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1The 3D biogeochemical marine mercury cycling model MERCY – linking atmospheric Hg to methyl mercury in the marine food web.

Johannes Bieser[1], David Amptmeijer[1], Ute Daewel[1], Joachim Kuss[3], and Corinna Schrum[1,2]
[1]Helmholtz Zentrum Hereon, Matter transport and Ecosystem dynamics, Geesthacht, Germany (johannes.bieser@hzg.de)
[2]Universität Hamburg, Institute for Marine Sciences Mittelweg 177, 20146 Hamburg , Germany
[3]Leibniz Institute for Baltic Sea research, Department for Marine Biogeochemistry, Seestraße 15, 18119 Rostock , Germany

Mercury (Hg) is a pollutant of global concern. Due to anthropogenic emissions, the global Hg burden has been ever
increasing since preindustrial times. Hg emitted into the atmosphere gets transported on a global scale and ultimately
reaches the oceans where it is transformed into highly toxic methylmercury (MeHg) that effectively accumulates along
the food chain. The international community has recognized this serious threat to human health and in 2017 regulated
Hg under the UN Minamata Convention.
Currently, the first effectiveness evaluation of the Minamata Convention on mercury is being prepared and besides
observations, models play a major role in understanding environmental Hg pathways and to predict the impact of policy
decisions and external drivers (e.g. climate, emission, and land-use change) on Hg pollution. Yet, the available model
capabilities are mostly focused on atmospheric models covering the Hg cycle from emission to deposition. With the
presented model for marine mercury cycling (MERCY) we want to contribute to the currently ongoing effort to further
our understanding of Hg and MeHg transport, transformation, and bioaccumulation in the marine environment with the
ultimate goal of linking atmospheric Hg emissions to MeHg in sea food. MERCY is the first fully resolved 3dbiogeochemical
model linking atmospheric Hg to MeHg in higher trophic levels. Most importantly, the MERCY model
is prgrammed in a way that allows for the coupling of the Hg chemistry, ecosystem, and bioaccumulation models with
most established hydrodynamic ocean models. This is achieved using the Framework for Aquatic Biogeochemical
Models (FABM).

In this talk we present the MERCY model and its application using different hydrodynamic drivers. Moreover, we
discuss its capabilities and shortcomings in reproducing the key Hg species Hg0, Hg2+, and MeHg as well as Hg loads
in biota. The presented model evaluation is a first step in establishing quality criteria for marine Hg modelling. We show
that the model can reproduce observed average concentrations of individual Hg species (normalized mean bias: HgT
(aq) -17%, Hg0 2%, MeHg -28%). Moreover, it is able to reproduce the observed seasonality and spatial patterns. We
find that the model error for HgT (aq) is mainly driven by the limitations of the physical model setup in the coastal zone
and the poor quality of data on Hg in rivers. Morover, the model error in calculating vertical mixing and stratification
contributes to the total Hg model error.
skill is in a range where further model improvements will be difficult to detect. Finally, for MeHg, we find that we are
lacking the basic understanding of the actual processes governing methylation and demethylation. Here, the model can
reproduce average concentrations but falls short in reproducing the observed value range. The results prove the
feasibility of developing marine Hg models with similar predictive capability as established atmospheric chemistry
transport models. Yet, there are still major knowledge gaps in the dynamics governing methylation and
bioaccumulation. Based on our findings we discuss these knowledge gaps and identify the major uncertainties in our
current understanding of marine Hg cycling from a modeller’s perspective.