Arsenic methylation;GSTT1;GSTM1;GSTP1 polymorphisms;and skin lesions

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摘要

Abstract

OBJECTIVE: We investigated whether primary and secondary arsenic methylation ratios were associated with skin lesions and whether GSTT1, GSTP1, and GSTM1 polymorphisms modify these relationships. METHODS: A case-control study of 600 cases and 600 controls that were frequency matched on age and sex was conducted in Pabna, Bangladesh, in 2001-2002. Individual well water, urine, and blood samples were collected. Water arsenic concentration was determined using inductively coupled plasma mass spectrometry (ICP-MS). Urinary arsenic speciation was determined using high performance liquid chromatography hydride with generator atomic absorption spectrometry and ICP-MS. Genotyping was conducted using multiplex polymerase chain reaction and TaqMan. RESULTS: A 10-fold increase in primary methylation ratio [monomethylarsonic acid (MMA)/(arsenite + arsenate] was associated with a 1.50-fold increased risk of skin lesions (multivariate odds ratio = 1.50; 95% confidence interval, 1.00-2.26). We observed significant interaction on the multiplicative scale between GSTT1 wildtype and secondary methylation ratio [dimethylarsinic acid/MMA; likelihood ratio test (LRT), p = 0.01]. No significant interactions were observed for GSTM1 or GSTP1 or for primary methylation ratios. CONCLUSION: Our findings suggest that increasing primary methylation ratios are associated with an increase in risk of arsenic-related skin lesions. The interaction between GSTT1 wildtype and secondary methylation ratio modifies risk of skin lesions among arsenic-exposed individuals.

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