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Sulfate Stimulation of Mercury Methylation in Freshwater Sediments

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■ The relationship between bacterial sulfate reduction and mercury methylation, as well as the in situ distribution of methylmercury in sediments, was studied in Quabbin Reservoir, MA. Fish methylmercury levels in Quabbin and other lakes affected by acid deposition are often elevated. However, the cause of acceleration of net methylmercury production or bioaccumulation in these lakes is poorly understood. Experimental additions of sulfate to either anoxic sediment slurries or lake water above intact sediment cores resulted in increased microbial production of methylmercury from added inorganic mercury. Sediment depth profiles of bacterial sulfate reduction and mercury methylation were similar, and specific inhibition of sulfate-reducing bacteria blocked methylmercury production at all depths. In situ methylmercury concentrations, like sulfate-reduction rates, were highest near the sediment-water interface and in shallow sediments. These data suggest that sulfate-reducing bacteria are important mediators of mercury methylation in lacustrine sediments and provide a possible mechanism for increased methylmercury bioaccumulation in water bodies affected by increased sulfate deposition.

Introduction

Methylmercury is a potent human neurotoxin, to which the fetus is particularly sensitive (1). Concentrations in fish from freshwater lakes are often elevated above guidelines for human consumption, and advisories have been released for a large number of lakes in eastern Canada, the north-central and northeast United States, Sweden, and Finland (3). While mercury pollution seen in past

decades arose from point source discharges of mercury into aquatic ecosystems (e.g., Minamata, Ottawa River, and Lake St. Clair), many of the aquatic ecosystems of current concern are influenced by acid deposition, but are not contaminated with aquatic point sources of mercury (4, 5).

Atmospheric deposition of mercury, even to remote areas, has increased since preindustrial times (6, 7). In addition, biogeochemical changes within acidified aquatic ecosystems can result in increased production and bioaccumulation of methylmercury (4, 8). For example, methylmercury concentrations in lake water (4) and in fish (9) increased, relative to the control basin, in the H₂SO₄-acidified basin of experimentally partitioned Little Rock Lake, WI. In this lake, both basins received equal atmospheric Hg deposition, and acidification alone resulted in increased methylmercury production. However, the quantitative importance of increased atmospheric Hg deposition relative to enhanced rates of methylmercury production in the widespread problem of excess methylmercury bioaccumulation is unknown.

Almost all of the mercury deposited from the atmosphere is in the inorganic form (10), while mercury accumulates in fish predominantly as methylmercury (2). In the Little Rock Lake study, atmospheric deposition of total Hg more than balanced total Hg accumulation in fish; however, deposition of methylmercury was not sufficient to account for methylmercury in the lake's biota (10). Because Little Rock is a seepage lake, an in-lake source must be invoked. Production of methylmercury has long been considered a biological process (11), occurring within lakes primarily via the bacterial methylation of inorganic mercury. However, the type(s) of microorganisms responsible for methylation in lacustrine systems, and the underlying mechanism(s) of methylation, are not well-known (5, 8). As a result, our basic understanding of the

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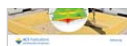
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