

## **Is it coming or going: Microbial community interactions with iron, BTEX and nutrients in a freshwater system**

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Benzene, toluene, ethylbenzene and xylene (BTEX) comprises one of the most widespread contaminants in terrestrial environments largely due to leaking of underground storage tanks for gasoline and oil into groundwater. Research to-date has focused on remediation efforts in subsurface systems; however, the groundwater-surface water interface is a critical zone that has received less attention. Iron mats are often found at these interfaces due to the flux of reduced iron from groundwater and oxidation at the surface, both chemical and biological. As insoluble iron oxides are highly reactive, they can sequester contaminants such as BTEX as well as nutrients including nitrogen and phosphorous. Therefore, their interactions with BTEX may subsequently affect the mobility and availability of these key nutrients as well. The goal of this study was to determine how the microbial communities associated with iron mats may affect the fate of BTEX and subsequently affects nutrient availability. In Greenville, NC two iron mats downstream of a BTEX seep and one iron mat upstream of the BTEX seep were analyzed using a suite of geochemical constituents, microbial community structure, and functional gene potential. Results suggest benzene may be degraded in the iron mats as benzene concentrations were typically lower in the iron mats than surrounding creek water samples and known benzene-degrading organisms *Dechloromonas* spp., *Hydrogenophaga* spp., and *Geobacter* spp. were present. These organisms are known to couple benzene degradation with nitrate reduction or iron reduction and genes associated with these processes were widespread. BTEX associated with iron oxides may competitively exclude phosphorous from the mats as total phosphorous concentrations were highest upstream of the BTEX seep and in the surrounding water compared to the BTEX impacted mats. Ongoing enrichment and cultivation studies, sorption experiments, and in-depth metagenomic analyses will aid in a better understanding of the specific interactions between the microbial communities, contaminants, and nutrients.