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Linking nitrifiers diversity to the flux of their key resources

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Introduction

To manage microbial communities it is critical to understand what shapes their diversity. More diverse community typically contribute to higher ecosystem function and resilience to perturbations. A number of ecological theories explain the existence of coexisting competitors. For example, **Resource-ratio theory** predicts that higher niche dimensionality (i.e. higher number of limiting resources) results in higher diversity. According to this theory, resource provision (and especially the number of limiting nutrients) has thus a strong influence on the diversity within microbial guilds. Here, we have selected biological nitrification as model process that is integral for removal of nitrogen and related species in drinking water production and wastewater treatment. We hypothesize that changing flux of potential limiting substrates for nitrifiers affects their diversity via modification of niche dimensionality. The first aim is to describe nitrifier diversity based on functional genes (*amoA* and *NxrB*) in drinking water biofilters and wastewater treatment plants, as they represent contrasting resource conditions to nitrifiers. The second aim is to correlate nitrifier diversity pattern to fluxes of potential limiting substrates. We sampled drinking water biofilters and wastewater treatment plants in Denmark and Sweden. In drinking water treatment plants biomass samples were sand collected from rapid sand filters, 5 samples from different points from top of the filter and at every 10cm over the depth of the filter (0-40cm). In waste water treatment plants nitrifying basins, inlet and inside the tank biomass was sampled in triplicates. Water samples were collected at source (raw water), under treatment (inside the tank) and treated water in triplicates at all sampling sites. We used Illumina sequencing and qPCR based on functional genes *amoA* (for ammonia oxidizing bacteria and archaea) and *NxrB* (for nitrite oxidizing bacteria *Nitrospira* and *Nitrobacter*) to describe the richness and dominance pattern of nitrifiers. Potential limiting substrates to nitrifiers such as Ammonium, Nitrite, Nitrate, Phosphate, Chloride, Sulphate and trace metals (Ca, Co, Cu, Fe, K, Mg, Mn, Mo, Na, Ni, Zn and P) were measured using ICP-MS, ICP-OES, Ion Chromatography, and spectrophotometric methods. The statistical analysis is based on non-metric multidimensional scaling and PCA. Not surprisingly, preliminary results show that nitrifiers abundance diversity is strongly affected by nitrogen loading. In wastewater treatment plants *Nitrospira* and *Nitrobacter* abundance in source water was in the range of 10^5 to 10^7 and 10^6 - 10^7 cells per gram sample wet weight respectively. Whereas, their abundance inside the nitrifying basin was two orders of magnitude higher than source water (10^8 - 10^9 cells per gram sample wet weight). In rapid sand filters *Nitrospira* abundance was always higher by one order of magnitude (10^7 cells per gram wet sand) compared to *Nitrobacter* (10^6

cells per gram wet sand) inside the rapid sand filters. We will use multidimensional analysis to further identify the link between resource provision and nitrifier density and provide experimental data to evaluate resource ratio theory in microbial guilds.