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Methylmercury Determination in Fish Samples by GC-ICP-MS and Species-Specific Isotope Dilution

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In the past, the accuracy and usefulness of isotope dilution mass spectrometry (IDMS) for analytical applications has been proven by many research groups. Particularly in speciation analysis where element species might not be stable throughout the analytical procedure, IDMS is a valuable tool for the investigation of species transformations. It can furthermore be used for calibration and to develop analytical methods in which transformations do not occur. The presented work contains results of speciation analysis of mercury in fish tissue. A combination of gas chromatographic (GC) separation with inductively coupled plasma mass spectrometric (ICP-MS) detection is used for this purpose.

The sample preparation includes an alkaline digestion with tetramethylammonium hydroxide (TMAH), followed by aqueous phase derivatization with sodium tetraethylborate (STEB). Analyte derivatives are purged from the sample digest solution and trapped in n-dodecane using a helium gas-stream. Isotopically labelled spikes, enriched with ^{204}Hg and ^{201}Hg for methylmercury and inorganic mercury, respectively, were added to the samples.

A batch of samples of edible fish tissue was analyzed for their content of methylmercury ($MeHg^{+}$) and inorganic mercury (Hg^{2+}). The IDMS-results are compared with data obtained from an Automated Mercury Analyzer (AMA).