



TITLE: STUDY OF METHYLATION SITES AND FACTORS IN CONTAMINATED AQUATIC SYSTEMS IN THE AMAZON USING AN OPTIMIZED RADIOCHEMICAL TECHNIQUE

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HIGHLIGHTS AND ACHIEVEMENTS

We confirmed that high methylation potentials (up to 22%) are found in roots of *Paspalum repens* and other floating macrophyte species such as *Eichhornia crassipes* and *Ludwigia helminthoryza* during both phases of the hydrological cycle, with a tendency for higher values in the wet season, confirming findings of previous studies, and a strong intra and inter-lake variation.

Hg methylation in macrophyte roots is carried out mainly in the root-associated periphyton, a complex and variable assemblage of benthic microalgae, fungi, bacteria and organic and inorganic detritus. However, no significant correlation was found in the first campaign between Hg methylation in samples of *Paspalum* sp. roots and the amount of periphyton in these samples.

We also verified that total plankton and phytoplankton are sites of a low (< 1 %) but easily detectable methylation.

Simultaneous in-situ determinations of Hg methylation potentials, bacterial activity and sulfate-reduction activity were made in the frame of this project, probably for the first time in tropical aquatic environments.

Preliminary analysis of data by the other research teams involved in the project suggest that the influence of terrigenous inputs on the Hg loads and cycling in the local aquatic environments may be hard to pinpoint, considering the moderate magnitude of these inputs in comparison to the inputs of the Tapajós river and the intense dynamics of the lakes themselves.

Pitfalls

- Heavy official bureaucracy and delays for issuance of permits for joint scientific expeditions involving foreigners in the Amazon, export of samples (except by mail) and for custom clearance, aggravated by biopiracy concerns.
- Increasing difficulties in obtaining commercial ^{203}Hg .
- Basic infrastructure problems caused partial loss of samples in one of the campaigns.