USGS Science in Florida, May 3-5, 2005, Orlando

An Evaluation of an Enclosed Method for the Determination of Total Mercury in Aquatic Life

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While past studies have addressed exposure levels in some species from locations in the Everglades ecosystem very few studies have attempted to comprehensively explore exposure levels on a large scale and no study has examined the strengths and weaknesses for existing analytical methods of measuring mercury in biological species. Although methods for analysis of mercury in biological samples already exist, combining historical datasets for comparison purposes are difficult because of the differences in the approach of sample preservation, analysis (i.e., fresh, wet, dry), and errors caused due to pre-treatment and handling of samples.

The overall objective of this study was to survey mercury concentrations in multiple trophic groups (alligator, largemouth bass, and frog) from several areas in south Florida to look for mercury exposure levels and potential differences in tissue mercury concentrations among locations. It is vitally important to use the most accurate sampling and analytical techniques to acquire mercury data for evaluating the magnitude of exposure and its impact on the health of wildlife species therefore the Direct Mercury Analyzer-80® was the instrumental choice for the analytical validation study. Finally, an evaluation of existing conventional analytical method was conducted that will provide the U.S. Geological Survey with an integrated approach for assessing trends of mercury exposure to biological organisms and allow comparisons of large data sets. These efforts strive to standardize methods for the purpose of understanding exposure levels in the Everglades ecosystem.

Multiple treatment (i.e., drying, chemical digestion, and oxidation) steps are often required during preparation of biological matrices for quantitative analysis of mercury. These multiple steps could potentially lead to systematic errors and poor recovery of the analyte. Presented in this study, a clean all-inclusive method was utilized to measure total mercury in fish tissue by integrating steps of drying, sample combustion and successive identification with atomic absorption spectrometry. We also evaluated the differences between the mercury concentrations found in samples that were homogenized and samples with no preparation. These results were confirmed with cold vapor atomic absorbance and fluorescence spectrometric methods of analysis. Finally, total mercury in wild captured largemouth bass (n=20) were assessed using the DMA-80 to examine interrelationships between mercury concentrations in muscle, liver and brain organs. Direct analysis of total mercury measured in muscle tissue was strongly (positively) correlated with muscle tissue that was homogenized before analysis ($r=0.81$, $p<0.0001$). Additionally, results using our integrated method compared favorably ($p<0.05$) with conventional cold vapor spectrometry with atomic absorbance and fluorescence detection methods. Mercury concentrations in brain were significantly lower than concentrations in muscle ($p<0.001$) and liver ($p<0.05$) tissues. This integrated method can measure a wide range of mercury concentrations (0-500 μg) using small sample sizes. Total mercury measurements in this study are comparative to the methods (cold vapor) commonly used for total mercury analysis and are devoid of laborious sample preparation and expensive hazardous waste.