



HAL
open science

Diversity of novel archaeal viruses infecting methanogens discovered through coupling of stable isotope probing and metagenomics

Vuong Quoc Hoang Ngo, François Enault, Cédric Midoux, Mahendra Mariadassou, Olivier Chapleur, Laurent Mazéas, Valentin Loux, Théodore Bouchez, Mart Krupovic, Ariane Bize

► To cite this version:

Vuong Quoc Hoang Ngo, François Enault, Cédric Midoux, Mahendra Mariadassou, Olivier Chapleur, et al.. Diversity of novel archaeal viruses infecting methanogens discovered through coupling of stable isotope probing and metagenomics. ISME18, 18th International Symposium on Microbial Ecology, Aug 2022, Lausanne, Switzerland. . hal-04359643

HAL Id: hal-04359643

<https://hal.inrae.fr/hal-04359643v1>

Submitted on 21 Dec 2023

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.

Diversity of novel archaeal viruses infecting methanogens discovered through coupling of stable isotope probing and metagenomics

Hoang Ngo¹, François Enault², Cédric Midoux^{1,3,4}, Mahendra Mariadassou^{3,4}, Olivier Chapleur¹, Laurent Mazéas¹, Valentin Loux^{3,4}, Théodore Bouchez¹, Mart Krupovic⁵, Ariane Bize¹

@ ariane.bize@inrae.fr

1. Université Paris-Saclay, INRAE, PROSE, 92761, Antony, France

2. Université Clermont Auvergne, CNRS, LMGE, F-63000 Clermont-Ferrand, France
3. Université Paris-Saclay, INRAE, MalAGE, 78350, Jouy-en-Josas, France

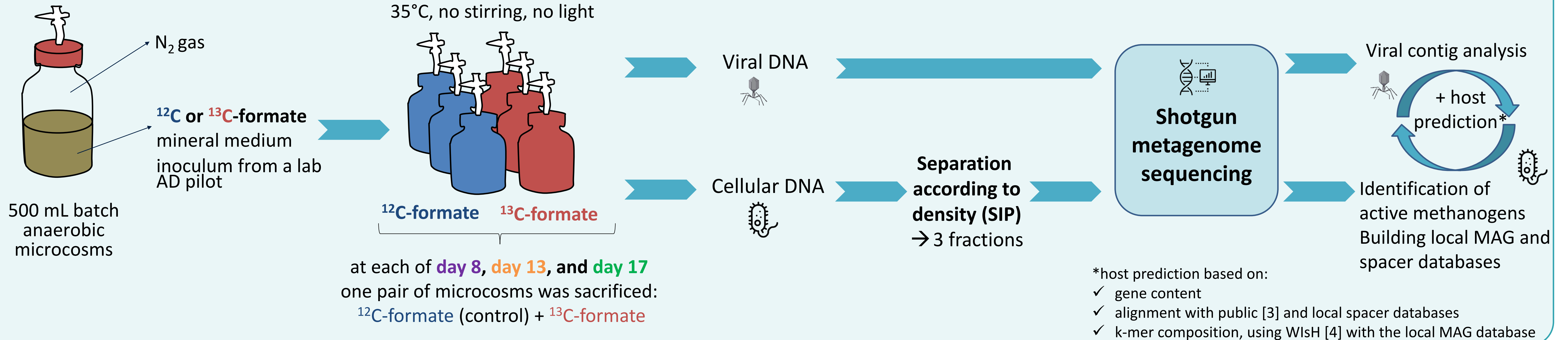
4. Université Paris-Saclay, INRAE, BioinfOmics, MIGALE bioinformatics facility, 78350, Jouy-en-Josas, France

5. Institut Pasteur, Université de Paris, CNRS UMR6047, Archaeal Virology Unit, F-75015 Paris, France

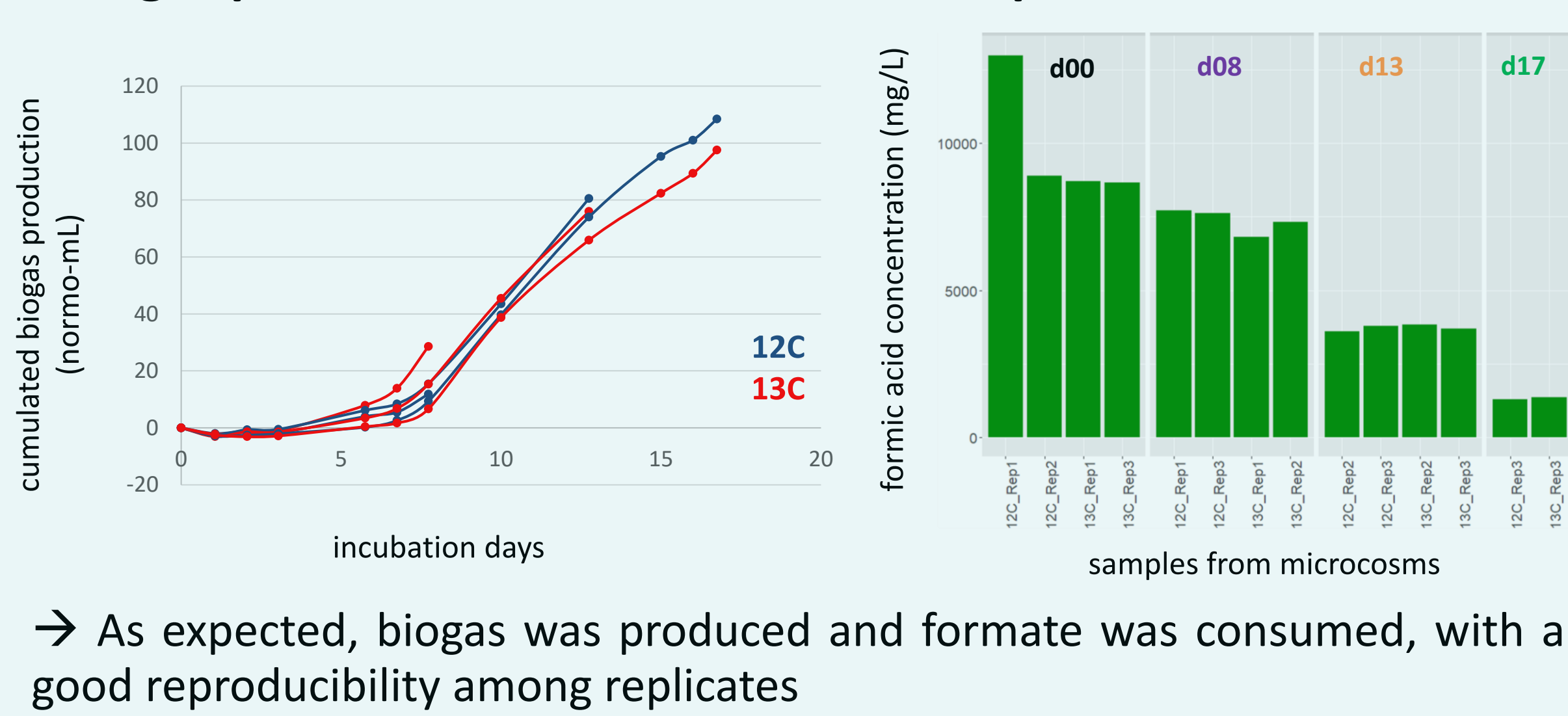
Context

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. Here, we explored the diversity of viruses infecting methanogens involved in AD processes. We developed an original coupling of **metagenomics** and **stable isotope probing (SIP)**, to identify viruses infecting formate-assimilating methanogens during AD. Only a dozen of **viruses of methanogens** have been isolated so far, mostly head-tailed.

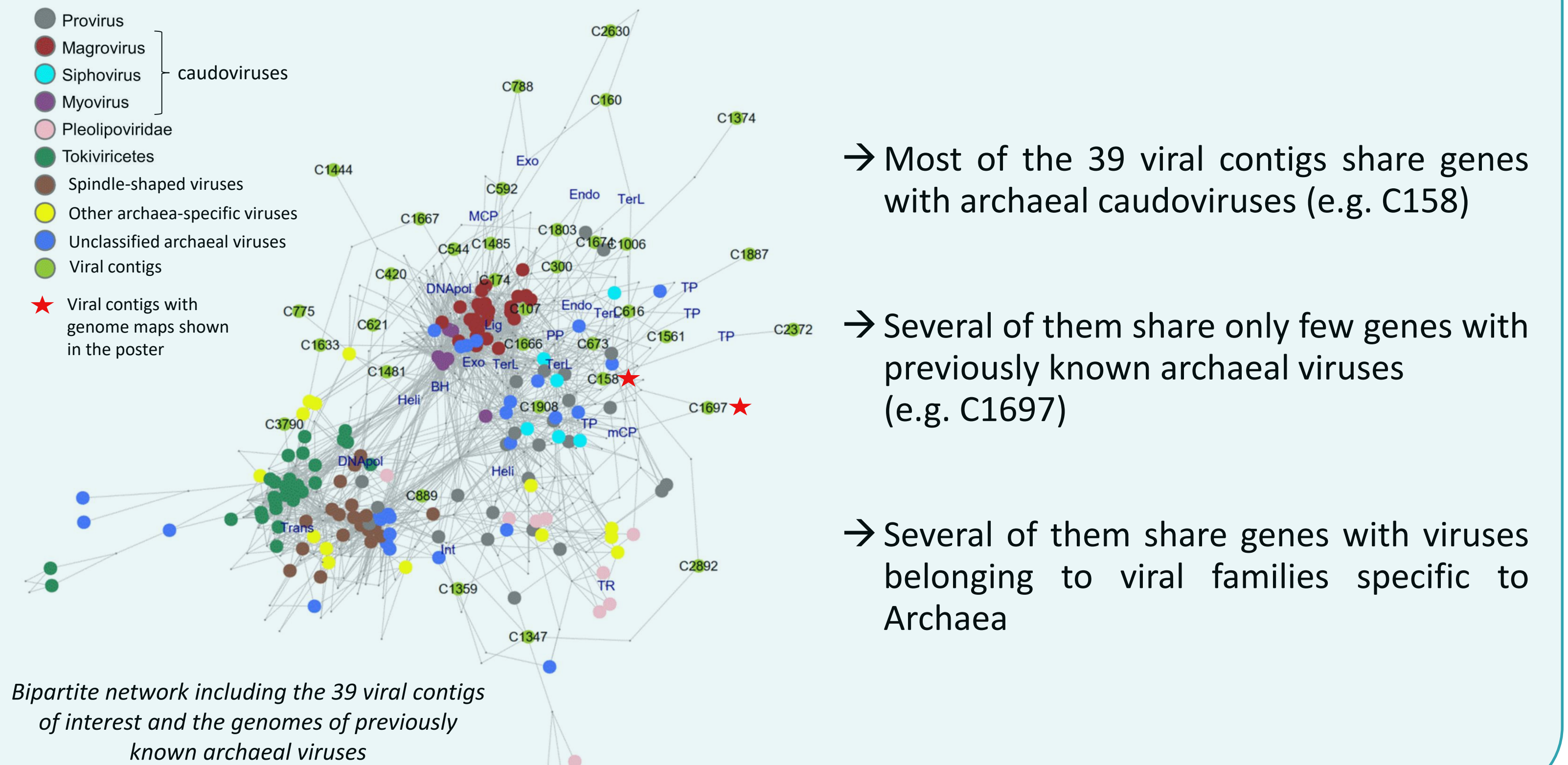
Experimental set-up



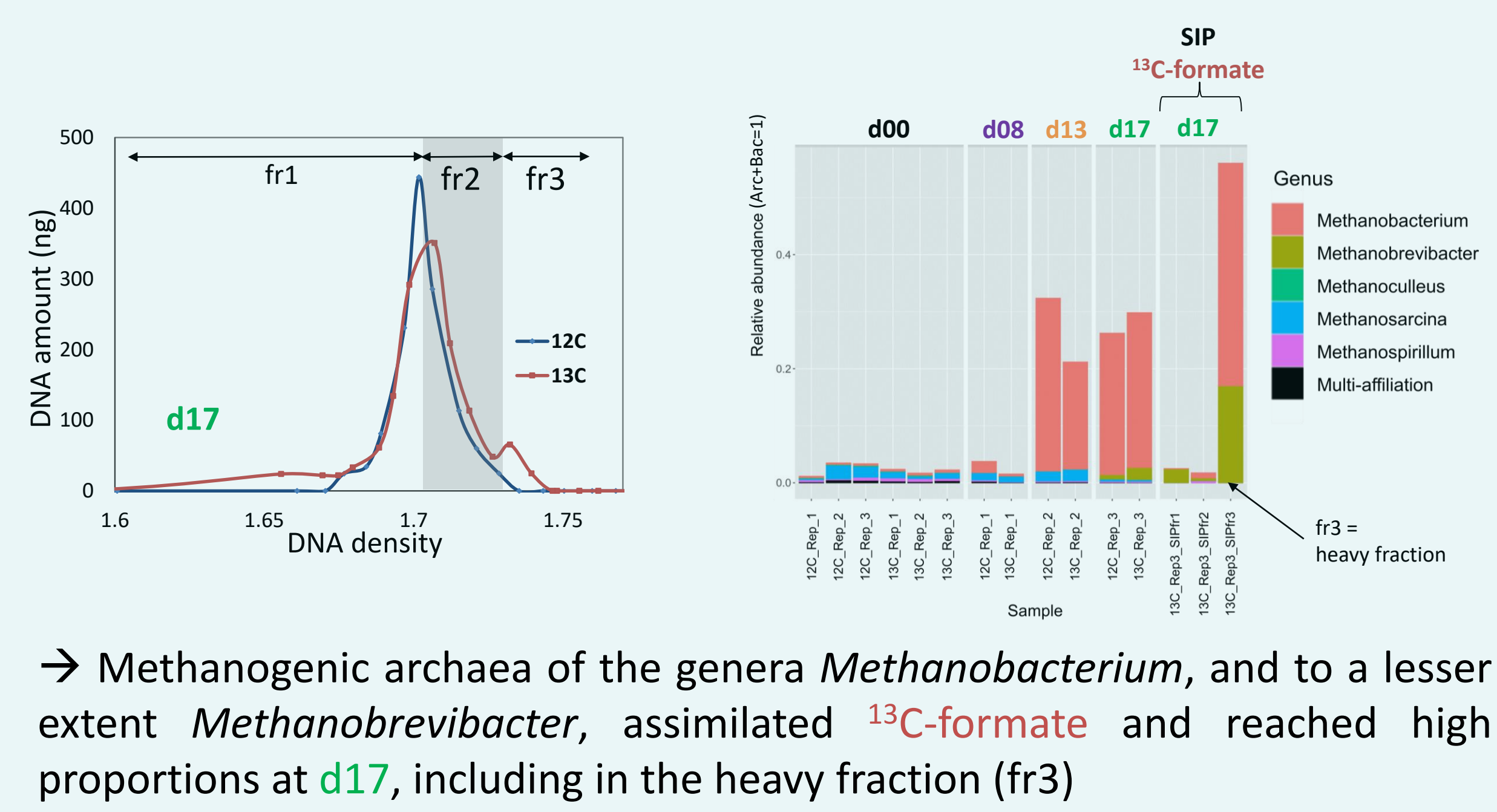
Biogas production and formate consumption



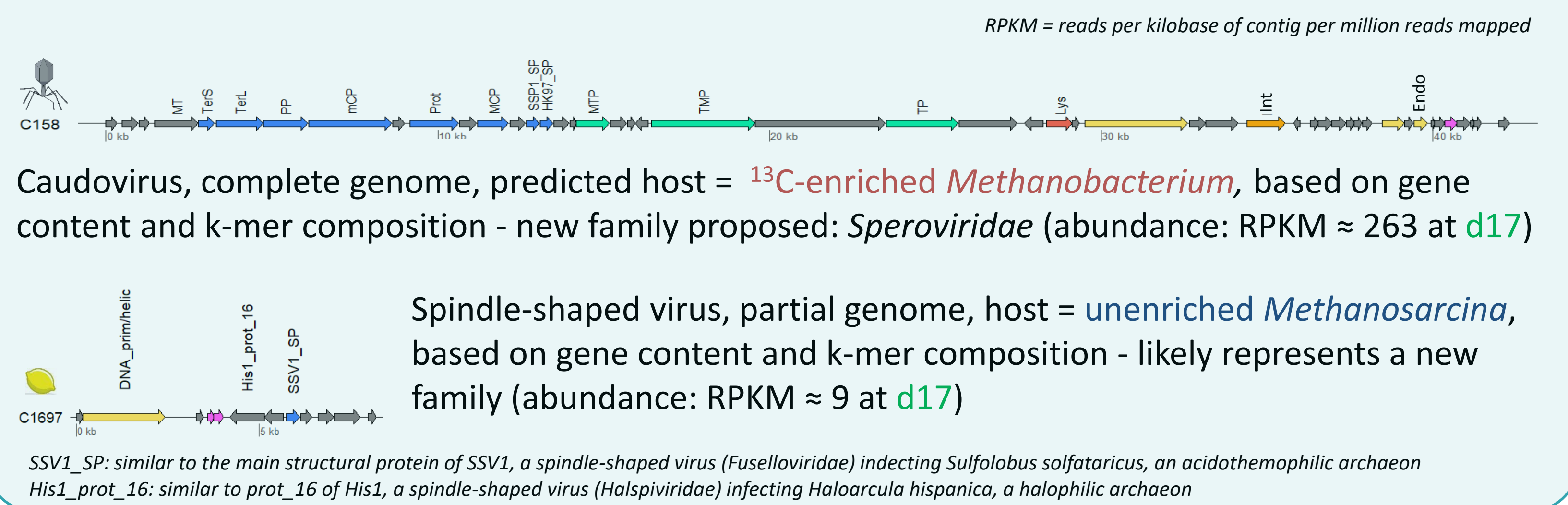
Bipartite network of 39 viral contigs predicted to have an archaeal host



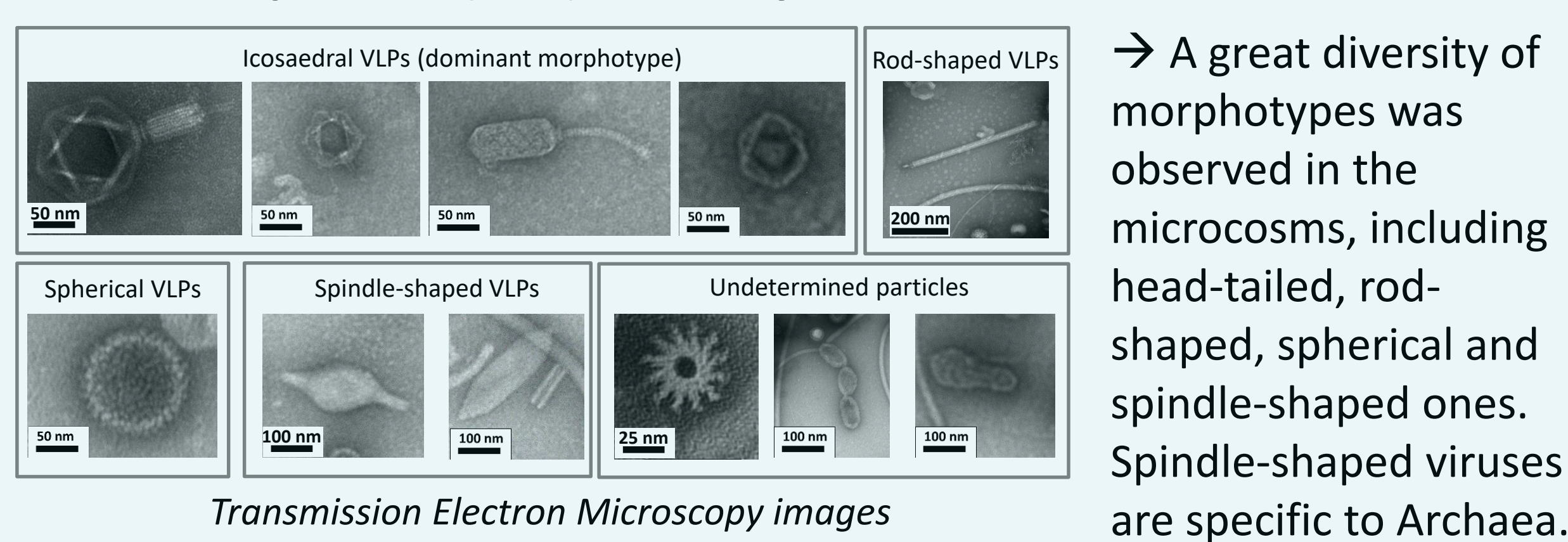
SIP and microbial community composition (16S metabarcoding)



Examples of viral contigs associated to ¹³C-enriched/unenriched methanogens



Virus-like particle (VLP) diversity



Conclusions

- ✓ Significantly expands the knowledge on the diversity of viruses of methanogens (one new caudovirus family, two putative new families of spindle-shaped viruses)
- ✓ Reinforces the notion of wide environmental and phylogenetic distribution of spindle-shaped archaeal viruses
- ✓ Work recently published: Ngo *et al*, *Environmental microbiology*, 2022, 1–16

Perspectives

- Original approach that can be applied to virtually any type of microbial community
- and coupled with other experimental methods for host identification (e.g. PhageFISH, epicPCR, ...).

References

- Sullivan MB, *et al*. Viral ecology comes of age. *Environmental Microbiology Reports* 2016
- Calusinska M, *et al*. Analysis of dsDNA and RNA viromes in methanogenic digesters reveals novel viral genetic diversity. *Environmental Microbiology* 2015
- CRISPRCasdb spacer: https://crisprcasdb.inrae.fr/Home/DownloadFile?filename=spacer_34.zip
- Galez C, *et al*. WISH: who is the host? Predicting prokaryotic hosts from metagenomic phage contigs. *Bioinformatics* 2017