Methylmercury distribution and formation in polluted agricultural soils.

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The biomethylation of mercury (Hg) is well studied in the marine environment due to the high bioaccumulation of monomethyl-mercury (MMHg) in the food chain. However, there is a lack of knowledge concerning MMHg formation in the terrestrial environment. Our aims with this study were i) to assess the small scale distribution of MMHg in polluted soils, which are regularly flooded and agriculturally used, and ii) to characterize soil parameters potentially driving MMHg formation in these soils. We compared Hg-polluted and soils from Valais (Switzerland) and from Wanshan (China).

We collected soils in 11 agricultural sites in both countries, ranging from background (0.05 mg*kg^{-1}) to high Hg (267.85 mg*kg^{-1}) concentrations. The soils were sampled along rectangular grids in 5-meter intervals. The resulting 380 individual soil samples were analyzed for Hg, MMHg, other relevant metals and standard soil parameters. To make this possible, we developed a high-throughput MMHg extraction and analysis method using HPLC-ICP-MS (detection limit: 0.2 µg*kg^{-1} in soil), which we will present, as well as results from an inter-laboratory comparison.

This dataset allowed us to show that in the contaminated Swiss sites, MMHg concentrations increased linearly with Hgtot concentrations while MMHg/Hg$_{tot}$ decreased with increasing Hg concentrations. In top soils of Swiss background sites, we found that Hg correlated with organic C concentrations, which is consistent with the property of natural organic matter (NOM) to efficiently adsorb airborne Hg. Further, MMHg/Hg$_{tot}$ was significantly higher in top soils than in the mineral soils of the Swiss background sites. We further suggest that MMHg/Hg$_{tot}$ varies with land-use types (crops vs. pasture).

The results from the Chinese sites will also be presented and compared to those of the Swiss sites in order to draw general conclusions about MMHg formation and distribution in soils.