

## Periphyton communities in mercury impacted surface water body

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Mercury (Hg) is a persistent contaminant threatening the environment and human health. Past and present Hg contaminations of surface waters are of major concern due to the potential of Hg to accumulate in biota and magnify along the food chain. Primary producers, such as periphytic communities, are the entry point of Hg in food webs. Therefore understanding the relationship between Hg contamination and its uptake by periphyton is crucial to get a better comprehension of Hg fate in natural waters. The link between Hg contaminations, accumulation and periphyton composition was thus explored in several cascade reservoirs on River Olt basin in Rm Valcea region (Romania) contaminated by Hg from past activities of a chlor-alkali plant. Periphytic communities grown on artificial substrata for two weeks were studied in four sites along the Hg pollution gradient (Babeni (B), Zavideni (Z) and Dragasani (D)) and in a upstream reference site, Valcea (V). Results demonstrated a higher Hg content in periphyton collected in Babeni and Dragasani. The BAF ranged from  $1.7 \times 10^7$  L/kg for a periphyton from Dragasani to  $3.8 \times 10^6$  L/kg for Zavideni. The degree of colonization decreased from ca. 60% for the reference site to 28% for Babeni, similarly to the biotic fraction. Phylogenetic diversity characterisation revealed that *Protobacteria* were the most abundant phylum in the periphytic communities at all sites. High cyanobacterial counts were found in Babeni, while *Bacteroidetes* dominated in the other sites. qPCR analysis demonstrated that the abundance of mercuric reductase genes (*merA*) responsible for Hg reduction and demethylation decrease in periphyton (B>Z>D~V) with decrease of total Hg concentrations in water. By contrast the abundance of *dsrA* genes specific for sulphate reducing bacteria and *Geobacter* cytochrome *c* oxidase gene – *gcs* (B~D>Z>V) were better correlated with the amount of Hg content in periphyton. The abundance of *HgcB* gene was much higher in periphyton from Zavideni than that from Babeni. Taken together, the results show a strong effect of Hg contamination on periphyton community composition and point out their suitability as Hg contamination bioindicators.