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

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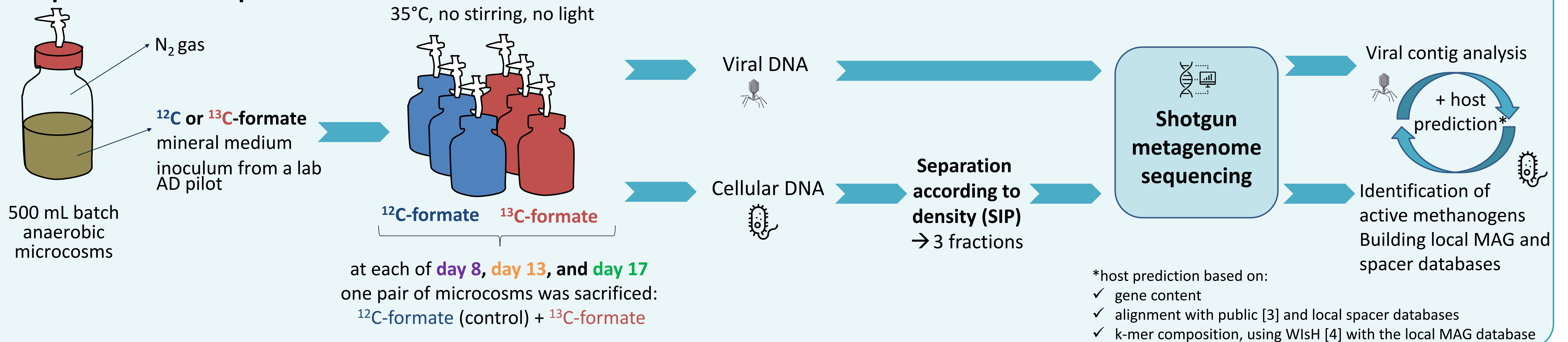
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5. Institut Pasteur, Université de Paris, CNRS UMR6047, Archaeal Virology Unit, F-75015 Paris, France

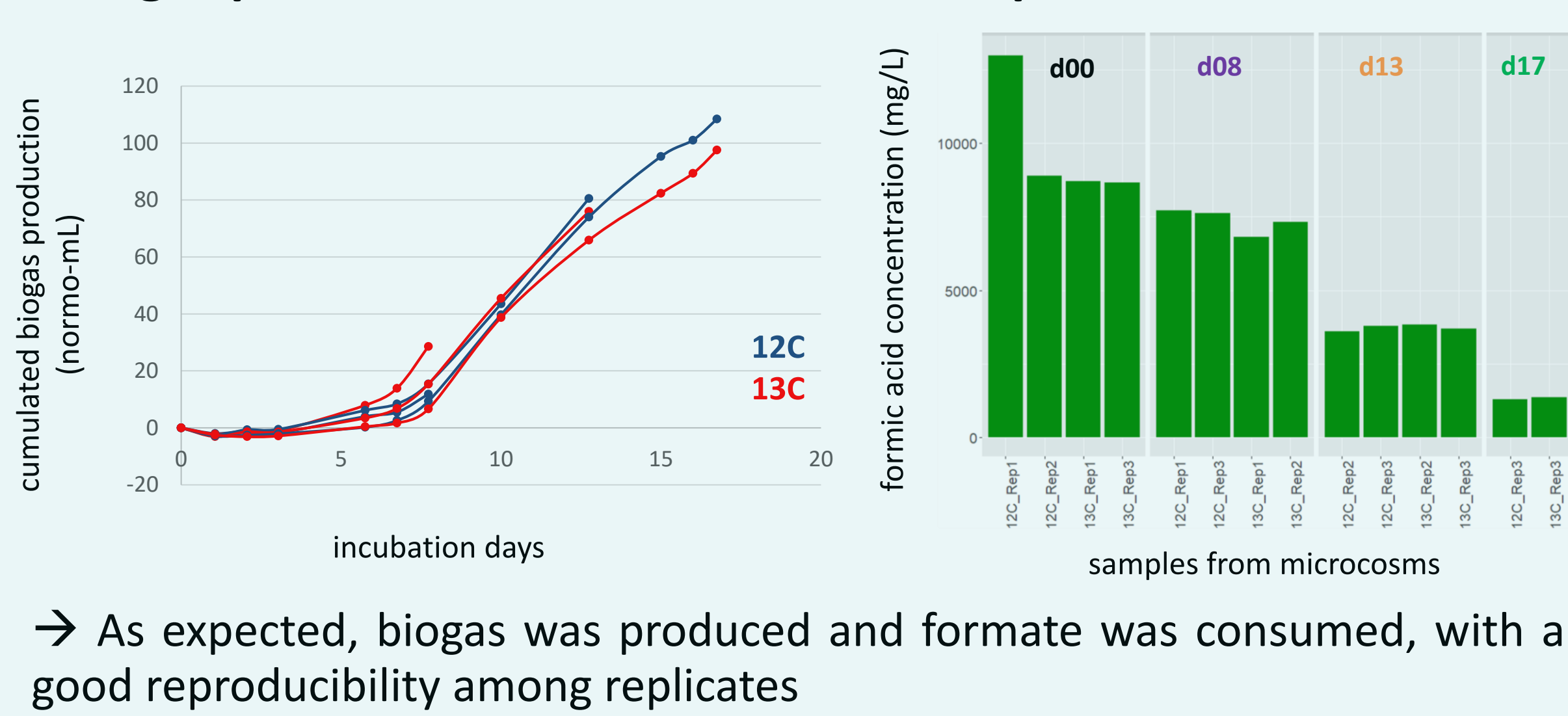
Context

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.

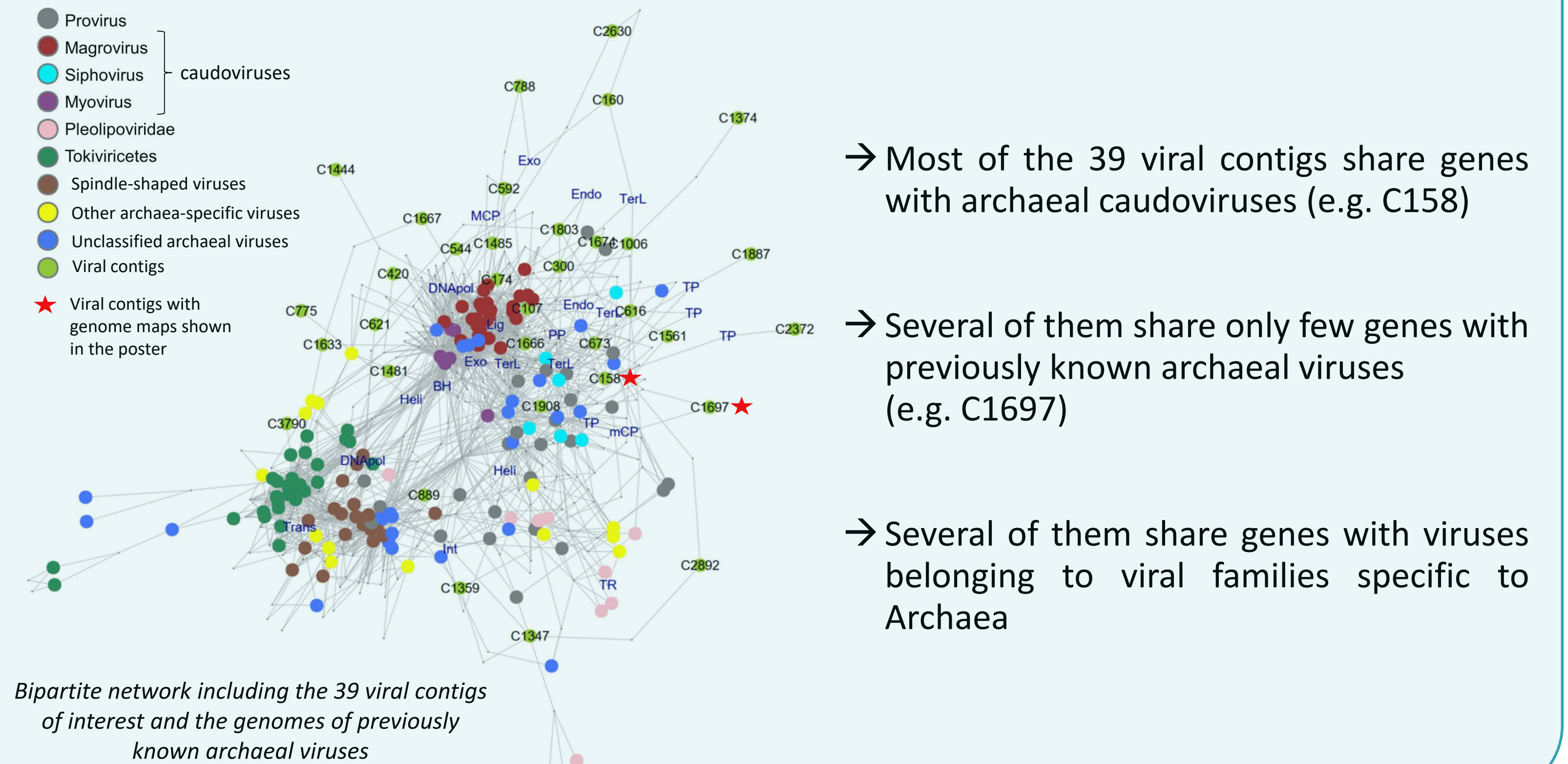
Experimental set-up



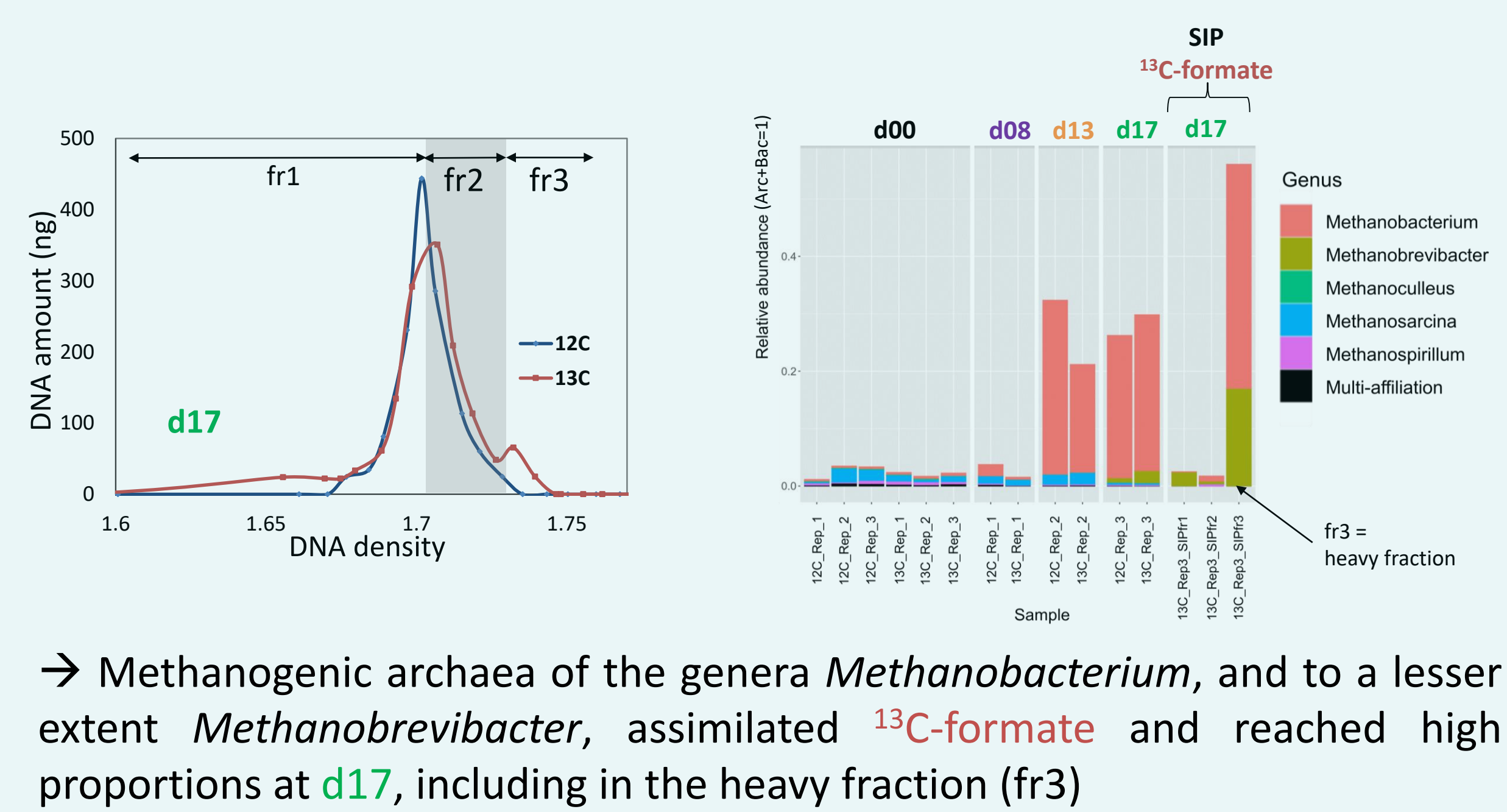
Biogas production and formate consumption



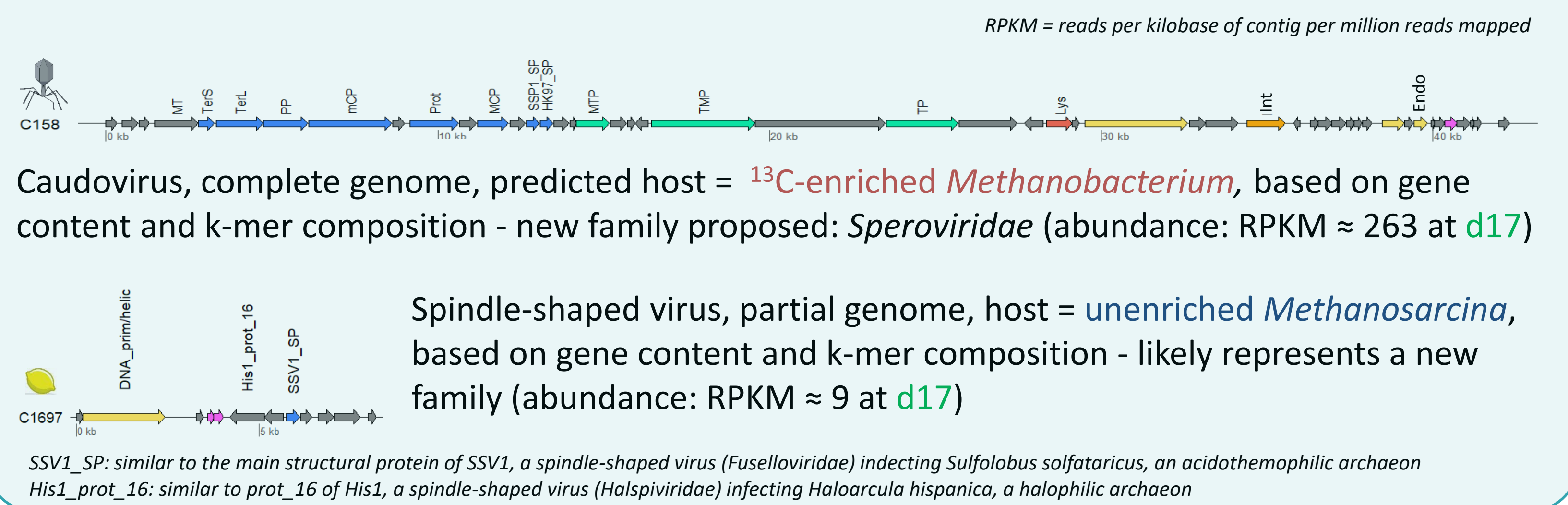
Bipartite network of 39 viral contigs predicted to have an archaeal host



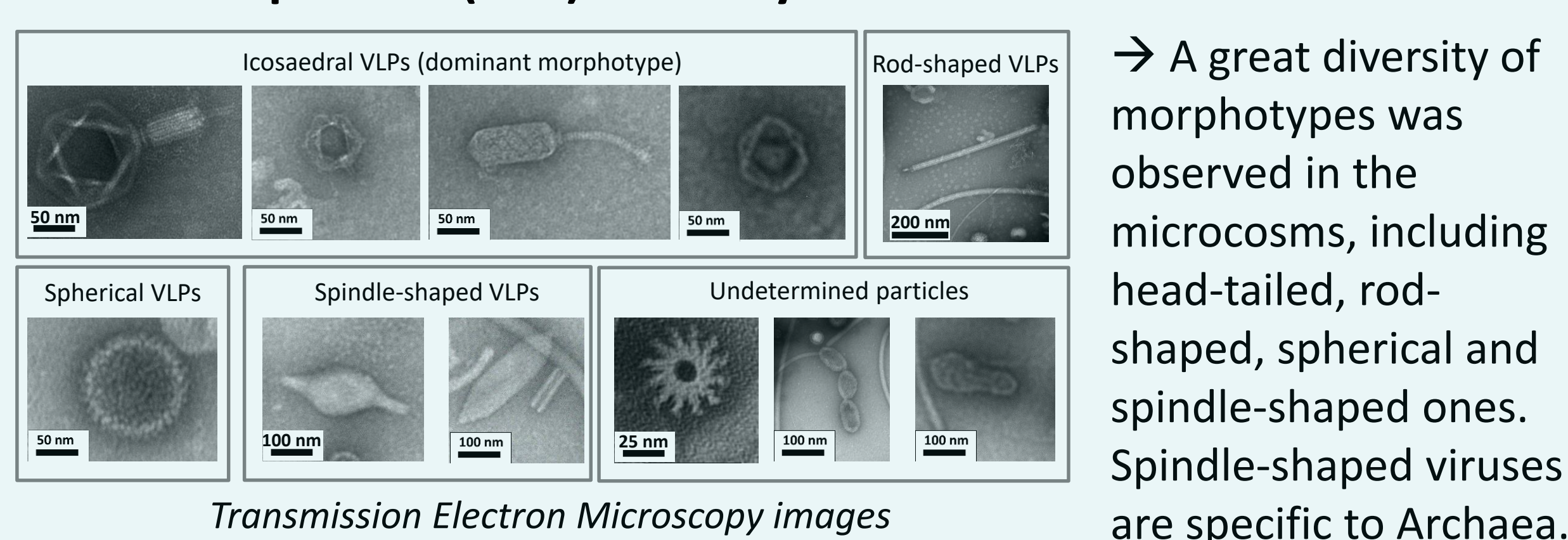
SIP and microbial community composition (16S metabarcoding)



Examples of viral contigs associated to ^{13}C -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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