

Mercury Amalgam and Antibiotic Resistance Antibiotic-Resistant Bacteria and Environmental Mercury Pollution: A Correlation

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Some bacteria that occur naturally in soils and in lake trout in Maine have developed a high level of resistance to antibiotics, and researchers who have conducted several studies on bacterial resistance to environmental toxins suggest there is a correlation between mercury pollution and the organisms' increasing resistance to antibiotics. Mercury contamination has become ubiquitous in Maine as pollution from Mid-Atlantic and Midwestern states is funneled over the state by jet stream winds and the heavy metal falls to earth in precipitation. Maine currently receives more than three times the Environmental Protection Agency's acceptable limit, according to a national monitoring network. To study the effects of increased mercury levels in Maine soils and aquatic environments, Colby College scientists designed studies to test bacteria found in hatchery lake trout and in four soil test sites.

Scientists, using microbiological and molecular biological approaches, found that the bacteria exhibited high resistance to mercury; all samples were shown to tolerate at least 20 parts per million. Soil mercury levels in Maine are approximately 7 parts per trillion. In further laboratory tests, the same bacteria also showed resistance to some of 22 different antibiotics, with some samples exhibiting resistance to as many as 14 of the 22 antibiotics tested. This high level of antibiotic resistance was observed in bacteria from environments where there had been no known application of antibiotics, either to the soil or to the water and feed at the hatchery where the trout were raised. So the usual cycle of increasingly virulent strains of bacteria overcoming the effects of targeted antibiotics doesn't appear to be the explanation.

Researchers found a common mercury resistance gene that produces a mercury detoxifying enzyme in many of the bacteria they were studying. They suggest that the organisms' resistance to antibiotics is most likely attributable to an environmental influence, possibly the presence of mercury contamination in the soil and the intermittent presence of mercury in the hatchery's water.

Bacteria naturally develop resistance to toxins in their environment. Unlike many organisms, bacteria share their DNA with one another in exchanges unrelated to reproduction. They adapt, and survive, by acquiring genes that allow them to resist toxins. The mercury-resistant genes and antibiotic-resistant genes are found together on mobile genetic elements.

Significantly, the data from the Colby study suggest that mercury pollution may, through natural selection processes, be favoring bacteria that also resist multiple

antibiotics. Further, since mercury is now ubiquitous in the Maine environment, the process may be fostering a significant reservoir of antibiotic resistant bacteria, and the mobility of the genes in bacteria could easily transfer these traits to human pathogens. The reservoir of resistant bacteria may contribute another threat to the future efficacy of antibiotics needed to treat infections and illnesses in humans. The research has been conducted at Colby College in Waterville, Maine, by undergraduate students working with Professor Frank A. Fekete Ph.D. and Assistant Professor Keith A. Johnson Ph.D. in the Department of Biology. In each of the last three years, students have expanded the research and added to the growing body of information on the effects of mercury in the selection of antibiotic-resistant bacteria by studying bacteria isolated from the human oral cavity and from stream sediment as well as from soil and the gastrointestinal tract of lake trout. The research has been sponsored by funding from the Natural Science Division of Colby College, an institutional grant to Colby from the Howard Hughes Medical Institute, and the Maine Department of Inland Fisheries and Wildlife. The research will be presented at the 58th Annual Meeting of the American Society for Microbiology in Salt Lake City, Utah on Tuesday, May 21, 2002.

Background information:

The earth's crust is estimated to contain a concentration of ~ 0.5 parts per million (ppm) of mercury. However, mercury is emitted into the biosphere due to natural processes and human activity and is able to move through the biosphere. The major anthropogenic sources of mercury include the burning of fossil fuels, mining and smelting activities, and metal processing. While the relative contribution of mercury from human activities remains uncertain, recent estimates indicate that since 1890 approximately 200,000 tons of mercury have been emitted into the atmosphere from these sources. About half of current total mercury emissions eventually enter the global atmospheric cycle, while the remainder is removed through local or regional cycles.

With an atmospheric residence time ranging from one and a half to two years, global atmospheric circulation systems can carry mercury emissions anywhere on the globe before transformation and deposition occur. Mercury emitted in the Midwest and Mid-Atlantic States may be carried many miles before being deposited with precipitation in Maine and in the other New England States.

Concern over the long-range transport of mercury and the amount of mercury being emitted from anthropogenic sources led the National Atmospheric Deposition Program (NADP) to expand its sampling, and the Mercury Deposition Network (MDN) was created in 1995. The main objective of the MDN is to collect weekly samples of precipitation so that total wet deposition of mercury in North America may be determined.

Mercury is toxic to humans and bacteria. Bacteria have evolved efficient enzymatic detoxification mechanisms so that they may adapt to the metal's toxic effects. The bacterial genes responsible for mercury resistance reside on various genetic elements, some of which are mobile and can be transferred readily and efficiently to other bacterial species. Genes conferring resistance to antibiotics are located on the same transferable genetic elements. Many studies have shown that both mercury and antibiotic resistances are closely linked on the same mobile genetic element. Antibiotic resistance is a serious health concern. Many multi-drug-resistant strains of bacteria have emerged worldwide. Exposing a microbial population to an antibiotic will select antibiotic resistant bacteria and allow them to transfer their resistance genes on to other bacteria via genetic transfer mechanisms. This natural phenomenon is exacerbated by the misuse and overuse of antibiotics to treat viral infections and by the widespread use of antibiotics in animal husbandry. The Colby College studies were designed to examine environmental factors that may

also be selecting for and increasing antibiotic resistance. According to data obtained from the MDN, Maine receives significant mercury contamination (more than three times the Environmental Protection Agency's acceptable limit) borne on the jet stream from Mid-Western and Mid-Atlantic States. The objectives of these studies were to investigate the effects of elevated mercury levels in soil and aquatic environments on microorganisms in soil and in the gastrointestinal tracts of hatchery-grown lake trout. The level of mercury tolerance was determined among soil bacteria at the four Maine MDN monitoring sites and among gastrointestinal bacteria from fish at a local hatchery. Subsequently the antibiotic resistance profiles of each mercury-tolerant isolate was evaluated. From these results, we hope to gain a better understanding of how increased mercury levels are selecting for mercury-resistant bacteria and how this then influences bacterial antibiotic resistance in both soil and aquatic environments.