

## TOWARDS A MORE ACCURATE PREDICTION OF BIOTRANSFORMATION – EXPLORING LINKAGES BETWEEN MICROPOLLUTANT BIOTRANSFORMATION AND MICROBIAL COMMUNITY CHARACTERISTICS

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Protection of human and environmental health critically depends on appropriate management of the risks involved in the use of over 100,000 man-made chemicals. The release of chemicals into the water cycle leads to exposure of aquatic organisms and potentially also humans with largely unknown consequences. Degradation by microbial communities (i.e., biotransformation) is key to reducing exposure to chemicals, but might also lead to the formation of persistent transformation products. The ability to predict rates and products of microbial biotransformation for a broad variety of chemical contaminants accurately is therefore essential not only for chemical risk management but also in the context of contaminated site remediation or the development of green chemical alternatives. In my talk, I will discuss novel experimental and data mining approaches to improve our understanding of why and how biotransformation efficiency differs between microbial communities, and how these differences are modulated by chemical structure. In particular, I will demonstrate how we combine biotransformation experiments with activated sludge communities, transformation product identification via high-resolution mass spectrometry screening, and high-throughput sequencing of the microbial communities to identify possible linkages between environmental conditions, community characteristics (i.e., functional and taxonomic composition and diversity) and their biotransformation potential for different classes of trace organic contaminants. For two examples, i.e., oxidative N-dealkylation of tertiary amides, amines and phenylureas, and hydrolysis of primary amides, I will discuss follow-up experiments, including inhibition, purified enzyme and pure culture studies, to validate the hypothesized linkages between enzyme abundance and biotransformation rate constants.

**Keywords:** Metatranscriptomics, (Q)SBRs, Activated Sludge, Trace Organic Contaminants, Biotransformation Pathways

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