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► 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-04359643>

Submitted on 21 Dec 2023

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

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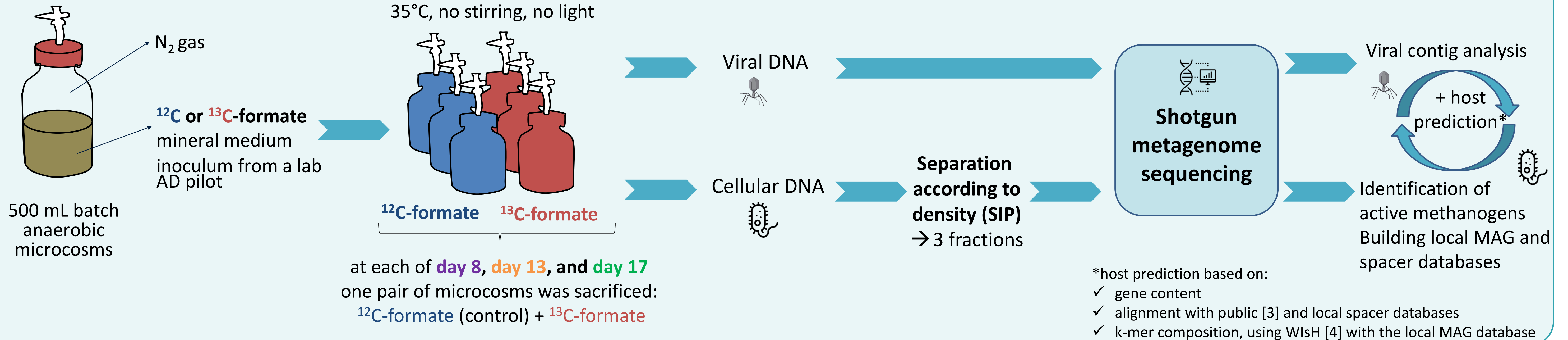
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5. Institut Pasteur, Université de Paris, CNRS UMR6047, Archaeal Virology Unit, F-75015 Paris, France

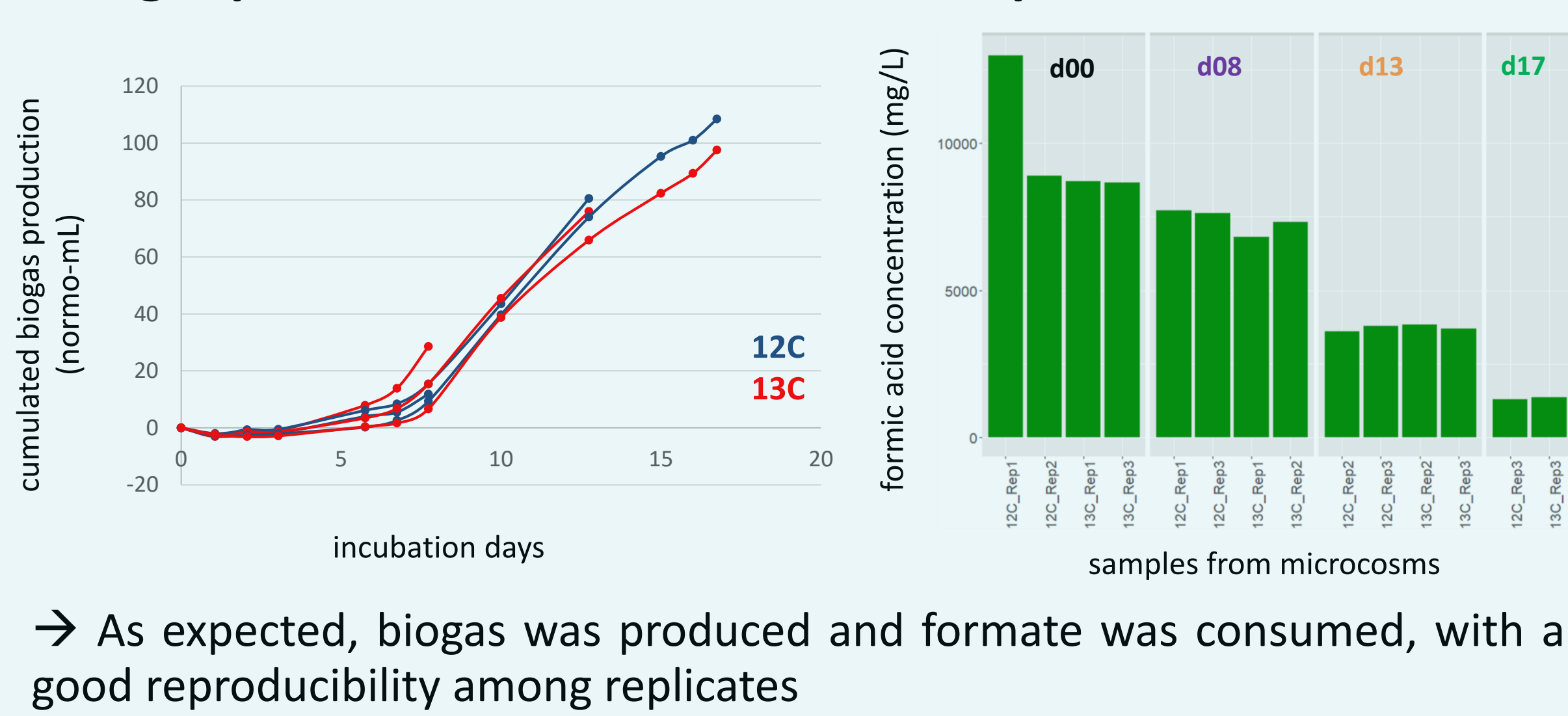
Context

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.

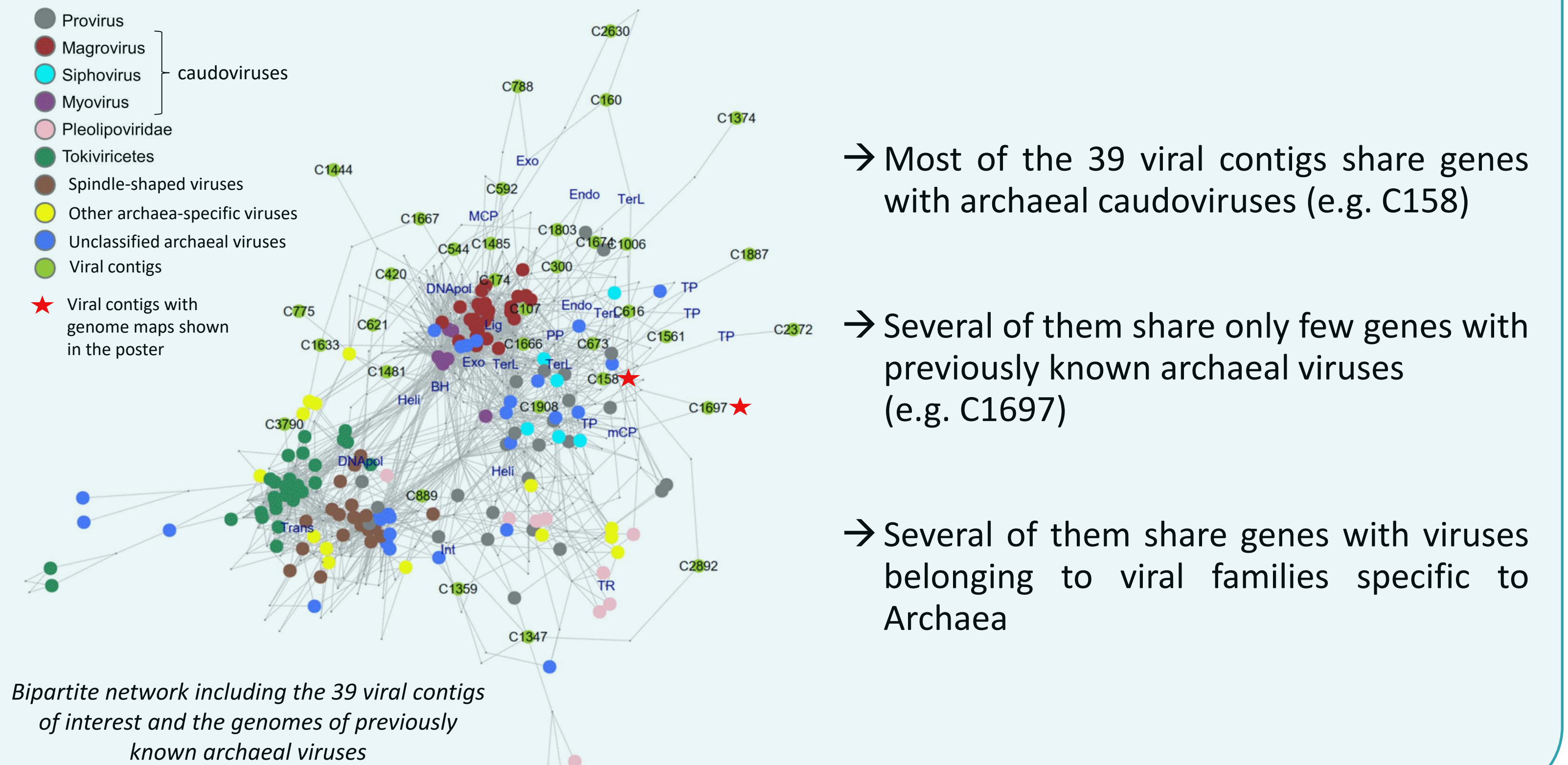
Experimental set-up



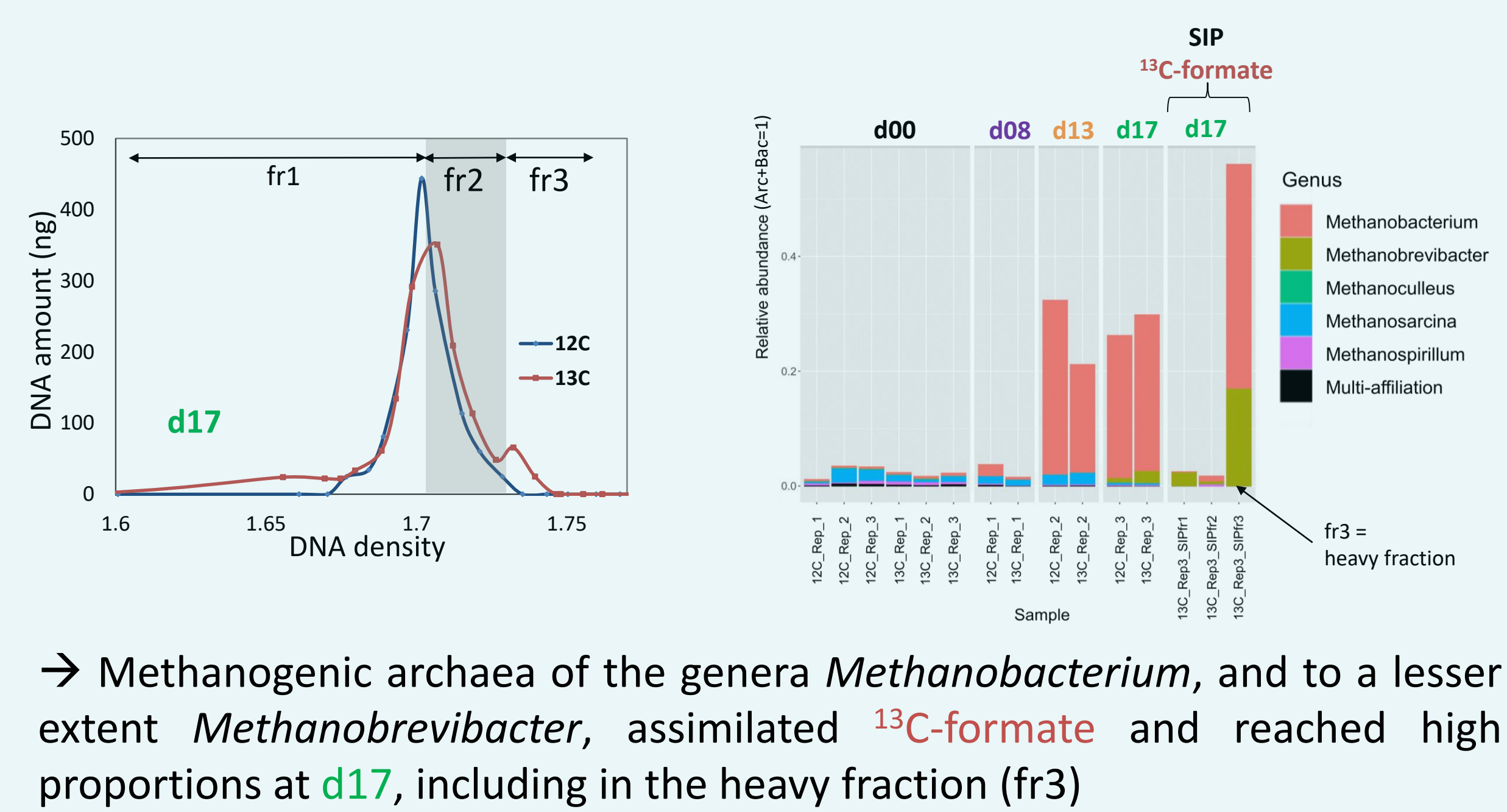
Biogas production and formate consumption



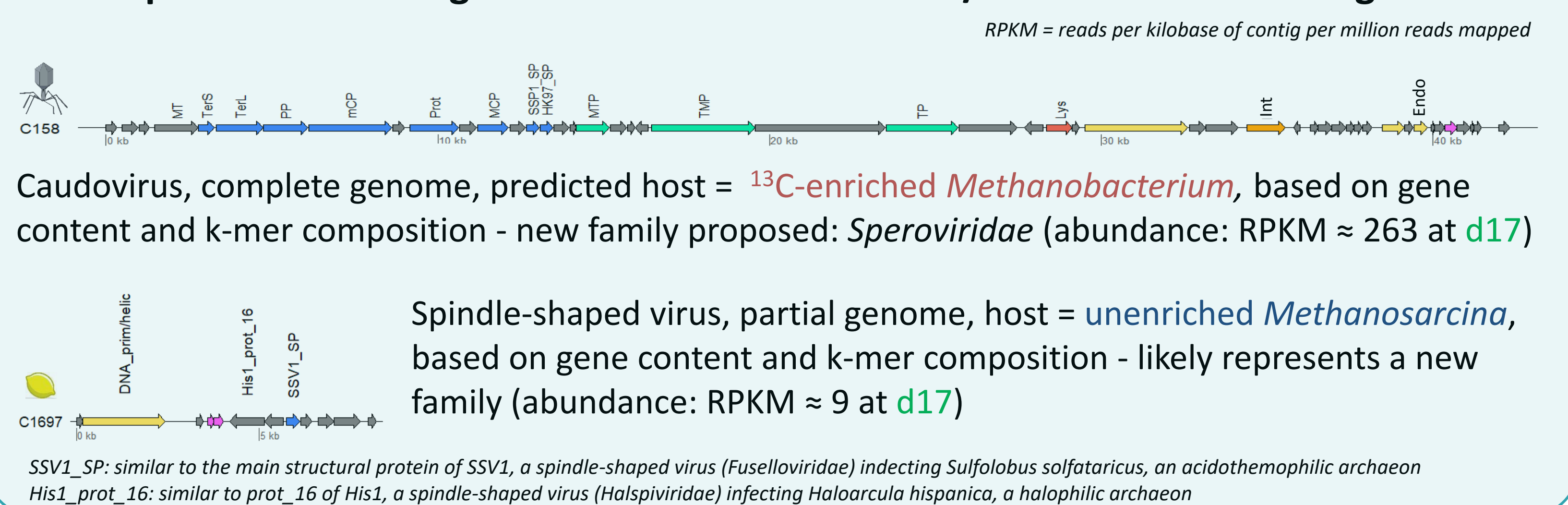
Bipartite network of 39 viral contigs predicted to have an archaeal host



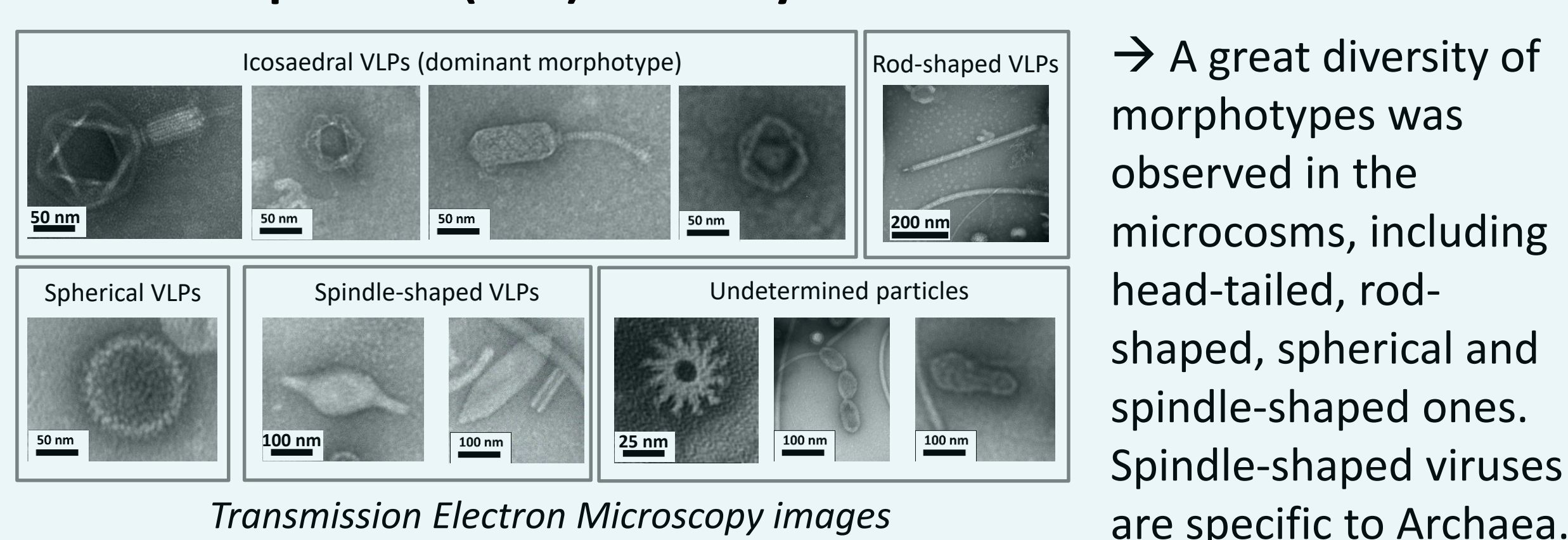
SIP and microbial community composition (16S metabarcoding)



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, ...).

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