Evolution of microbial communities and nutrient removal performances in aerobic granular sludge sequencing batch reactor during change of substrate

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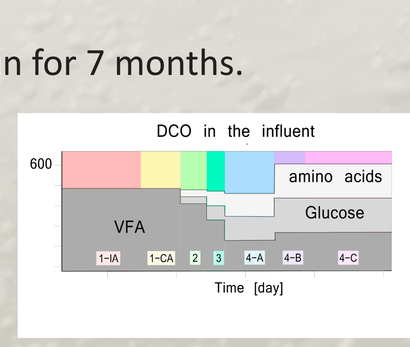
Context

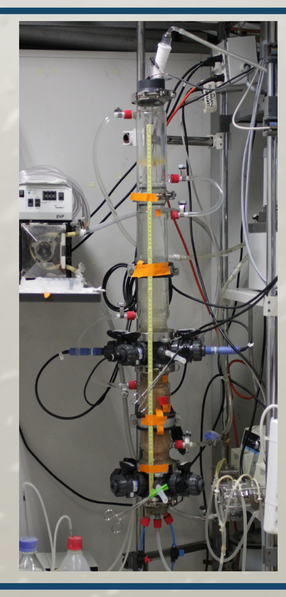
- Aerobic granular sludge (AGS) is a promissing alternative wastewate treatment to the conventional activated sludge system.
- AGS present various advantages like an enhanced settlability, the persence of different red-ox conditions at the same time.
- AGS allow substantial space, energy and chemical saving.
- Phosphate accumulating organisms often found in high proportions in AGS allow biological phosphorus removal

Methodology

- An AGS sequencing batch reactor was run for 7 months.
- The composition of the synthetic wastewater was progressively changed from volatiles fatty acids (VFA) to a mix of VFA, glucose and amino acids.



- The COD, Phosphorus (P) and Nitrogen (N)-removal performances were monitored.
- The community composition structure was estimated by amplicon sequencing weekly biomass samples

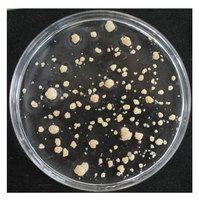


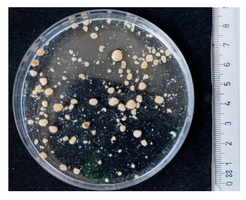
Objectives

- Maintain the reactor nutrient removal during despite the substrate change
- Identify the taxa implicated in P-, N-removal.

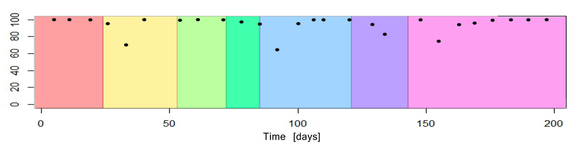
Results

Granule size at the before and after the change of substrate

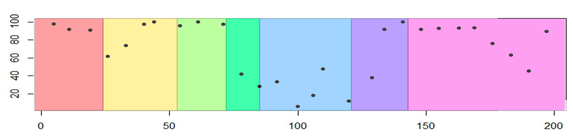




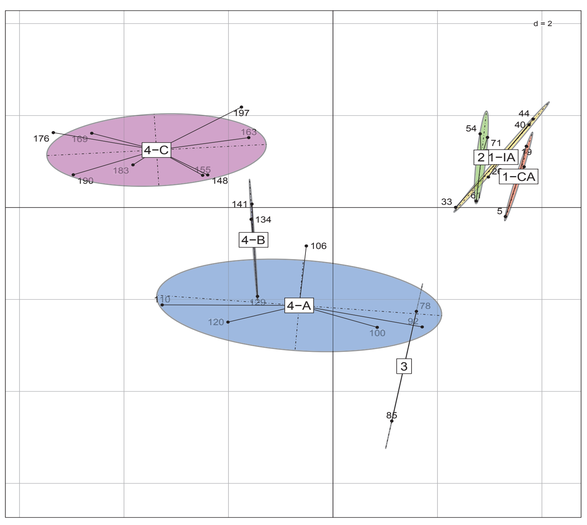
Evolution of ammonium removal



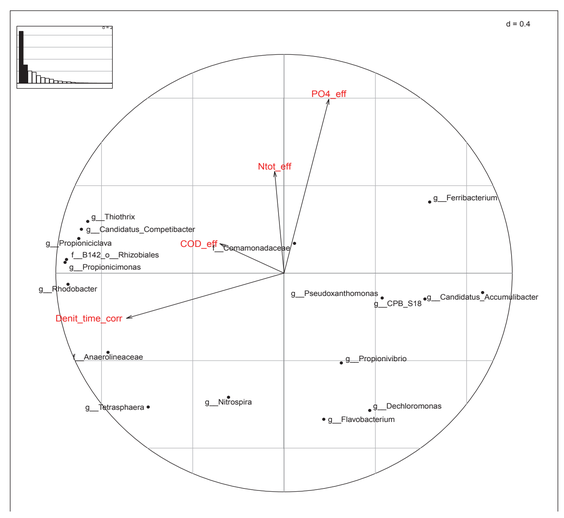
Evolution of phosphate removal



Principal component analysis of the samples performances and main bacterial genus abundances

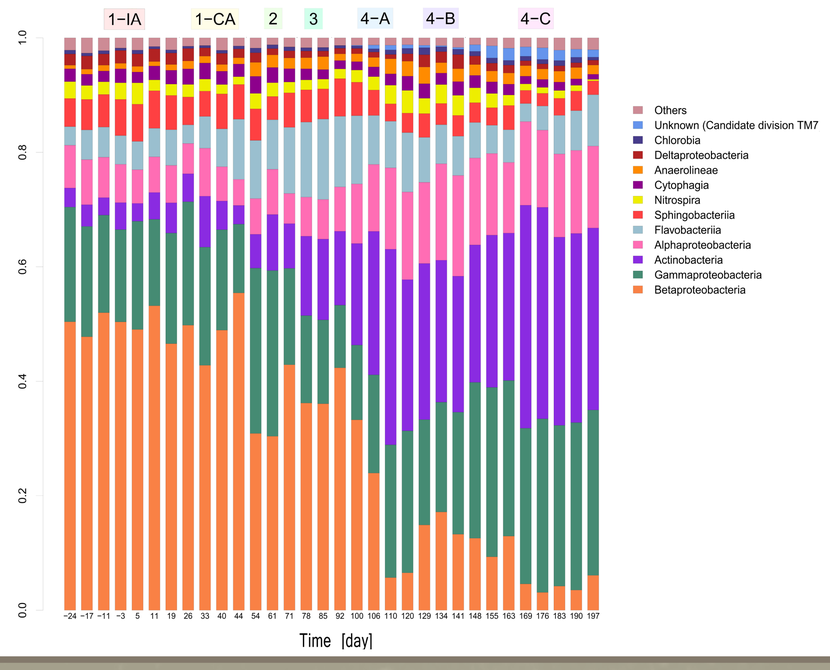


The sample are clusterd according to the operating conditions

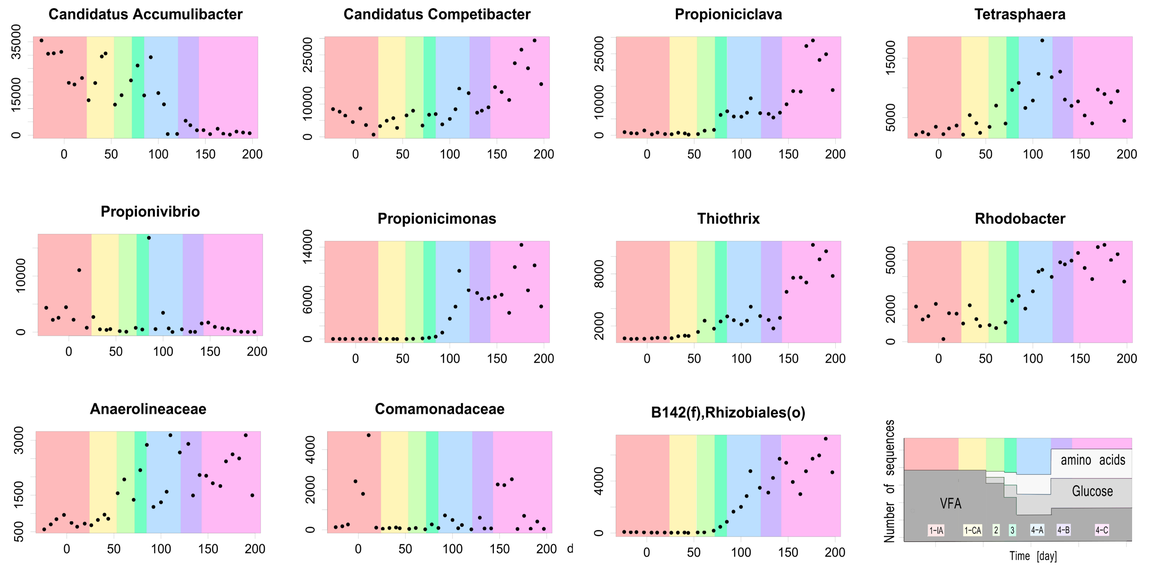


Composition of the two main axis, where PO4_eff is the P-removal efficiency, Ntot_eff is the total N-removal efficiency, COD_eff is the chemical oxygen demand removal efficiency and Denit_time_corr is the estimated time required for complete denitrification

Evolution of main bacterial classes abundances during the substrate change, estimated from the number of rRNA sequences detected in each biomass sample



Evolution of the abundance of some bacterial genus through the experiment



Conclusion

- The reactor nutrient removal performances remained good dispite the substrate change and the bacterial community change.
- The abundance of the known phosphate accumulating organisms is low at the end of the experiment, but high amounts of phosphate were removed from the water.
- Undetermined OTUs from Rhizobiales, Anaerolineaceae and Comamonacaceae were detected in high abundance in the reactor running with mixed substrate

Outlook

- Determine witch organisms are responsible for P-removal with the mixed substrate.
- Identify the metabolisms and roles of uncharacterised taxa usign whole metagenomic and metatranscriptomic analysis.

AGS = Aerobic Granular Sludge
PAO = Phosphate accumulating organism
P-removal= Phosphorus removal
N-removal = Nitrogen removal
COD = Chemical oxygen demand