



HAL
open science

Microbial community dynamics during the co-digestion of manure and the organic fraction of household waste

Franciele Pereira Camargo, Céline Roose-Amsaleg, Sabrina Guérin-Rechdaoui, Vincent Rocher, Elise Alibert, Carlyne Lacroix, Anne Goubet, Chrystelle Bureau, Lays Paulino Leonel, Adriano Luiz Tonetti, et al.

► To cite this version:

Franciele Pereira Camargo, Céline Roose-Amsaleg, Sabrina Guérin-Rechdaoui, Vincent Rocher, Elise Alibert, et al.. Microbial community dynamics during the co-digestion of manure and the organic fraction of household waste. 4th International Conference on Biogas Microbiology (ICBM-4), May 2022, Braga, Portugal. hal-04486518

HAL Id: hal-04486518

<https://hal.inrae.fr/hal-04486518>

Submitted on 2 Mar 2024

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

Microbial community dynamics during the co-digestion of manure and the organic fraction of household waste

Franciele Pereira Camargo^{1,4}, Céline Roose-Amsaleg², Sabrina Guérin³, Vincent Rocher³, Elise Alibert³, Carlyne Lacroix³, Anne Goubet⁴, Chrystelle Bureau⁴, Lays Paulino Leonel⁵, Adriano Luiz Tonetti⁵, Maria Bernadete Amâncio Varesche¹, Ariane Bize^{4*}

¹Department of Hydraulics and Sanitation, School of Engineering of São Carlos, University of São Paulo, São Carlos, SP, Brazil

²CNRS, ECOBIO-UMR 6553, Univ Rennes 1, 35000 Rennes, France

³Syndicat Interdépartemental Pour l'Assainissement de l'Agglomération Parisienne (SIAAP), Colombes, France

⁴Université Paris-Saclay, INRAE, PROSE, 1 rue Pierre-Gilles de Gennes, CS10030, 92761 Antony, France

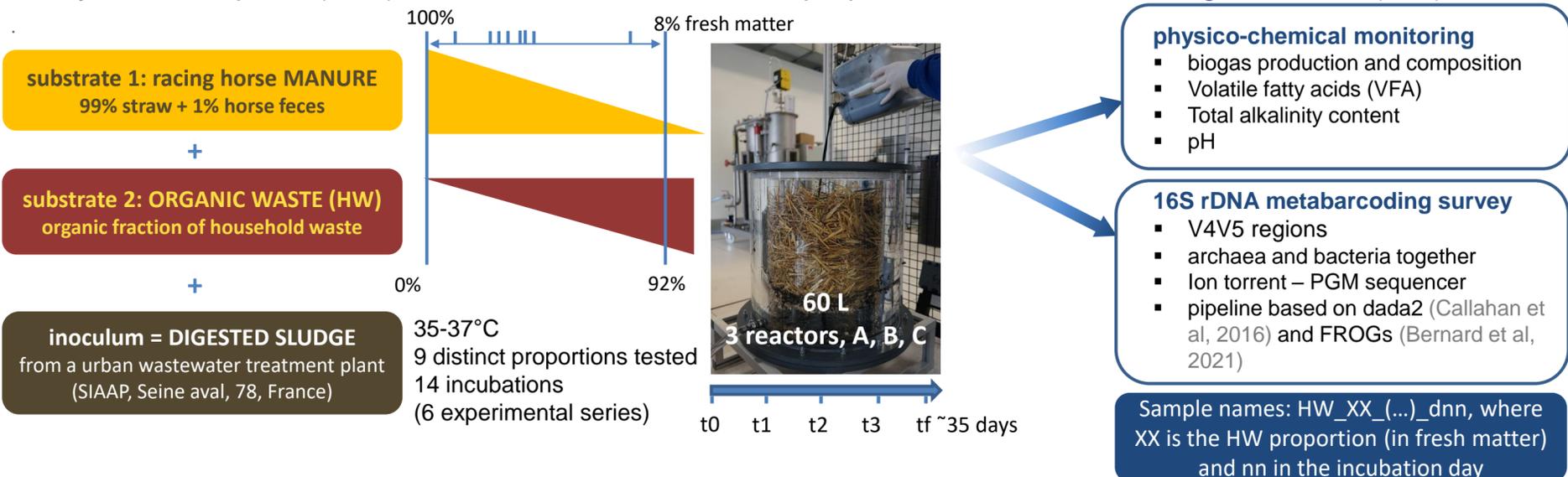
⁵Sanitation and Environmental department, School of Civil Engineering, Architecture and Urban Design, University of Campinas, Brazil



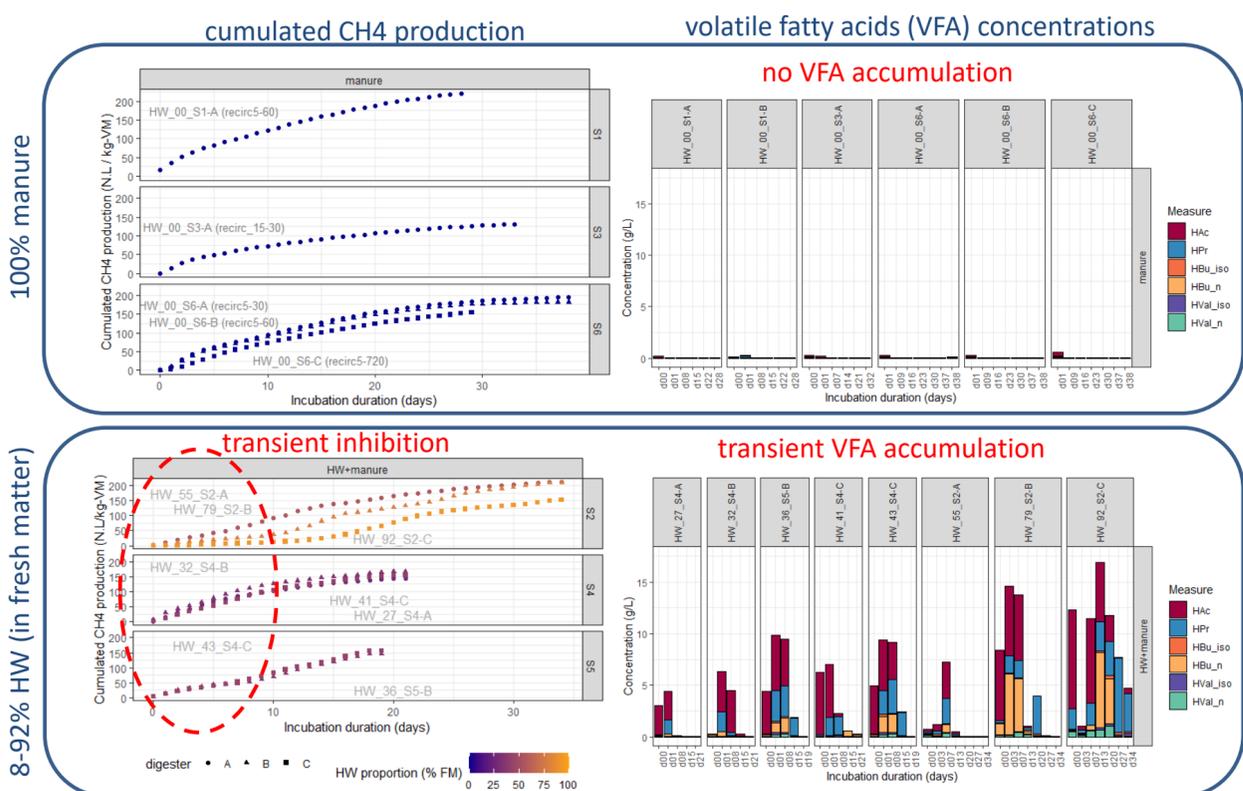
1. Introduction: co-digestion of organic waste is an attractive option for territories but requires optimization

Organic waste co-digestion enables to valorize different types of locally produced waste and to optimize biogas production in digestion plants. However, the operating conditions need to be adapted to the waste stream nature. We studied the dry batch mesophilic co-digestion of **reconstituted racing horse manure** and the **organic fraction of residual household waste (HW)**, in 60 L pilot reactors. We identified optimal proportions of co-substrates and evaluated the effects of their initial proportions on **microbial community** dynamics during **anaerobic digestion (AD)**.

2. Dry batch AD pilots (60 L) were used to assess various proportions of manure and organic waste (HW)



3. Increasing, but transient, acidic inhibition occurs with increasing proportions of organic waste (HW)

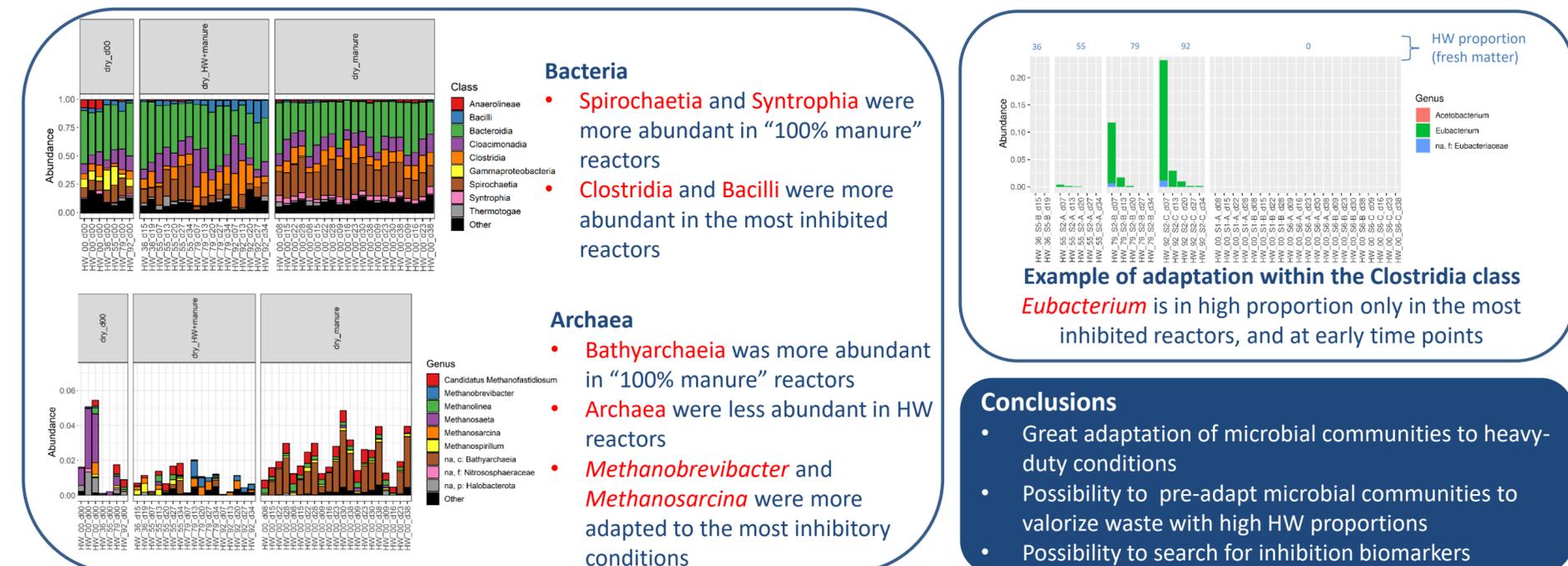


The total cumulated methane volume was overall little affected by the presence of HW. However, a transient acidic inhibition occurred when manure was co-digested with HW, and increased with higher HW proportions. It was caused by VFA accumulation and can be related with the higher degradation rate of HW compared to manure. Indeed, HW must be richer in readily-fermentable compounds compared to the highly lignocellulose-rich manure.

A maximal concentration of 16.9 g(VFA).L⁻¹ was reached in the reactor with the highest HW proportion (92%), at day 13. Acetic and propionic acids (Hac and HPr) were generally the dominant VFAs. However, concentrations in butyric acid (Hbu) increased with higher HW proportions, reaching 7.4 g.L⁻¹ at day 13 in the reactor with 92% of HW.

4. The microbial community composition is greatly influenced by both the use of HW and the acidic inhibition

A selection of 66 samples was analyzed by 16S rDNA metabarcoding (>15 000 sequences per sample).



References

Callahan BJ, McMurdie PJ, Rosen MJ, Han AW, Johnson AJ, Holmes SP. DADA2: High-resolution sample inference from illumina amplicon data. *Nature methods*. 2016 Jul;13(7):581-3.

Bernard M, Rué O, Mariadassou M, Pascal G. FROGS: a powerful tool to analyse the diversity of fungi with special management of internal transcribed spacers. *Briefings in Bioinformatics*. 2021 Nov;22(6):bbab318.



This work was conducted in the framework of the research program MOCOPEE (<http://s513518674.siteweb-initial.fr/>)