A window into the past of Hg microbiology

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Mercury (Hg) is a naturally occurring global pollutant that has, since the late 1700s, been increasingly remobilized in the environment by anthropogenic activities. The continued importance of Hg as a chemical of concern to human health was underscored by the recent ratification of the Minamata convention (2017), requiring governments to regulate Hg emissions, reduce Hg mining, supply, trade and waste, to limit its environmental impacts. One area where data is scarce, and which could aid in managing Hg pollution, is in determining the lag in aquatic ecosystem response to a change in atmospheric Hg deposition. Indeed, whereas the total concentration of metals can be determined from environmental archives, there is currently no means of tracking their bioavailable and often toxic, fractions. For Hg in particular, this fraction represents a substrate for the production of toxic methylmercury.

To address this issue, we hypothesized that microbial DNA stored in environmental archives and encoding for Hg detoxification metabolism, such as the mercuric reductase gene (*merA*), can be used to evaluate historical deposition of Hg. We predicted that increasing selective pressure from anthropogenic mercury would affect the evolutionary trajectory of aquatic microbes over broad continental scales and inform on the fraction of bioavailable Hg. For this, we recovered and analyzed DNA in dated sediment cores from Canada and Finland, and reconstructed the past demographics of microbes carrying genes encoding for MerA using models known as Bayesian relaxed molecular clocks.

We found that the evolutionary dynamics of *merA* exhibited a dramatic increase in effective population size at the end of the 18th century, which coincided with both the Industrial Revolution, and with independent measurements of atmospheric Hg concentrations [1]. We show that this evolutionary response was both swift and synchronous across two continents in the Northern Hemisphere. We are cautiously optimistic that applying this approach to study the biological history of other metals, for which detoxification and homeostasis are genetically coded in microbes, will yield new insights into metal cycling.

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