Influent pathogenic bacteria may go straight into effluent in full scale wastewater treatment plants
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Microorganisms from wastewater are usually considered to be adsorbed onto the activated sludge flocs in wastewater treatment plants (WWTPs), consumed by protozoan or to die off. Therefore, the effluent is assumed to comprise primarily of those microorganisms that grow in the plant.

Standard techniques for detecting bacteria, particularly pathogens, in the effluent are based on culture-dependent methods, which may underestimate potential pathogenic bacteria escaping WWTPs in the effluent. Culture-independent DNA sequencing methods may resolve that.

Analysis of the microbial composition, combined with bacterial mass balances to calculate net growth and relative abundances in the influent, process tank and effluent of 14 Danish full-scale WWTPs.

The microbial community composition was examined by 16S rRNA gene amplicon sequencing (V1 to V3 region) and MiDAS curated taxonomy (http://midasfieldguide.org/).

The non-growing genus *Arcobacter* was among others found abundant in effluent. Some *Arcobacter* species are known pathogens, and failure to remove these from wastewater pose a potentially serious health safety problem.

The effluent microbial community was in some WWTPs very similar to the process tank community, in other plants influent and effluent communities were very similar while in some plants it was a combination.

This indicates that in some plants many microorganisms may go straight through the plant from influent to effluent without being incorporated into activated sludge flocs.

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