OF IN-UTERO ARSENIC EXPOSURE

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ABSTRACT

Background and Aims: There is a growing body of epidemiologic evidence that arsenic exposure in-utero, even at the low levels found in the United States, is associated with adverse reproductive outcomes and may contribute to long-term health effects in exposed individuals. Animal models, in-vitro studies, and human cancer data suggest that arsenic may elicit epigenetic alterations as its mode of toxicity, specifically, by altering the pattern of DNA methylation. This study aims to identify differences in the profiles of DNA methylation in infant cord blood samples associated with low-level chronic arsenic exposure in a U.S. cohort.
Methods: DNA methylation of cord-blood derived DNA from 150 infants involved in a prospective birth cohort in New Hampshire was profiled using the Illumina Infinium Methylation450K array. In-utero arsenic exposure was assessed using urine and toenail samples. Infinium methylation data were analyzed using the semi-supervised recursively partitioned mixture modeling approach.
Results: Ongoing analyses of the DNA methylation array data suggest differences in DNA methylation profiles associated with in-utero arsenic exposure, and the top loci identified in these analyses are being validated for their methylation status using bisulfite pyrosequencing.
Conclusions: This works demonstrates that arsenic may be acting through epigenetic mechanisms to produce its developmental effects. Prospective follow-up of these children will allow for the long-term assessment of the health-related risks associated with these alterations.

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