


Individual differences in arsenic metabolism and lung cancer in a case-control study in Cordoba, Argentina

Steinmaus, Craig , Yuan, Yan, Kalman, Dave, Rey, Omar A., Skibola, Christine F., Dauphine, Dave, Basu, Anamika, Porter, Kristin E., Hubbard, Alan, Bates, Michael N., Smith, Martyn T. and Smith, Allan H. (2010) *Individual differences in arsenic metabolism and lung cancer in a case-control study in Cordoba, Argentina*. Toxicology and Applied Pharmacology, 247 (2). pp. 138-145. ISSN 20600216

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Resumen

In humans, ingested inorganic arsenic is metabolized to monomethylarsenic (MMA) then to dimethylarsenic (DMA), although in most people this process is not complete. Previous studies have identified associations between the proportion of urinary MMA (%MMA) and increased risks of several arsenic-related diseases, although none of these reported on lung cancer. In this study, urinary arsenic metabolites were assessed in 45 lung cancer cases and 75 controls from arsenic-exposed areas in Cordoba, Argentina. Folate has also been linked to arsenic-disease susceptibility, thus an exploratory assessment of associations between single nucleotide polymorphisms in folate metabolizing genes, arsenic methylation, and lung cancer was also conducted. In analyses limited to subjects with metabolite concentrations above detection limits, the mean %MMA was higher in cases than in controls (17.5% versus 14.3%, $p=0.01$). The lung cancer odds ratio for subjects with %MMA in the upper tertile compared to those in the lowest tertile was 3.09 (95% CI, 1.08-8.81). Although the study size was too small for a definitive conclusion, there was an indication that lung cancer risks might be highest in those with a high %MMA who also carried cystathionine β -synthase (CBS) rs234709 and rs4920037 variant alleles. This study is the first to report an association between individual differences in arsenic metabolism and lung cancer, a leading cause of arsenic-related mortality. These results add to the increasing body of evidence that variation in arsenic metabolism plays an important role in arsenic-disease susceptibility.

Tipo de documento: Artículo

DOI: <https://doi.org/10.1016/j.taap.2010.06.006> Copy to clipboard

Palabras clave: Arsenic. Drinking water. Lung cancer. Metabolism.

Temas: [R Medicina > R Medicina \(General\)](#)

Unidad académica: [Universidad Católica de Córdoba > Facultad de Ciencias de la Salud](#)