

SINGLE NUCLEOTIDE POLYMORPHISMS IN METALLOTHIONEIN AND CHANGES IN HAIR MERCURY LEVELS

Yi Wang, *Department of Environmental Health Sciences, University of Michigan, Ann Arbor, USA*

Jaclyn Goodrich, *Department of Environmental Health Sciences, University of Michigan, Ann Arbor, USA*

Brenda W. Gillespie, *Department of Biostatistics, University of Michigan, Ann Arbor, USA*

Robert A. Werner, *Department of Environmental Health Sciences, University of Michigan, Ann Arbor, USA; Department of Physical Medicine and Rehabilitation, University of Michigan, Ann Arbor, USA*

Niladri Basu, *Department of Environmental Health Sciences, University of Michigan, Ann Arbor, USA*

Alfred Franzblau, *Department of Environmental Health Sciences, University of Michigan, Ann Arbor, USA*

Background and Aims: Mercury (Hg) is a potent neurotoxicant of concern to the general public. Recent studies suggested that several genes that mediate mercury metabolism are polymorphic in humans. We hypothesized that single nucleotide polymorphisms (SNPs) in metallothionein (MT) genes may underlie inter-individual differences in mercury metabolism.

Methods: Dental professionals (n=515) were recruited during the Michigan Dental Association (MDA) Annual Conventions in 2009 and 2010. Samples of hair and buccal swabs were collected. Self-administered questionnaires were completed for demographic information and estimating daily dietary Hg intake from fish.

Results: The sample consisted of 244 dentists (47.4%), 269 non-dentists (52.2%), and 2 unidentified (0.4%) and was predominantly Caucasian (90.5%). The arithmetic mean mercury level in hair (0.51 µg/g) was not significantly different from that (0.47 µg/g) of the US general population (NHANES 1999-2000). The mean estimated daily methylmercury intake was 0.084 µg/kg/day ranging from 0 to 0.98 µg/kg/day with 25% exceeding the current US EPA Reference Dose (RfD) of 0.1 µg/kg/day. A statistically significant difference was found in mean hair Hg levels of subjects with MT1M 3'UTR (T>C; rs9936471) TT and TC genotypes. Multivariate linear regression analysis found those with TC genotype had higher hair Hg levels than those with TT genotype (n=15) after controlling for estimated daily methylmercury intake from fish. Similar higher hair Hg levels were found in subjects with MT1E 3'UTR (G>T; rs708274) GG genotype compared to those with GT and TT genotypes (n=51).

Conclusions: The findings suggested that MT gene polymorphisms may influence mercury metabolism.