

Influence of external microorganism on the microbiome in anaerobic reactors. (No. IWA-550105)



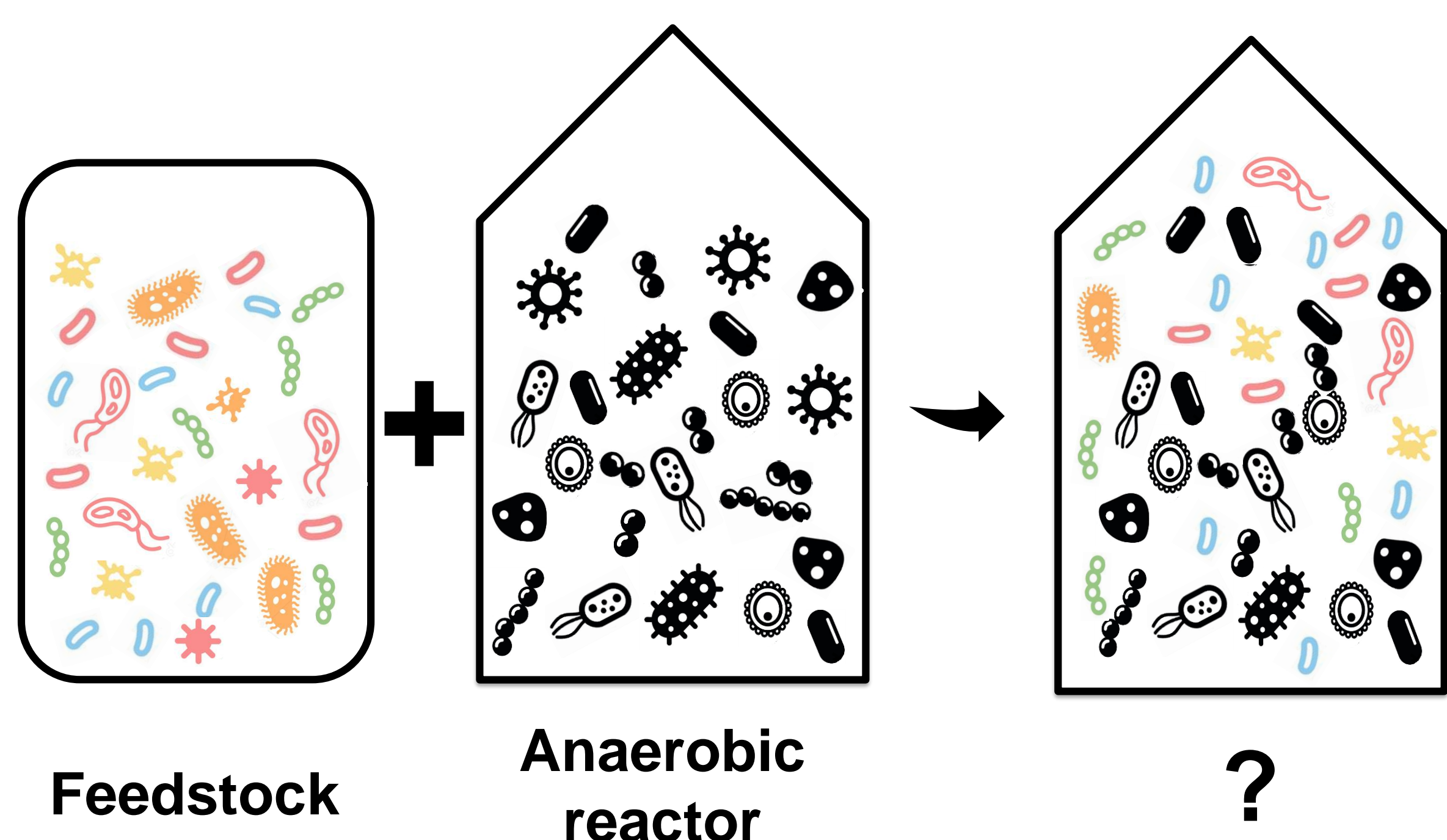
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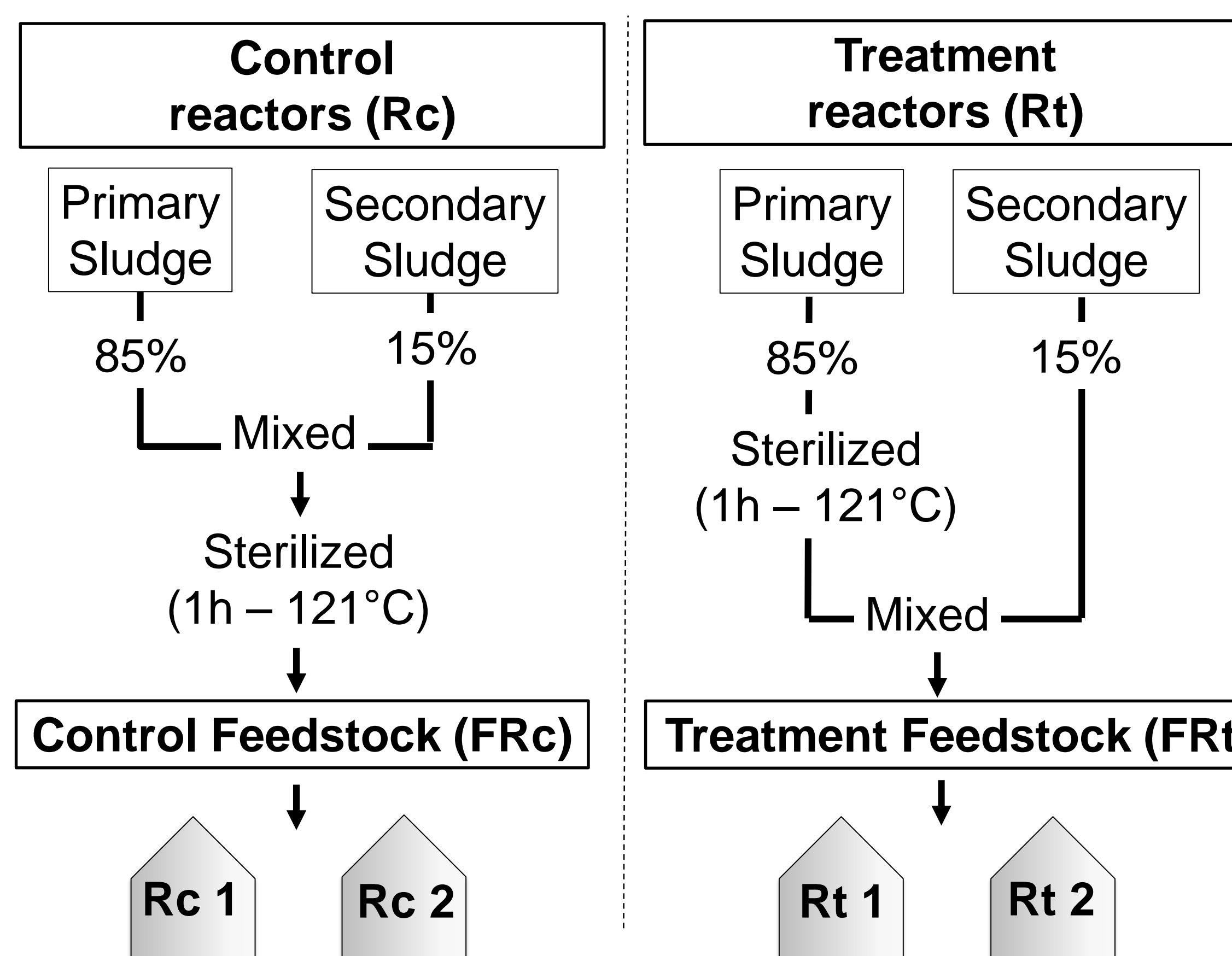
OBJECTIVE

Does the continuous entrance of external microorganism influence the microbiome in anaerobic reactors?



METHODS

TWO DIFFERENT TREATMENTS



16S rRNA gene massive sequencing

Physico-chemical parameters

Similar feedstock composition between treatments

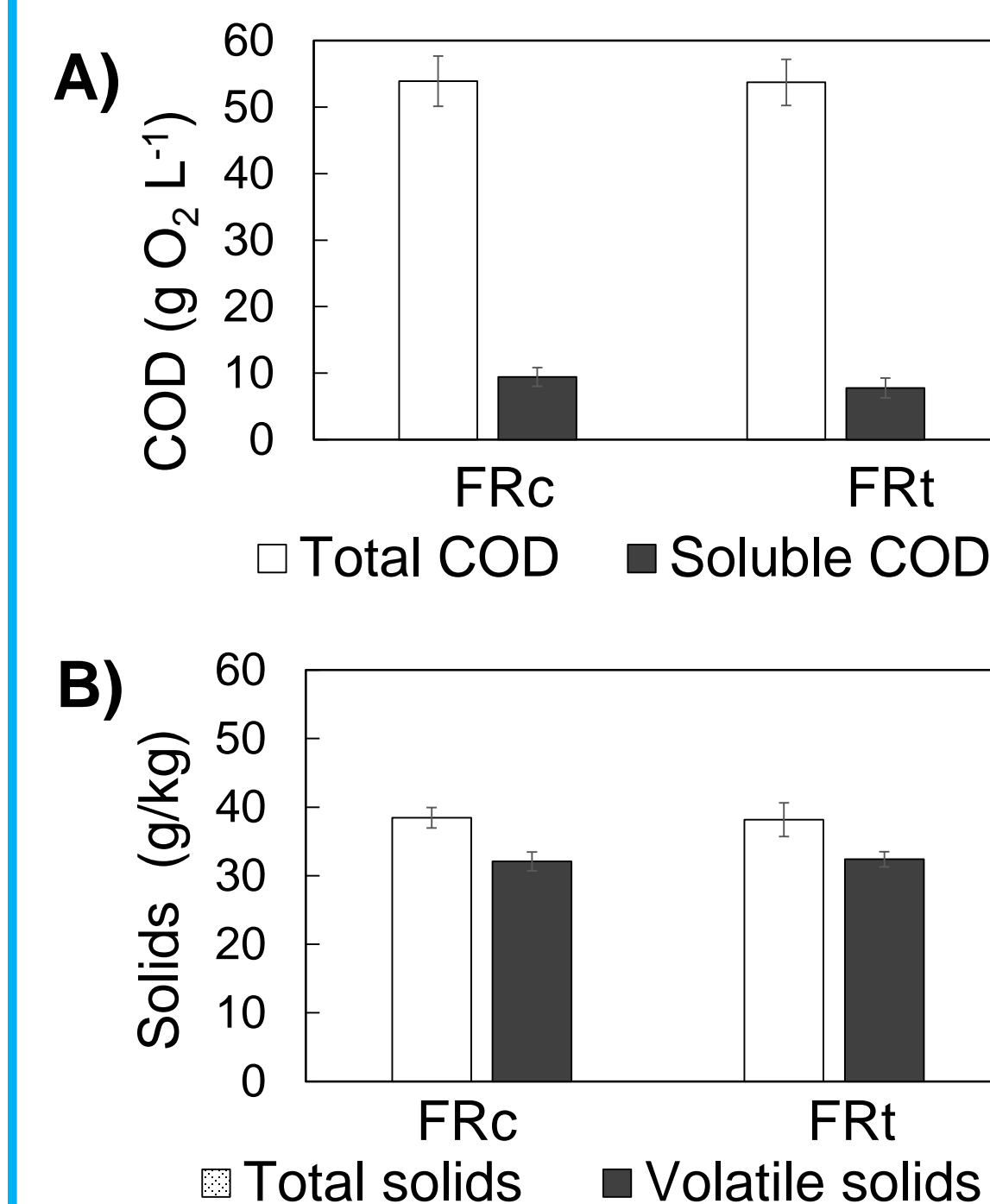


Figure 1 – Averaged feedstock values of A) chemical oxygen demand (COD) and B) solids. Vertical bars indicate standard deviation.

RESULTS AND DISCUSSION

STABLE AND SIMILAR BETWEEN TREATMENTS

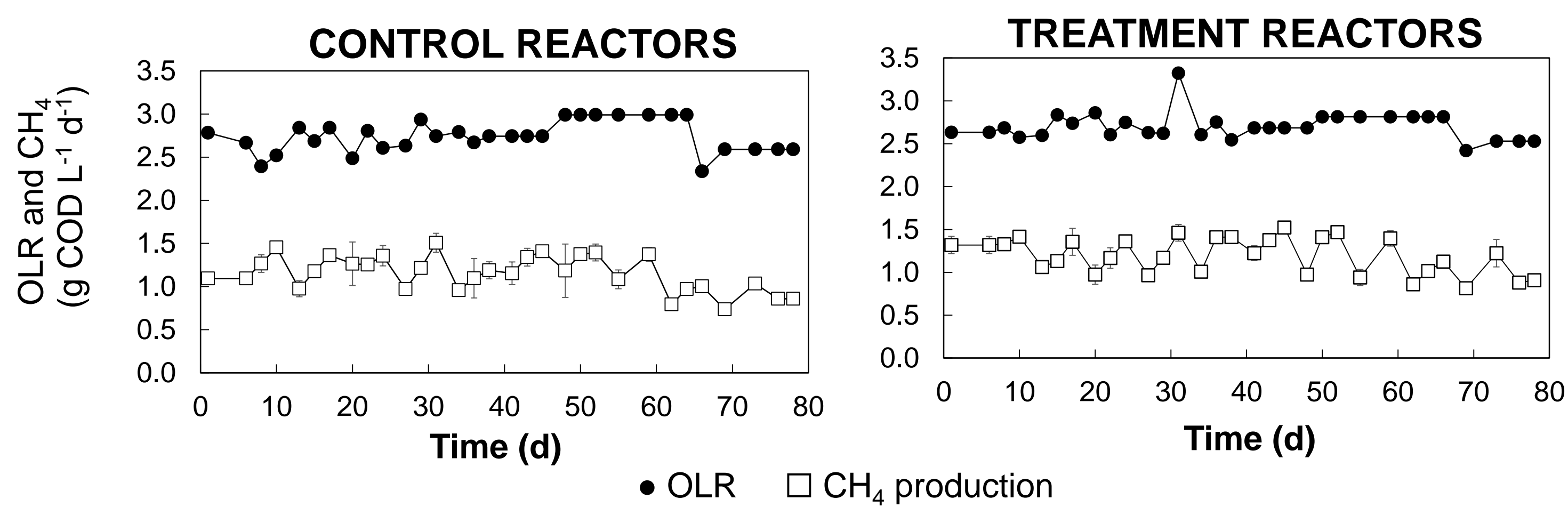
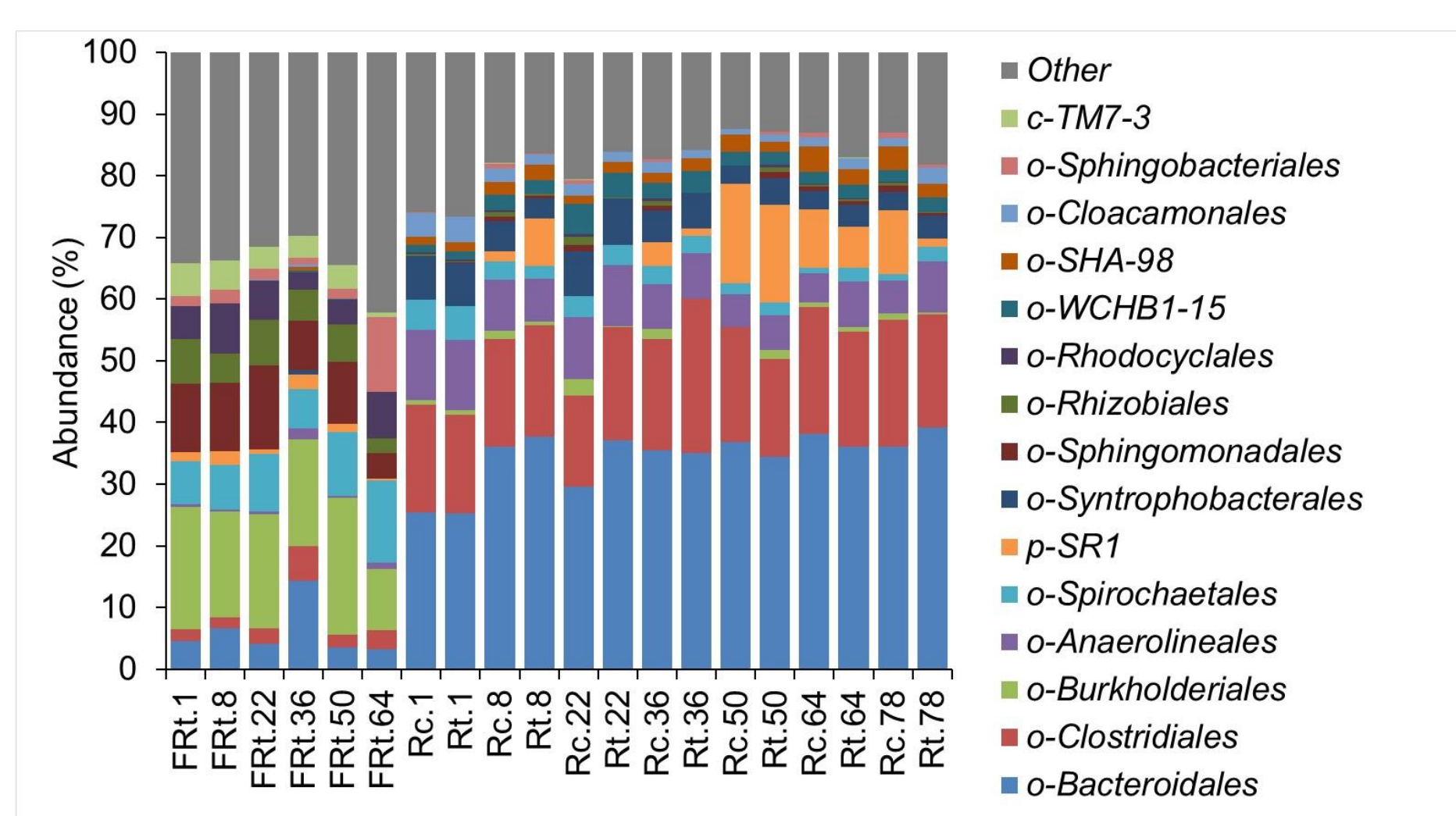


Figure 2- Organic loading rates and CH₄ production. Vertical bars: standard deviation among replicates

NO DISPLACEMENT OF MAIN RESIDENT MICROBIOTA IN THE REACTORS BY FEEDSTOCK MICROORGANISMS

A) BACTERIA

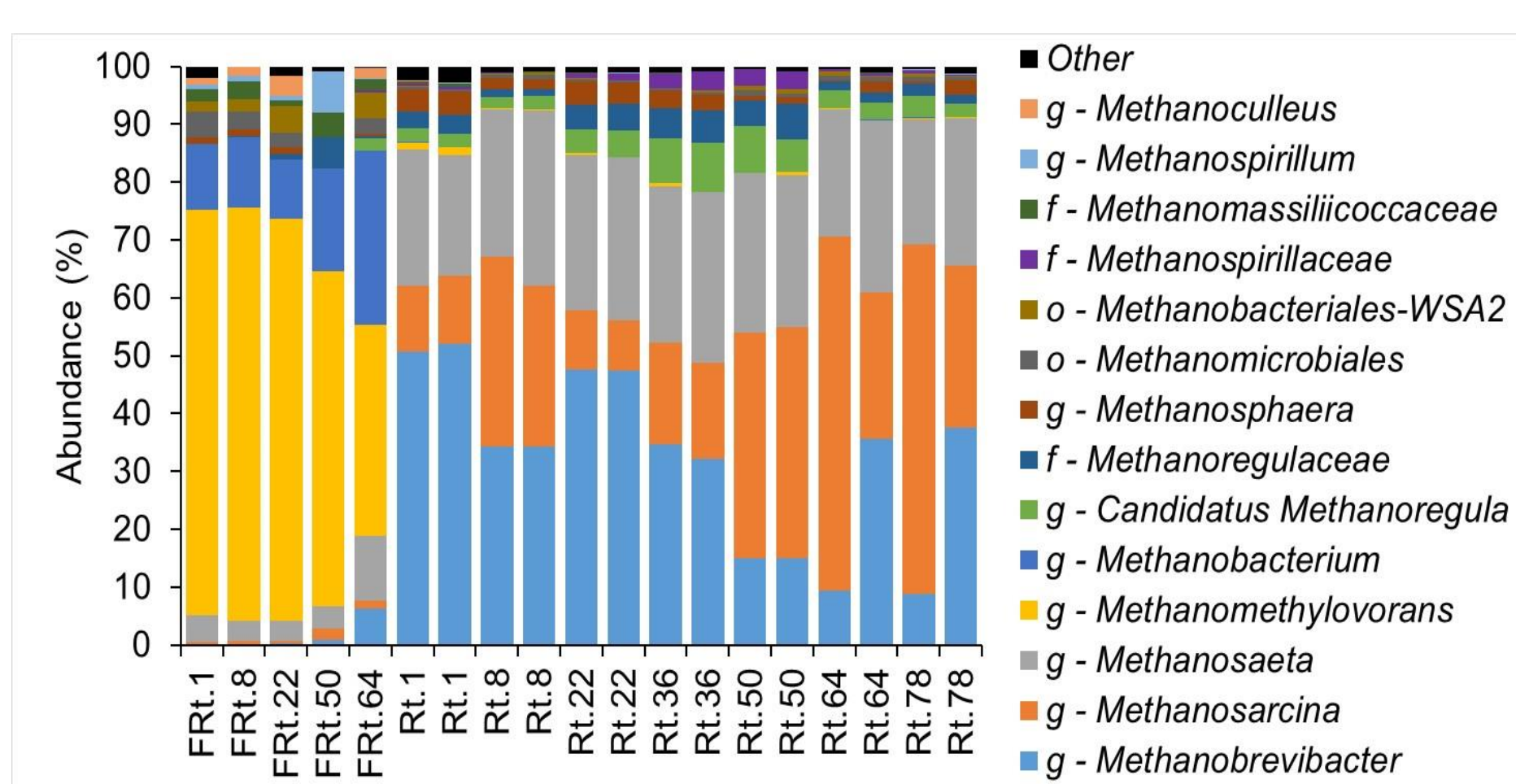


DOMINANT PHYLA

Reactors
Firmicutes and Bacteroidetes

Feedstock
Proteobacteria

B) ARCHAEA



DOMINANT GENERA

Reactors
Methanobrevibacter and Methanosarcina

Feedstock
Methanomethylovorans

Figure 4 – Top 10 prevalent A) bacterial orders and B) archaeal genera from day 1 to 78. In samples Rt and Rc the relative abundances were averaged between replicates. FRt: treatment feedstock

MICROBIOME STRUCTURE: FEEDSTOCK VS. REACTORS → DIFFERENT CONTROL VS. TREATMENT REACTORS → SIMILAR

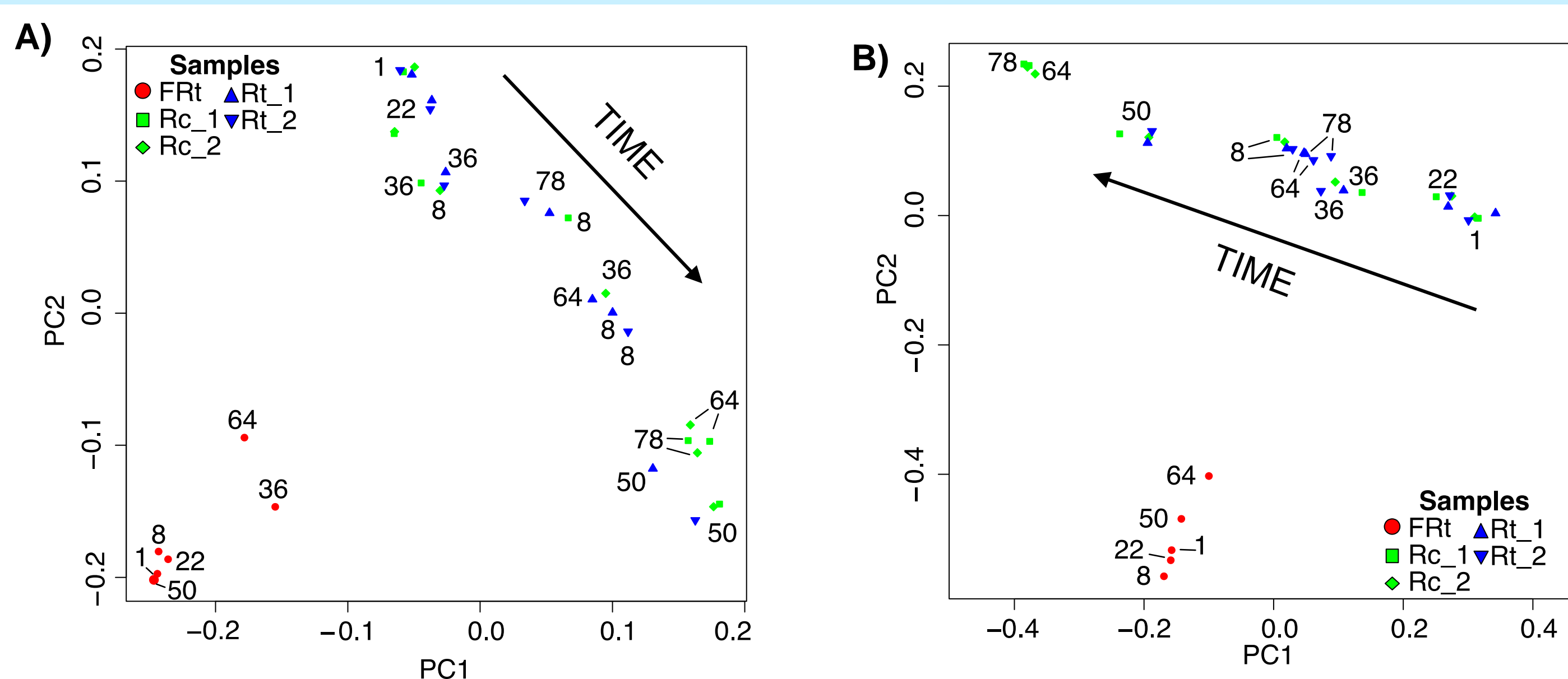


Figure 3 – Principal component analysis of A) bacterial and B) archaeal community. Labels correspond to the operational days.

CONCLUSIONS

- The feedstock microbial load does not influence the steady-state operation of AD reactors.
- AD process was maintained by the native AD microbiome present in the reactor seed.
- No severe influence of feedstock microbial load on AD digesters microbiome.

- REFERENCES
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ACKNOWLEDGEMENTS

PhD fellowship by CAPES (BEX-2160/2015-03) Foundation, Ministry of Education of Brazil, Brasília – DF 70040-020, Brazil. The authors belong to the Galician Competitive Research Group GRC/GPC2013-032 and to the CRETUS Strategic Partnership (AGRUP2015/02). All these programmes are co-funded by FEDER (UE). The authors acknowledge the computational support from Centro de Supercomputación de Galicia - CESGA