

Identification of the 'Active' Fraction and Metabolic Pathways in Trace Organic Contaminants Removal Using Stable Isotope Probing

The widespread presence of trace organic contaminants (TOrc), such as the endocrine disrupting compound bisphenol-A (BPA), has been cause for growing concern due to persistence in the environment and potential ecological impacts. Despite progress made in understanding the removal of TOrc in biological wastewater treatment processes, there is still a lack of consensus regarding the identity of microorganisms active in biodegradation and the exact removal mechanisms involved. This research aimed to develop a clear understanding of the microbial 'active' fraction in activated sludge which is responsible for the assimilation of a selected TOrc, BPA. Through the use of DNA stable isotope probing (DNA-SIP), BPA assimilating organisms were identified. This active fraction of BPA assimilation included bacteria related to *Sphingobium* spp., *Sphingomonas* spp., *Pussilimonas* spp., and *Variovorax* spp.. Results from this work also confirm that prior or time-course exposure to BPA as well as bioreactor process conditions influence microbial community structure and function. Added understanding of TOrc removal mechanisms could be derived through continued investigation into microbial functions associated with BPA removal.

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