

Characterizing Arsenic Contamination and its Effects on the Microbiomes of South Central Puget Sound Lakes.

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Legacy arsenic (As) contamination in freshwater ecosystems in the south-central Puget Sound region is a product of prolonged pollution from the ASARCO copper smelter (1912-1993) in Tacoma, WA. We hypothesize that As is a significant selective pressure for As-tolerant and resistant microbiota in freshwater urban lakes. To test this hypothesis, water, sediment, periphyton, and Chinese Mystery Snails (CMS) were sampled from three lakes with differing concentrations of As; Lake Killarney (20 ppb As), Steel Lake (2 ppb As), and Trout Lake (< 1 ppb As). Previous studies have shown that As hyper-accumulates in periphyton and transfer As to primary consumers, influencing CMS gut microbiota and physiological health. Thus, CMS can be indicators of the ecosystem's overall health as well. Inductively coupled plasma-mass spectrometry (ICP-MS) and 16S rRNA amplicon sequencing were performed for all sample types from every lake for quantification of total As levels and microbial composition. Preliminary experiments comparing As-contaminated and control lakes have shown that bacterial community composition in periphyton differs, suggesting selection for As-tolerant species. The observation of overlapping phyla between lake periphyton communities and in snail guts, indicates the possibility that As exposure can alter CMS gut microbiota. Ongoing work involves the optimization of a quantitative polymerase chain reaction (qPCR) assay of total bacterial load and various As metabolizing genes. These genes are widespread across bacteria and confer resistance/tolerance to As via respiratory arsenite oxidation, respiratory arsenate reduction, inorganic arsenic detoxification, and organic arsenic methylation.