Hg dynamics in Arctic top predators: insights from a captive experiment on hooded seals Cystophora cristata.

PINZONE M.[1], TESSIER E.[2], BÉRAIL S.[2], AMOUROUX D.[2] AND DAS K.[1]

[1] *University of Liège*

[2] *CNRS/UNIV PAU & PAYS ADOUR*

Arctic predators like true seals have been experiencing a strong increase in Hg levels in their tissues in the last 150 years. This is in contrast with other terrestrial animals or other parts of the world. Dietary Hg accumulates and biomagnifies in marine food webs in its most toxic form, monomethylmercury (MMHg). Hg seven stables isotopes (^{196}Hg, ^{198}Hg, ^{199}Hg, ^{200}Hg, ^{201}Hg, ^{202}Hg and ^{204}Hg) undergo both mass-dependent and mass-independent fractionation (MDF and MIF, respectively) as a result of abiotic and biotic reactions occurring in the environment and within the organism. For this reason, they are a promising tool for tracing Hg cycling in the natural environment. The interpretation of Hg isotopic data remain however a challenge, especially when taking into account species such as Arctic true seals, which have highly complex life styles and metabolism. In 2012, six pups of hooded seals *Cystophora cristata* were captured on the ice edge of the Greenland Sea and kept in captivity for 2 years. During this period, they were fed on a constant diet made of Norwegian herring *Clupea harengus* and vitamin complements. This allowed us to study Hg kinetic in an Arctic top predator without the influence of age, distribution and diet specialization. The main objective was to select the tissue in which the information about Hg pathways would be conserved, leading to the optimal tracing of Hg sources along the food web. Total Hg (THg) concentrations were determined on a Milestone direct mercury analyzer, while MeHg and IHg concentrations were determined by isotope dilution-gas chromatography-inductively coupled plasma-mass spectrometer (ID-GC-ICP-MS) following microwave-assisted extraction and aqueous phase derivatization. Mercury isotopic composition analysis was performed using cold vapor generation (CVG) with multicollector-inductively coupled plasma-mass spectrometer (MC-ICP-MS, Nu Instruments). The analysis was conducted in seal muscle, liver, hair, and kidney, plus muscle of herring. Hg speciation changed significantly among tissues. Hair and muscle were predominantly enriched in MMHg (range: 84 to 98% and 74 to 95%, respectively) relative to liver and kidney (range: 7 to 38% and 4 to 27% respectively) that tend to mainly accumulate iHg. δ^{202}Hg values were positively related with levels of MMHg ($p > 0.0001$, $R^2 = 0.531$). With higher values found in hair, followed by muscle, liver and kidney. Δ^{199}Hg and Δ^{201} values were not influenced by Hg species composition in tissues, as well as slope values of Δ^{199}Hg/Δ^{201}Hg. When calculating the isotopic trophic enrichment between herring and hooded seals' tissues, a significant ^{202}Hg enrichment resulted between seal hair and kidney and herring ($p = 0.011$ and $p < 0.001$), indicating important MDF between the ingested prey and these tissues. Instead, a significant MIF (Δ^{199}Hg and Δ^{201} values) was observed only between seals' kidney and herring ($p = 0.0003$). Our results show that: (1) Hg isotopic composition reflects Hg molecular speciation; (2) as a result of isotopic incorporation during tissue turnover, hair and kidney present a strong trophic MDF; and (3) with the exception of kidney, MIF signal is conserved in all tissues during assimilation of prey items. Based on these observations, we believe that muscle is the optimal monitoring tissue for tracing of Hg sources since both the MDF and MIF signals are conserved from prey to predator. The important MDF observed in hair instead, make this tissue the best option for the analysis of Hg biomagnification along food webs.

Oral preference