

Mercury Analysis for Fish Consumption Advisories

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ABSTRACT

Sportfish tissue (n=189) collected during 1999-2000, were analyzed for total mercury by inductively coupled plasma/atomic emission spectrophotometry (ICP/AES) and thermal decomposition, amalgamation/atomic absorption spectrophotometry (TDA/AAS) to compare methods. Total mercury measurements using these techniques were not significantly different ($\alpha = 0.05$). TDA/AAS is a precise technique for the analysis of total mercury in fish tissue, and is less expensive, easy to use and rapid (6 min/assay).

Mercury residue data for sportfish samples (n=211) collected from lakes across the US were statistically analyzed to develop a predictive model for total mercury. Significant parameters were the feeding pattern of the fish (i.e., bottom feeder vs. predator) and the sampling location ($p < 0.05$). Regression models were developed for bottom-feeders ($p < 0.0001$, r -square = 0.45) and predators ($p < 0.0001$, r -square = 0.73).

INTRODUCTION

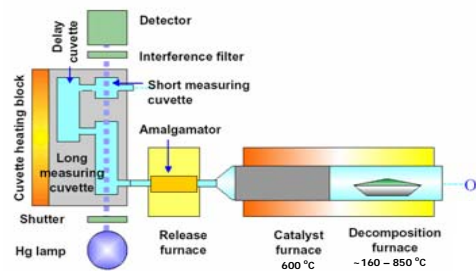
Mercury is naturally present in the environment and it also enters through the combustion of fossil fuels and waste. Methyl mercury, is the most toxic form because it bioaccumulates in fish (EPA, 2001). The toxicity of methyl mercury is especially important because it can cross the placenta, move into breast milk and pass the blood brain barrier (EPA, 2001). Fetuses and infants exposed to mercury have been found to exhibit various symptoms relative to the degree of exposure ranging from coordination and developmental delays, to brain damage, mental retardation and blindness (EPA, 2001).

The main route of human exposure to mercury is through the consumption of contaminated fish. The EPA has issued advice to pregnant and nursing women and women of childbearing age, to limit their consumption of sportfish (EPA, 2001). The FDA has also issued an advisory for shark, swordfish, tilefish and king mackerel due to high content of methyl mercury (FDA 2001). Unfortunately, the development of sportfish consumption advisories for mercury are limited by the sample throughput and testing cost. Therefore, the objectives of the research were: to demonstrate that TDA/AAS is as precise as ICP/AES for the measurement of total mercury in fish tissue; and to develop a predictive model for total mercury in fish tissue.

METHODS

Sportfish samples (n=189) collected by the Indiana Department of Environmental Management (1999-2000) were analyzed by ICP/AES and TDA/AAS. ICP/AES analyses were carried out by En Chem, Inc. (Madison, Wis.) using SW-846 Methods 6010B (EPA 2003). Analysis by TDA/AAS was carried out using a mercury analyzer (Model DMA-80, Milestone, Inc. Monroe, CT) which was calibrated using standard reference materials TORT-2 and DORM-2 (National Research Council of Canada) in the range of 0-470 ng total Hg.

Figure 1. Thermal decomposition, amalgamation, atomic absorption spectrophotometer



Predicting total mercury in lake fish:

Total mercury (ppm) concentrations were measured in fish which were collected from lakes across the US as a composite of 4-5 fish. The bottom feeders were homogenized whole, while the predators were filleted prior to homogenization. These data were analyzed using SAS (Cary, NC) to obtain a regression model to predict total mercury. Parameters included: fish length (cm), fish weight (g), weight/length ratio, sampling location, feeding pattern (i.e., bottom feeder vs. predator). The data were normalized and the analysis of variance for the multivariate model was carried out with the progressive removal of insignificant parameters.

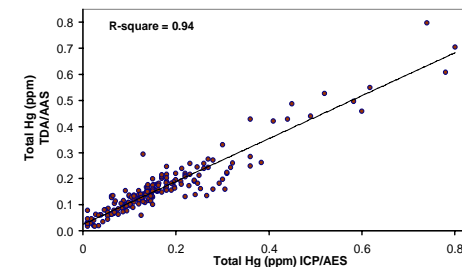
Table 1. Species and mean mercury concentrations

Bottom-feeders	Total Hg (mean ± S.D)
Brown bullhead	0.05 ± 0.05
Channel catfish	0.08 ± 0.06
Common carp	0.08 ± 0.04
White sucker	0.07 ± 0.05
Predators	
Largemouth bass	0.32 ± 0.21
Northern pike	0.28 ± 0.11
Smallmouth bass	0.56 ± 0.24
Walleye	0.30 ± 0.22

RESULTS

Analysis of total mercury by TDA/AAS was not significantly different ($p > 0.05$) from ICP/AES for fish tissues with residues between 0 and 1.0 ppm.

Figure 2. Comparison of total mercury in fish tissue as analyzed by TDA/AAS and ICP/AES



Predicting total mercury in lake fish:

1. Feeding pattern and location were the most significant ($p < 0.05$) predictors for total Hg.
2. Predators (0.34 ± 0.21 ppm) had significantly ($p < 0.05$) more mercury than bottom-feeders (0.08 ± 0.05 ppm).

Therefore, two separate models were obtained to predict total mercury for bottom feeders and predators. Lakes were divided in groups according to the mercury concentrations in fish from those locations.

Table 2. Advisory groups and consumption frequency

Advisory Groups	Hg (ppm)	Populations*
Group 1	<0.16	1 meal/week
Group 2	0.16 – 0.65	1 meal/month
Group 3	>0.66	DO NOT EAT

*At-risk populations include pregnant, lactating, or those that will become pregnant and children <15 yrs.

Regression equations ($\alpha = 0.05$) :

Bottom-feeders:

$$\text{Log [Hg]} = -0.1848 - 1.2174 * (\text{Group 1})$$

Predators:

$$\text{Log [Hg]} = -0.1895 - 1.8979 * (\text{Group 1}) - 0.9532 * (\text{Group 2})$$

CONCLUSIONS

- TDA/AAS was a precise analytical technique for the analysis of total mercury in fish tissue. Significant benefits of this technique relate to its ease of use, lower cost and rapid throughput.
- Regression models can be used to predict total mercury in predators and bottom-feeders for lakes across the US.
- However, increasing the amount of residue data with a more efficient technique, like TDA/AAS, will further improve the prediction models for total mercury.

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