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Characterization of virus-host dynamics in anaerobic digesters under abiotic stress











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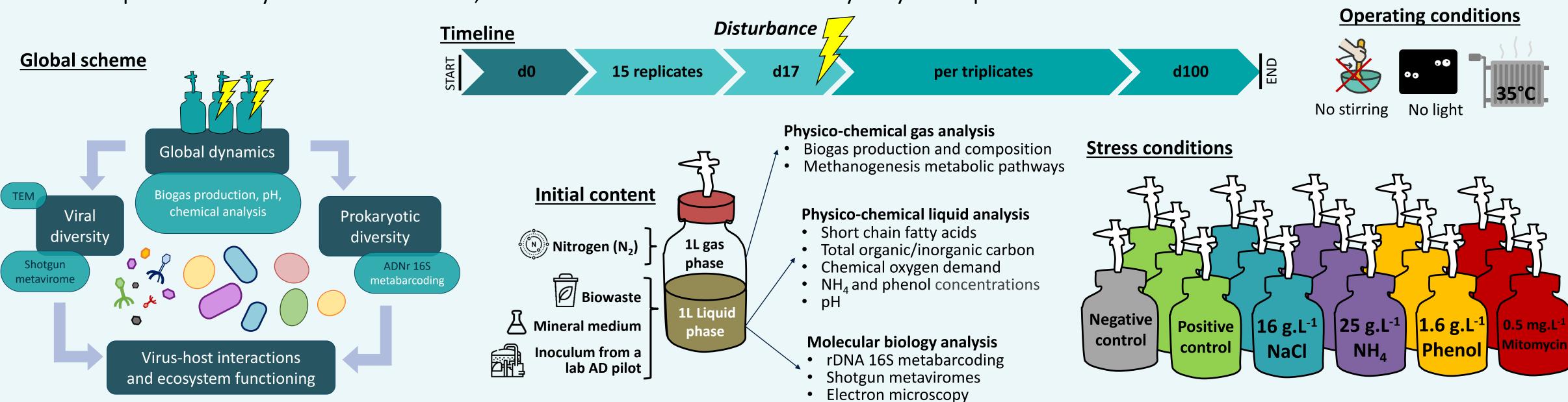
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Context

Viruses of microbes are major players in various ecosystems, typically affecting the structuration and dynamics of microbial communities [1]. They nevertheless remain poorly explored in anaerobic digestion (AD) plants [2], where biowaste is valorised into methane-rich biogas. The AD process ecosystems are very sensitive to disturbance, leading to inhibition and loss of methane production [3]. We were therefore interested in better understanding the interplay between abiotic disturbance, microbial community composition, including the viromes, and process performance.

Experimental design

The variations of both viral and prokaryotic populations were monitored in batch AD microcosms under abiotic stress, during a hundred days. Four distinct abiotic disturbances were tested in triplicates: during incubation, either NaCl, NH₄Cl or phenol was injected into the reactors, as inhibitors previously reported in full-scale plants. Mitomycin C was also tested, since it can induce the activation of lytic cycle for proviruses.



CH. Impact on gas production d17: Disturbance d17: Disturbance 6000 <u>5000</u> rction 4000 8g 2000 Cumulated productions of total biogas (left) and CH₄ (right)

→ We confirmed a significant impact of the tested stresses on biogas production, although with variable intensity

DESeq model

Time evolution comparison: 2 time points, 2 conditions

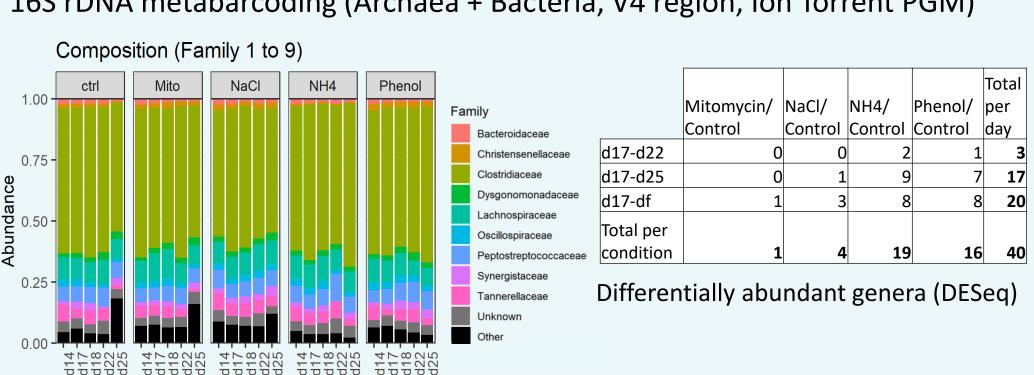
model.matrix(~ condition + condition:replicate + condition:day, data)

Identification of prokaryotic genera or viral contigs showing differential evolutions compared to the control.

Considering the high biological variability among replicates, the model took into account the intra-condition variability

Microbial community dynamics

16S rDNA metabarcoding (Archaea + Bacteria, V4 region, Ion Torrent PGM)



- → Clostridiaceae was the most abundant family in all samples.
- → No shift was visible at rank family but there was an impact at a finer level: 20 distinct genera presented significantly different dynamics

Metaviromes

Methods

- Shotgun sequencing of 30 selected metaviromes (Illumina, 2 x 150 bp)
- Coassembly (Megahit) with a snakemake pipeline developed in our lab [4]
- Virus detection with tools such as VIBRANT . [5], CheckV [6] and VirSorter2 [6]

Coassembly statistics

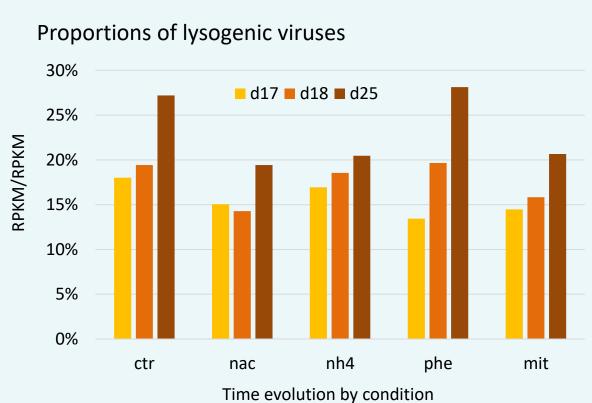
- 10⁵ contigs longer than 1,000 bases
- N50 = 3,886 bases
- 45,914 putative viral contigs (VIBRANT) including 2,815 with the status "complete"
- 430 highly reliable viral contigs (detected by at least two distinct tools)
- 64,10⁶ mapped reads per sample on average (representing 97.5% of the reads)

Solution Differentially abundant viral contigs (DESeq) Upset plot presenting set intersections Differentially abundant contigs

→ 127 viral contigs were differentially abundant when comparing time evolutions (before and after disturbance). 16 of them were common among conditions NaCl, NH₄ and Phenol on day 25

Time-bomb hypothesis [8]

Stress could increase the proportion of particles from temperate viruses, by activating the lytic cycle of proviruses.



→ Looking further into the induction of prophages in phenol disturbance experiment could be interesting

Conclusions

- ✓ The significant impact of the tested stresses on biogas production was confirmed
- ✓ Microbial community's shifts were more significant on day 25
- √ 127 viral contigs were differentially abundant

(4) Perspectives

- ☐ Analysis of viral contigs of interest (host prediction, taxonomic affiliation, gene content)
- ☐ Auxiliary metabolic genes (AMG) will be particularly interesting to study further

Centre









References

sequences. Microbiome 2020

- 1. Sullivan MB, et al. Viral ecology comes of age. Environmental Microbiology Reports 2016
- 2. Calusinska M, et al. Analysis of dsDNA and RNA viromes in methanogenic digesters reveals novel viral genetic diversity. Environmental Microbiology 2015
- 3. Chen Y, et al. Inhibition of anaerobic digestion process: A review. Bioresource Technology 2008
- 4. https://forgemia.inra.fr/cedric.midoux/workflow_metagenomics 5. Kieft K, et al. VIBRANT: automated recovery, annotation and curation of microbial viruses, and evaluation of viral community function from genomic
- 6. Nayfach S, et al. CheckV assesses the quality and completeness of metagenome-assembled viral genomes. Nat Biotechnol 2021 7. Guo J, et al. VirSorter2: a multi-classifier, expert-guided approach to detect diverse DNA and RNA viruses. Microbiome 2021
- 8. Paul JH, et al. Prophages in marine bacteria: dangerous molecular time bombs or the key to survival in the seas? The IsmeJournal 2008