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Project: "Impact of process dynamics on microbial communities and $N_2O$ formation in wastewater systems"

In order to generate insight on how environmental variables, microbial community composition and microbial interactions contribute to $NO/N_2O$ emissions in both nitrification and denitrification processes, two different research approaches will be taken: (i) lab-scale studies with enrichment cultures and (ii) full-scale studies in different types of wastewater treatment plants in the Netherlands. Studying $N_2O$ emissions from wastewater systems is not only important for the future mitigation of emissions from full-scale wastewater treatment plants, it also provides a convenient system- more realistic than a pure culture but less complex than a soil sample- to study these emissions.

Initially, lab-scale continuous enrichment cultures in chemostats, accompanied with genomic/transcriptomic analysis and microbial community analysis, will be used as a tool to study denitrification pathway sharing and its importance in $N_2O$ emissions in denitrifying microbial communities. Special attention will be given to $N_2O$ reducing microorganisms, and to denitrification as a potential $N_2O$ sink in nitrification/denitrification processes. To dig further into the topic of denitrification as a potential $N_2O$ sink, $N_2O$ consumption kinetics of activated sludge will be studied in batch cultures in collaboration with the UMB nitrogen group (Partner 1). In later studies, the chemostat system will be used to study the effect of dynamic conditions (regarding dissolved oxygen concentrations, nitrite accumulation, COD/N ratio, consumption of internal storage compounds, pH, and presence of toxic compounds) on $N_2O$ emissions in both denitrifying and nitrifying communities.

Complementing the lab-scale work, $N_2O$ emissions will be studied in full-scale Anammox wastewater treatment plants (in collaboration with Paques- Partner 13) and other wastewater treatment systems (Demon, Nereda, and conventional activated sludge systems). Microbial community composition and the metagenomic/metatranscriptomic signature of these systems will be analyzed (together with Bioclear- Partner 11) in order to search for correlations with $N_2O$ emissions- potentially leading to the development of a molecular tool to predict these emissions.