An analysis of variability in the methylmercury burden of marine mammals using stable mercury isotopes

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Methylmercury (MeHg) is a neurotoxin that biomagnifies in aquatic food webs. High concentrations of inorganic Hg have been observed in many marine mammals and unique detoxification pathways have been proposed to explain the relatively lower proportion of MeHg in some organs compared to those of non-mammalian species. Examples include *in vivo* formation of insoluble crystalline HgSe in the liver of seals and whales. However, little effort has been made to quantitatively link detoxification mechanisms to the variability in MeHg burden and potential health implications. This study uses Hg stable isotopes to understand how MeHg metabolism alters internal MeHg body burden in marine mammals (long-finned pilot whale: *Globicephala melas,* and ringed seals: *Phoca hispida hispida*). We present a physiologically-based toxicokinetic model that examines the relative importance of changing diet, age, and internal demethylation for changes in MeHg burdens in various biological compartments, constrained by measured total Hg, MeHg and stable Hg isotopes in various organs. These data suggest pilot whales develop the capacity to demethylate methylmercury at an early life stage and this occurs primarily in the liver and kidney. In contrast, results indicate that different mechanisms of demethylation take place in seal pups and adults. The findings of this study improve understanding of variability in MeHg exposure within and among marine mammal species across different life stages, which can be extended to better understand MeHg metabolism in human populations.