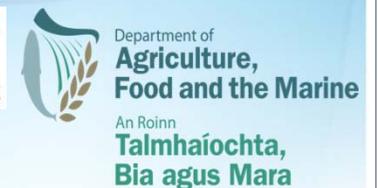


Task 5: Molecular ecology analysis for bioreactors

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Objectives

- ④ To investigate changes in the **microbial ecological structure** of laboratory-scale and meso-scale intermittently aerated sequencing batch reactors (**IASBRs**) treating dairy influents and in **water reuse systems**.
- ④ To correlate **ecological shift** with the **biological nutrient removal profiles** in the bioreactors (efficiency and stability).
- ④ PCR cloning, sequencing and analysis of **relevant functional gene** diversity during high efficiency nutrient removal.

Literature review

④ Biological nutrient removal. Nitrogen and phosphorus.

Key nutrients causing **eutrophication** in waterways.

Nitrogen removal: simultaneous nitrification-denitrification (SND), partial nitrification, anammox.

AOB/AOA (ammonia-oxidizing bacteria/archaea) NOB (nitrite-oxidizing bacteria)

Phosphorus removal: enhanced biological phosphorus removal (EBPR).

PAOs (phosphorus accumulating organisms)

SND and phosphorus removal in one single reactor.

DPAOs (denitrification phosphate accumulating organisms)

References: S. Tsuneda (2005), Raymond J. Zeng (2003).

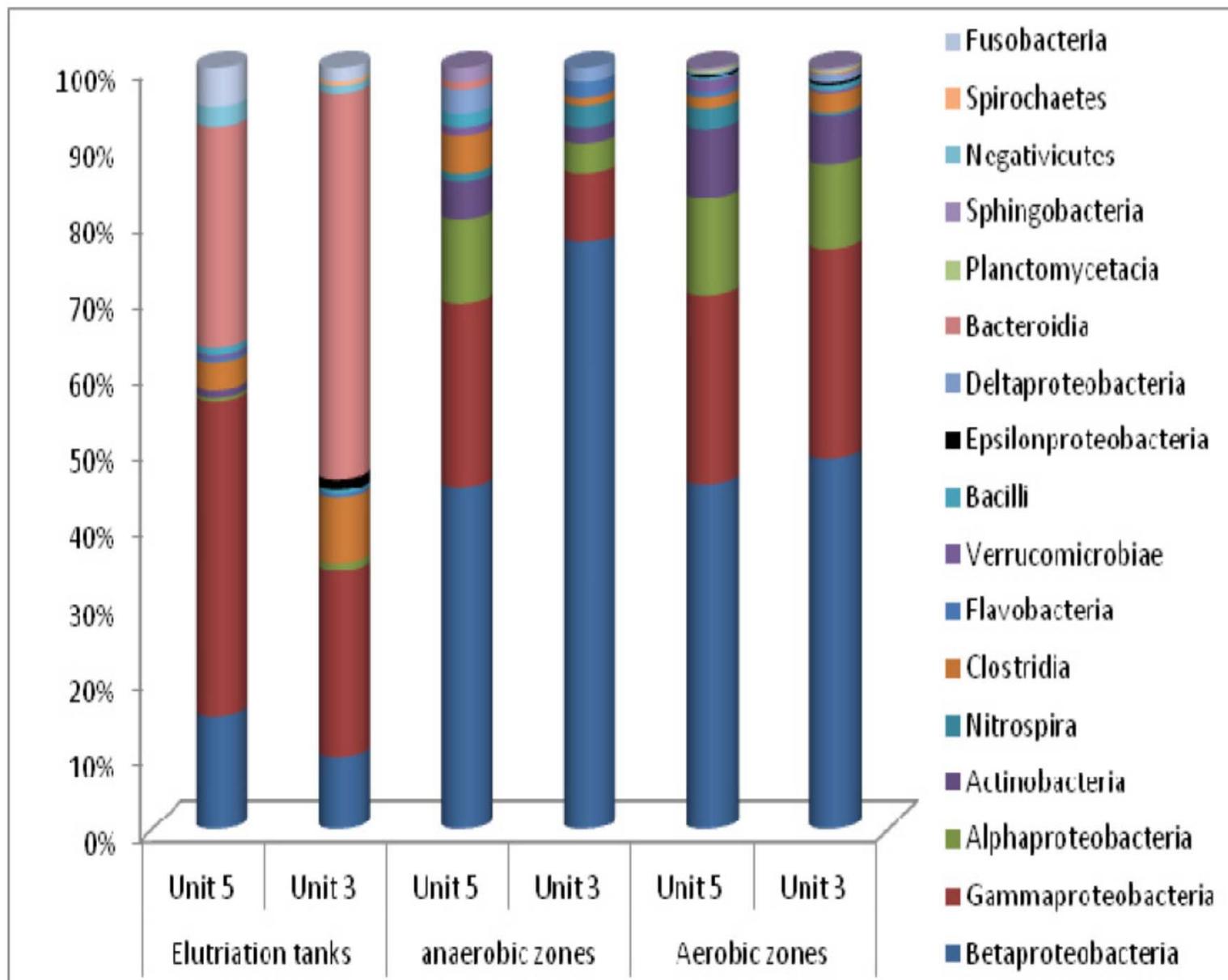


Figure 1: Microbial diversity within different zones of the treatment in a WWTP.
 Source: I.Kamika et al., 2014. (Int. J. Environ. Res. Public Health 2014,11,2876-2898)

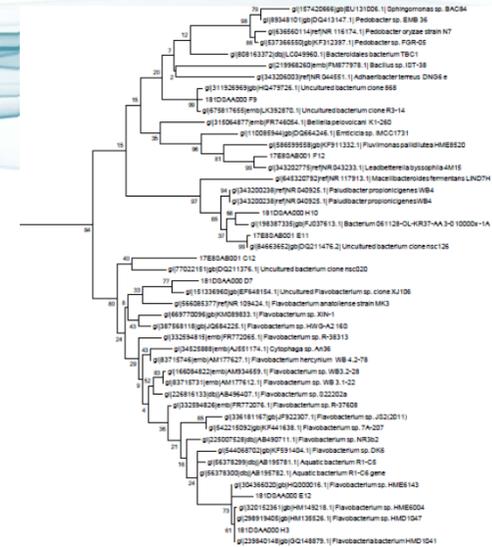
Molecular analysis of IASBR

16S Clone library

Material and Methods

1. Three samples, one from each reactor: **R1, R2, R3** in day 63 since starting.
2. **DNA extraction:** Mobio PowerSoil Isolation kit.
3. **PCR amplification** with the pair of primers: 27F/1492R (1500bp length).
4. **Cloning** and screening: Qiagen PCR Cloning^{Plus} kit. Kanamycing and ampiciline selection.
5. **Sequency:** Sanger sequencing (Macrogen).

Results



Groups (phyla) of species (85-99%similarity, excluding uncultured bacteria):

- Actino
- Bacte
- Leadb
- Firmic
- Planct

- Time consuming and laborious.

- Many clones have to be sequenced to ensure most of individual species in the sample are covered.

Successful identification of know species but inconsistent for the purpose of comparative assessment of reactors overtime.

Proteobacteria. Arcobacter sp., Campylobacteraceae sp., Comamonas sp., Acidovorax sp., Rhodospirillum rubrum, Ferritribacterium sp., Castellaniella sp., Alcaligenes sp., Delftia sp.,

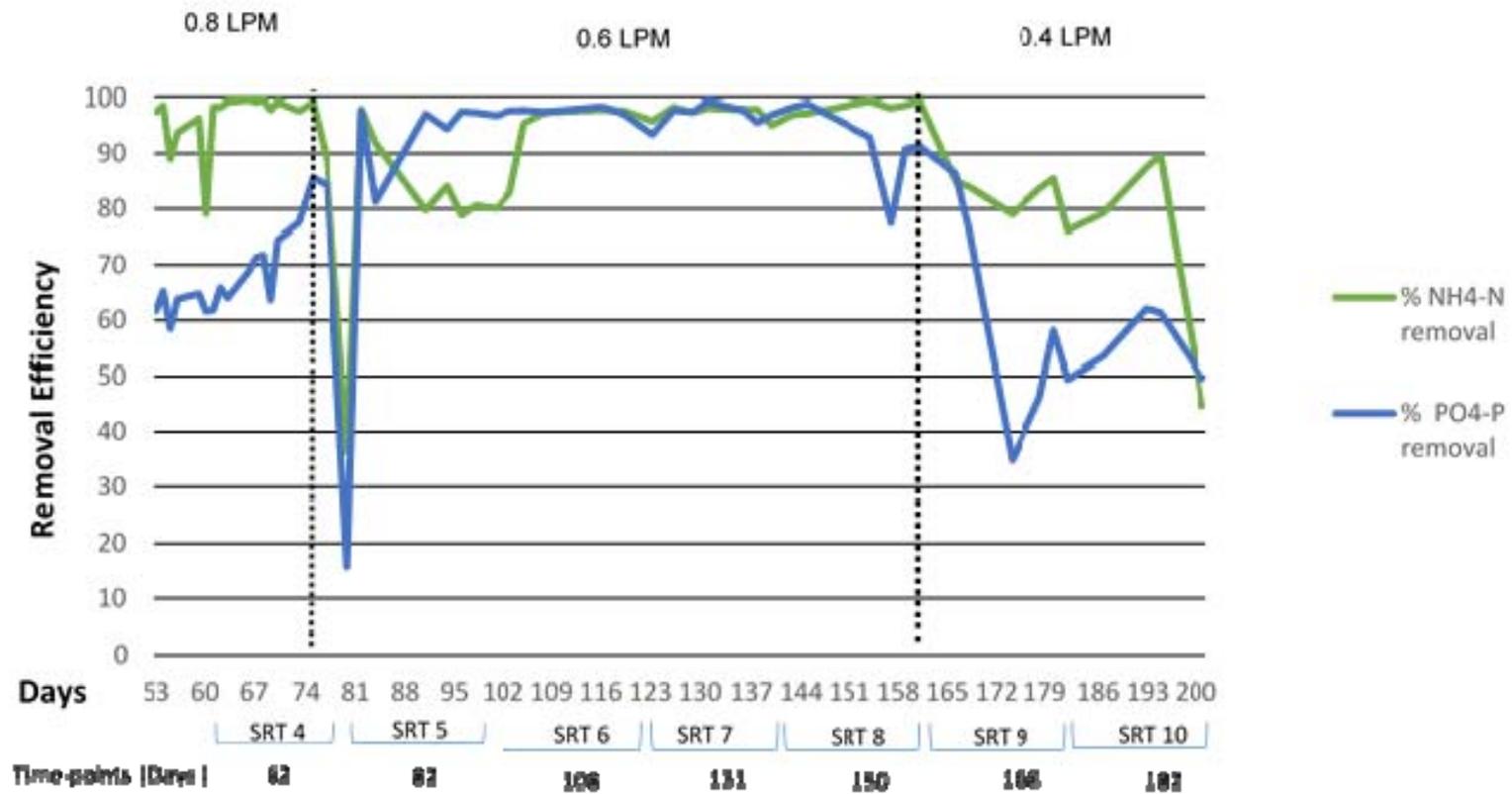
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Molecular analysis of IASBR

HRT : 4 days

SRT: 20 days

Nutrient removal efficiency in reactor 3



Molecular analysis of IASBR

Microbial ecology structure in R3

- Material and Methods

1. Nine samples from **R3** along the 201 days setup: **T₀, T₁, T₂, T₃, T₄, T₅, T₆, T₇, T₈**.
2. **DNA extraction:** Mobio PowerSoil Isolation kit.
3. **454-Pyrosequencing** using the universal primers: U905F/U1492R for the regions V5-V9 in the 16S (Wang&Qian, 2009; Gao et al., 2015). 35 nucleotide barcodes were added in each pair of primers (~650 bp length).
4. **Bioinformatics analysis:** QIIME.

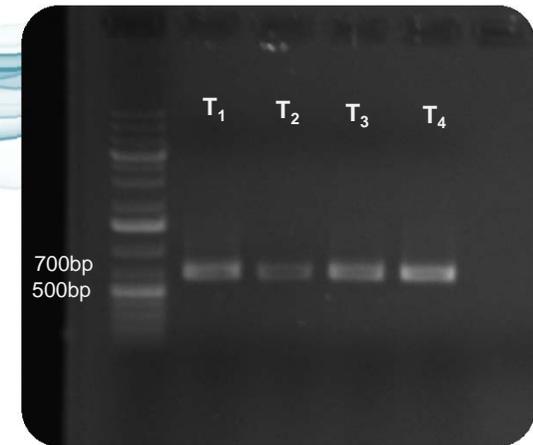


Figure 2: PCR product for samples T₁ to T₄

Regular parameters:

- Cycle and aeration period lengths
- Temperature (11°C)
- Hydrolic retention time (HRT)
- Solid retention time (SRT)

Variable parameter:

- Air flow

Future Prospects

- To link physicochemical parameters with the molecular microbiology studies of IASBR systems.
- To understand how the microbial communities do perform and recover after breakdown events.
- Microscopy and clone specific probes for FISH (fluorescence *in situ* hybridisation) analysis.
- To determine the ecology in meso-scale IASBR.

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Thanks for your attention



DairyWater