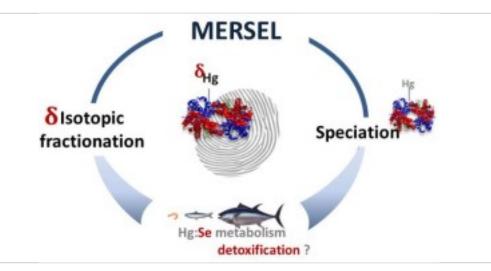# MERSEL

Pushing speciation frontiers for investigation of mercury and its detoxification by selenium in key organisms

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Mercury (Hg) pollution is considered a major environmental problem. Due to its extreme toxicity, Hg has been recently included in the list of the top ten chemicals of major public health concern by the World Health Organization. Once released in the environment, it is transformed, principally in aquatic ecosystems, by microorganisms into the neurotoxic methylmercury. Its hazardous effect is biomagnified through the trophic chain, resulting in serious social and health effects. However, Hg metabolic pathways in biota remain elusive. Its understanding is crucial to elucidate its (eco)toxic effect as well as its biogeochemical cycle. Bioavailability, mobility and toxicity of an element are dependent of its chemical forms. Hg binding with proteins has been evoked as a cause for toxicity and the role of selenium (Se) as antagonist for Hg toxicity is acknowledged but not understood so far.

MERSEL is a multidisciplinary research project, which main objective is to advance the understanding of Hg metabolic pathways in living organisms paying also attention to its (antagonist) interaction with Se. The project is based on the development of new analytical approaches that combines speciation and natural isotopic fractionation in a unique pattern. Speciation provides valuable information about reactivity and potential toxicity of the metabolites. Complementary, the natural abundance isotopic signature adds a dynamic dimension, comprising the life history of the target element, its (pollution) source and reaction tracking. The resulting (bio)molecular and isotopic signature will be precious in the insight of Hg in biota and its detoxification mechanisms, including its relation with Se. On a long term prospective, this highly innovative methodology could be extended to other metal/loids and push back frontiers in life and environmental sciences related to them.

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