Biomarkers of exposure, effect, and susceptibility of arsenic-induced health hazards in Taiwan.

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Abstract

Long-term exposure to inorganic arsenic from drinking water has been documented to induce cancers and vascular diseases in a dose-response relationship. A series of molecular environmental epidemiological studies have been carried out to elucidate biomarkers of exposure, effect, and susceptibility for arsenic-related health hazards in Taiwan. Arsenic levels in urine, hair, and nail are biomarkers for short-term (<1 year) internal dose, skin hyperpigmentation and palmoplantar hyperkeratosis are for long-term (many years) internal dose, and percentage of monomethylarsonic acid in total metabolites of inorganic arsenic in urine may be considered as an exposure marker for biologically effective dose. The biomarkers of early biological effects of ingested inorganic arsenic included blood levels of reactive oxidants and anti-oxidant capacity, genetic expression of inflammatory molecules, as well as cytogenetic changes including sister chromatid exchange, micronuclei, and chromosome aberrations of peripheral lymphocytes. Both mutation type and hot spots of p53 gene were significantly different in arsenic-induced and non-arsenic-induced TCCs. The frequency of chromosomal imbalances analyzed by comparative genomic hybridization and the frequency of loss of heterozygosity were significantly higher in arsenic-induced TCC than non-arsenic-induced TCC at specific sites. Biomarkers of susceptibility to arsenic-induced health hazards included genetic polymorphisms of enzymes involved in xenobiotic metabolism, DNA repair, and oxidative stress, as well as serum level of carotenoids. Gene-gene and gene-environment interactions are involved in arsenic-induced health hazards through toxicological mechanisms including genomic instability and oxidative stress.