



Mercury in Sentinel Biota as Indicators of Atmospheric Mercury Deposition at National Estuarine Research Reserve Sites from Maine to Florida

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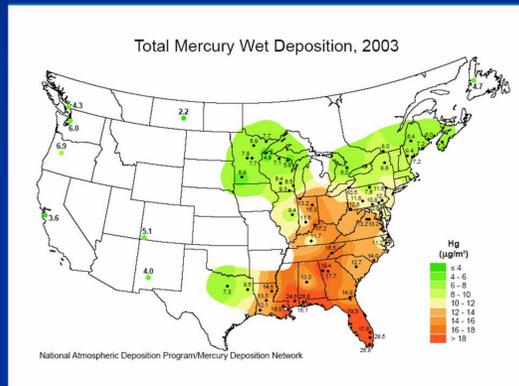
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BACKGROUND

Atmospheric deposition of mercury expresses an increasing gradient from north to south along the Atlantic coast.



If this gradient translates into a comparable gradient in mercury bioaccumulation in biota, then we have a basis to infer changes in mercury concentrations in biota in response to changing mercury deposition over time.



A rich array of National Estuarine Research Reserve (NERR) sites along the Atlantic seaboard provides an opportune set of well characterized sampling locales with minimal impacts of local mercury sources with which to test this hypothesis.



APPROACH

Under similar ecological and biogeochemical conditions, we hypothesize that mercury concentrations in the mummichog, *Fundulus heteroclitus*, will parallel the atmospheric deposition gradient. This small fish is an inhabitant of the shallow margins of its food web depends strongly on benthic microalgae (Currin *et al.*, 2003). This is important because atmospherically deposited mercury is thought to be rapidly removed from the water column to sediments where mercury methylation takes place near the sediment: water interface and where benthic microalgae reside. This provides a short physical and trophic pathway to bioaccumulation by mummichog.



Mercury was also measured in the American oyster, *Crassostrea virginica* collected subtidally from the same areas. The oyster, *Ostrea edulis* was sampled at the Wells reserve in Maine. Oysters provide a measure of methylmercury entry into the seston, again a short pathway mercury methylation, and



In a secondary hypothesis, we tested whether shallow marsh habitats are critical sites of and bioaccumulation. It was hypothesized that estuarine tidal concentrations in and dilution of whether shallow marsh habitats are critical sites of and bioaccumulation. It was hypothesized that estuarine tidal concentrations in and dilution of



SAMPLE DESIGN

We attempted to minimize, to the extent possible, the influence of other factors across NERR sites that can influence mercury methylation and bioaccumulation.

- Sites were located in the more marine areas of the reserve with average salinities above 16 psu.
- Sites were located away from known anthropogenic inputs (*e.g.* outfalls, major upstream watershed drainage).
- Sites were located near marshes preferably *Spartina* spp. with tidal creek drainage. An effort was made to find paired sites, one near the headwaters of a tidal creek and a second site where the tidal creek enters a larger, better flushed drainage. See the adjacent figure.

Sampling Period: Sampling occurred in August and September when young of the year fish have grown and are inhabiting marsh habitats.

Biota Sampling:

Fundulus heteroclitus: 20 individuals per site over a range of sizes using minnow traps (baited with dog food), dip net, or seines

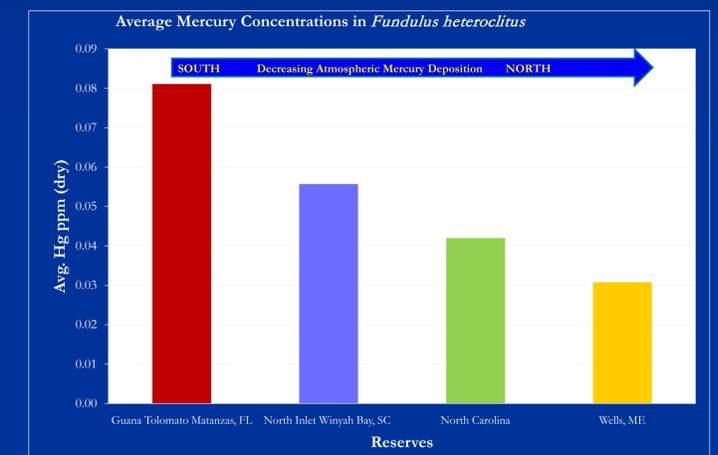
Oysters: 8 individuals collected by hand

ANALYSIS

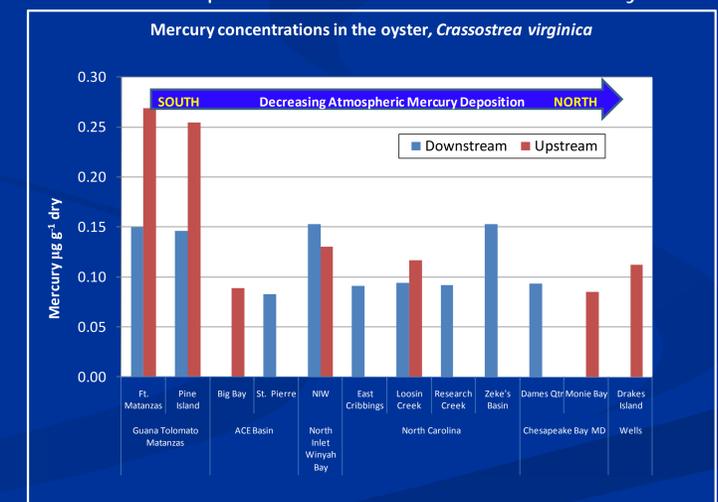
Fundulus and oyster samples were freeze dried before analysis. Whole fish or homogenized subsamples of larger fish and oysters were analyzed using EPA method 7473 using a Milestone DMA-80 Direct mercury Analyzer.

RESULTS

Average mercury concentrations in *Fundulus* decrease from south to north at the four sites at which we have completed analyses, paralleling the declining atmospheric gradient. Upstream and downstream sites showed no significant differences. They were pooled as a result.



Average mercury concentrations in oysters were higher at upstream than downstream sites at the Florida reserve, Guana Tolomato Matanzas, but not elsewhere. This reserve had significantly higher mercury concentrations at the upstream sites than at more northerly reserves.



Preliminary results provide modest support for the two hypotheses. This year's effort will repeat the 2009 sampling at all 13 NERRS reserves to provide greater geographic coverage and test year to year stability in the patterns. Methylmercury analyses will provide a fuller test of the hypotheses.

We thank the staffs of the participating reserves for collecting samples and providing information on the habitats of their reserves.