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

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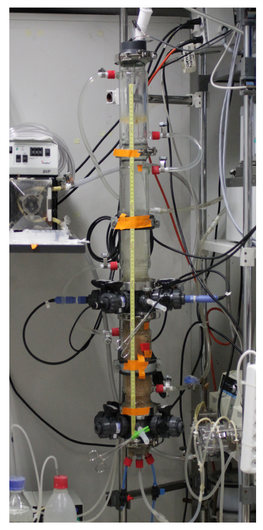
Context

- Aerobic granular sludge (AGS) is a promissing alternative wastewate treatment to the conventional activated sludge system.
- AGS present various advantages such as enhanced settlability and presence of different red-ox conditions simultaneously in the granules.
- AGS allows substantial space, energy and chemical savings.
- Phosphate accumulating organisms (PAO) often found in high proportions in AGS allow biological phosphorus removal

Methodology

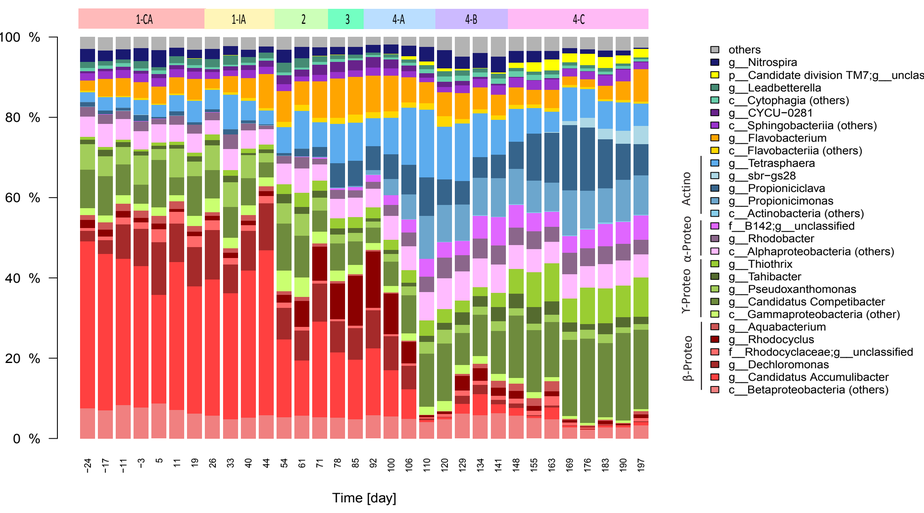
- An AGS sequencing batch reactor was run for 7 months.
- The composition of the synthetic wastewater was progressively changed from volatiles fatty acids (VFA) only to a mix of VFA, glucose and amino acids.
- The COD, Phosphorus (P) and Nitrogen (N)-removal performances were monitored.
- The bacterial community composition was analyzed by amplicon sequencing of weekly biomass samples.



Objectives

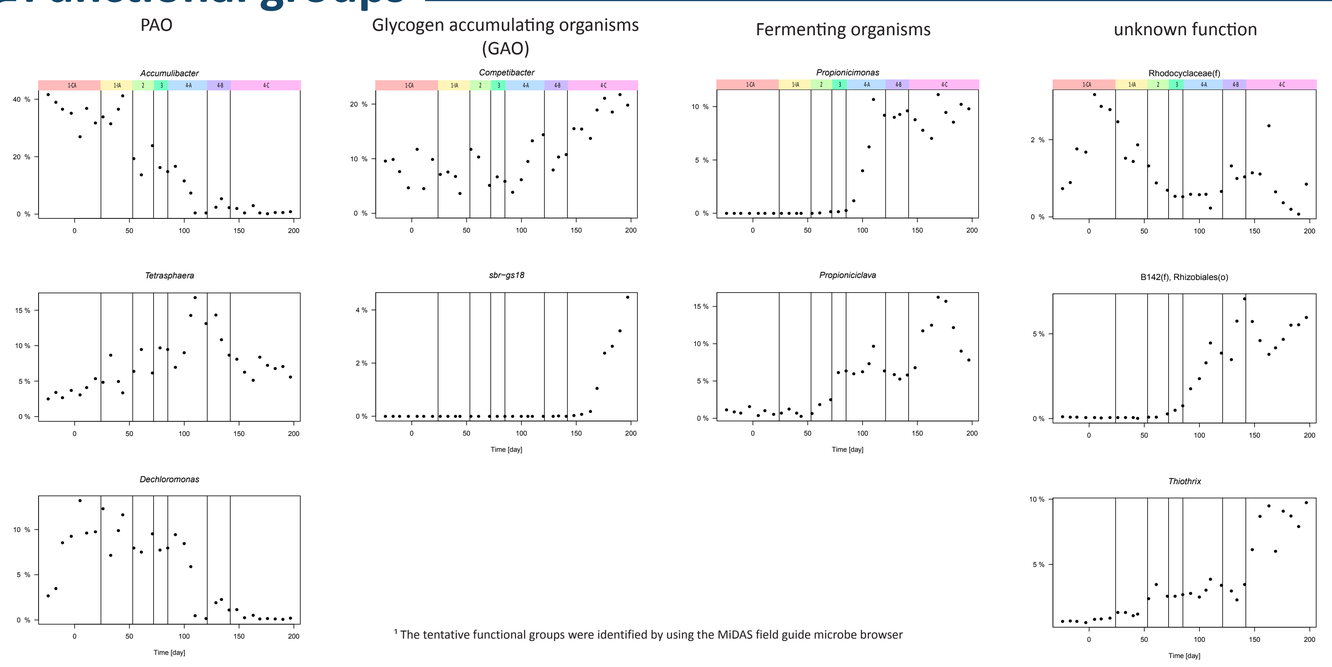
- Maintain the reactor nutrient removal during the substrate change
- Identify the taxa involved in P-, N-removal.

Microbial communities



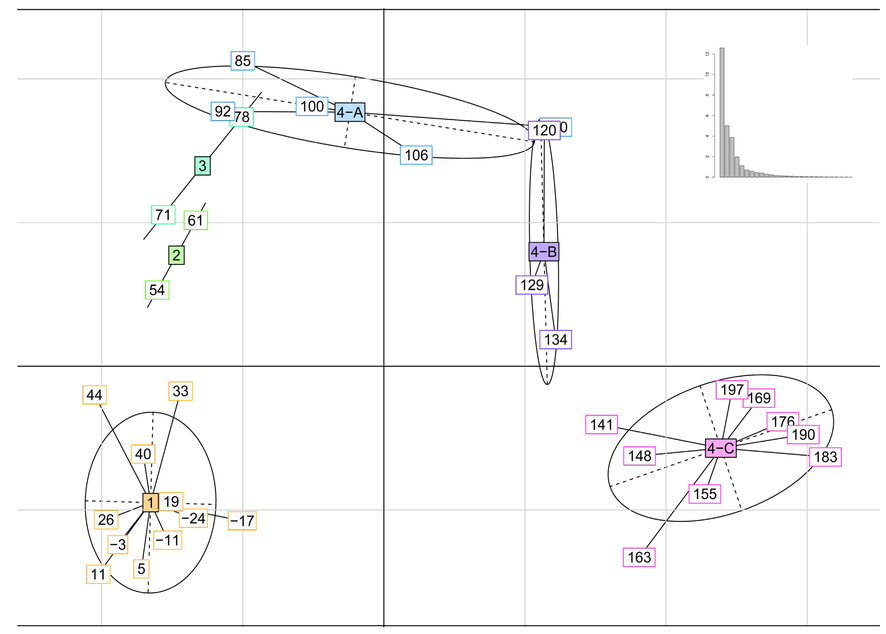
A clear shift was observed in the bacterial community composition through the experiment.

Functional groups[1]



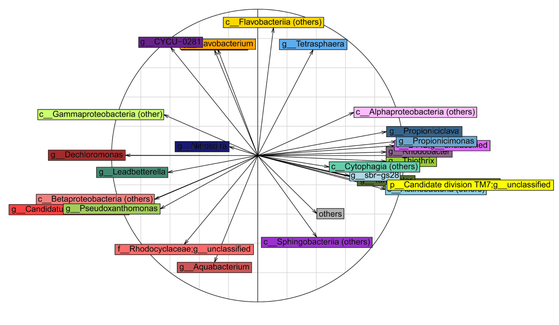
[1] The tentative functional groups were identified by using the MiDAS field guide microbe browser

Principal component analysis



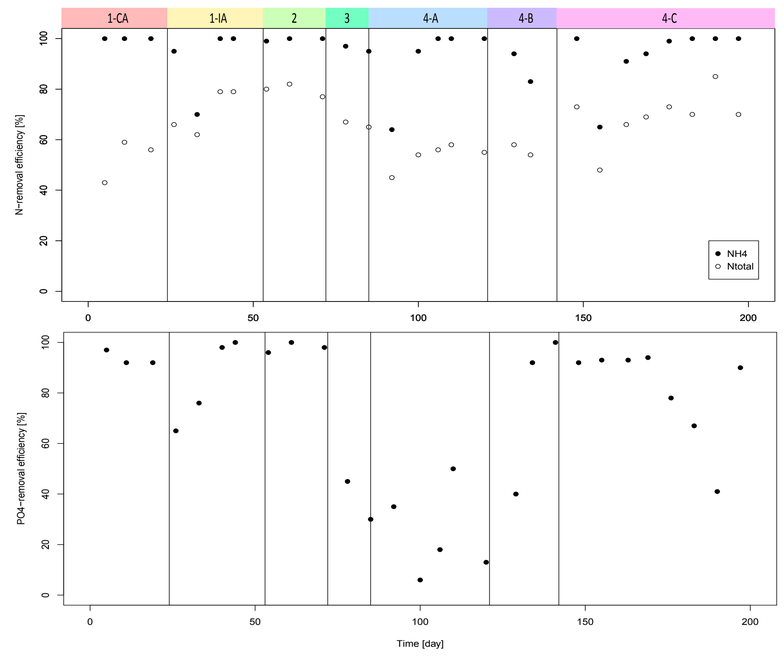
The samples are clustered according to the synthetic wastewater composition

Principal component analysis (PCA) of the biomass samples according to the main bacterial genus abundances.



Contribution of the different genera to the two main PCA axis.

Reactor performances



The nutrient-removal performances of the reactor were similar at the beginning and the end of the experiment.

Conclusion

- The N-removal performances remained good dispite the substrate change and the bacterial community change, whereas the P-removal experienced a drop during a certain period.
- The abundance of the known PAO 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

Outlooks

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

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

[1] **MiDAS Field Guide,** www.midasfieldguide.org/en/search/**,** accessed on 31.08.2016