

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

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



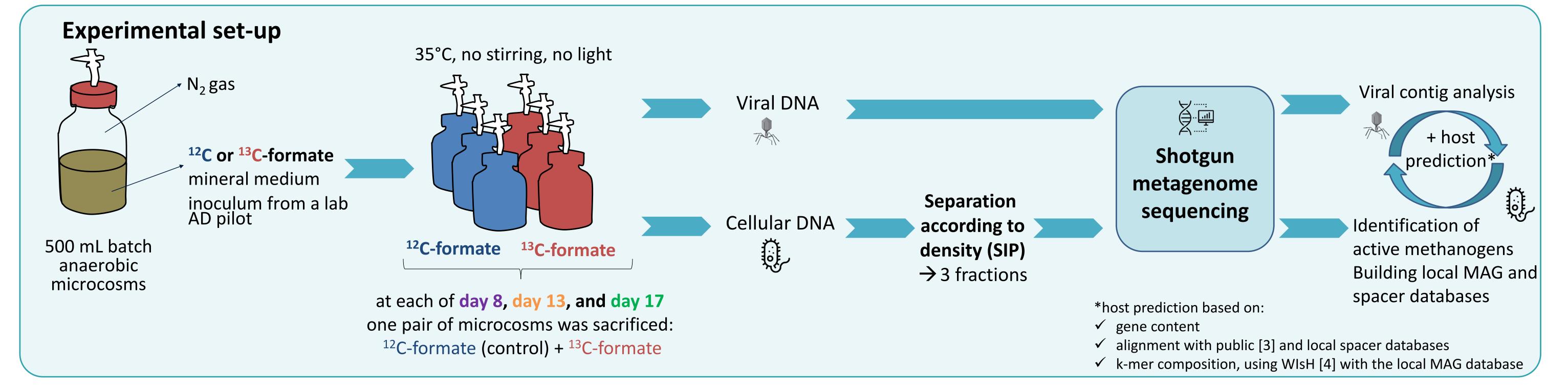
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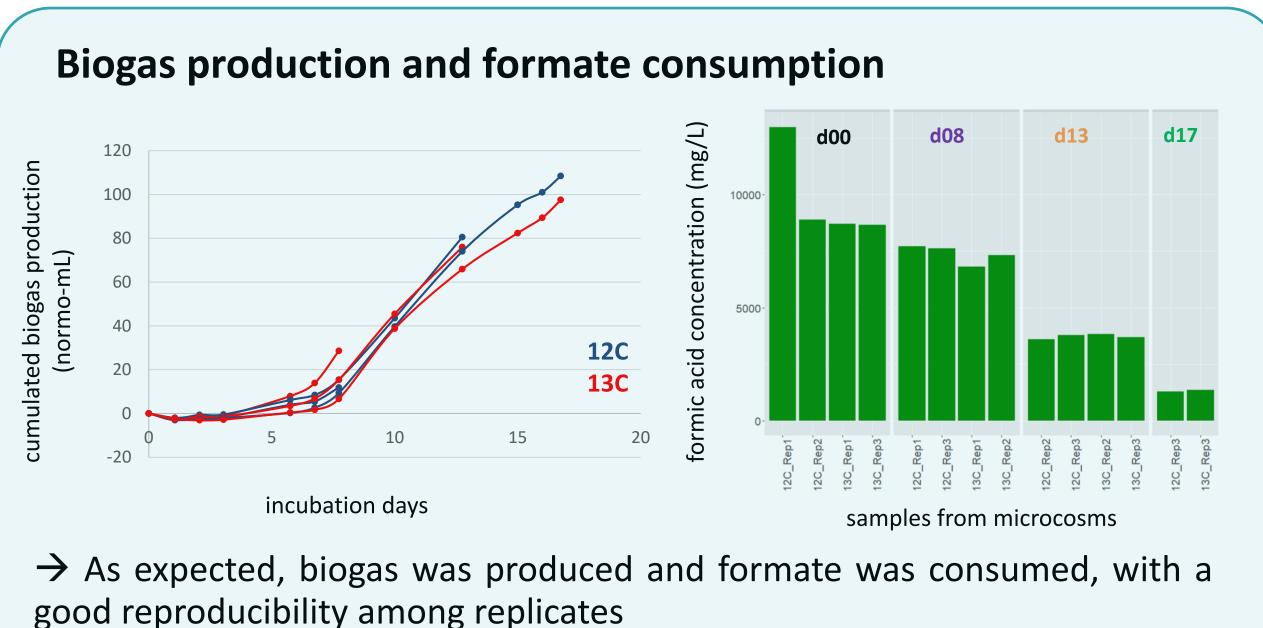
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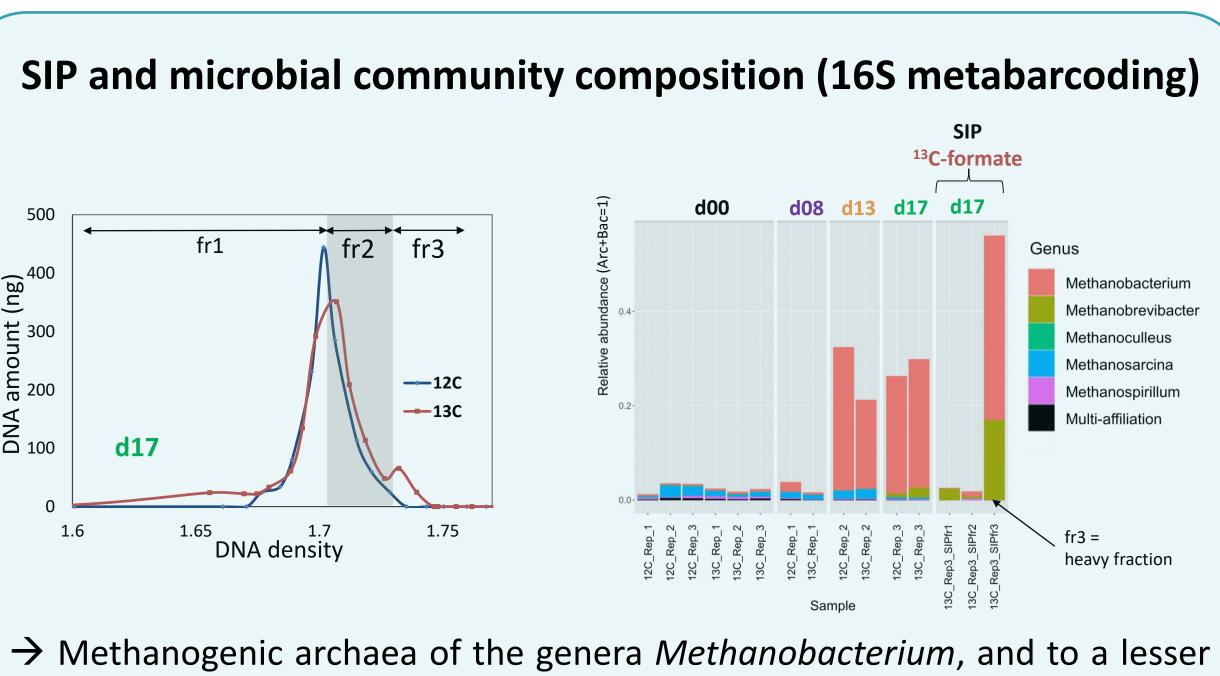
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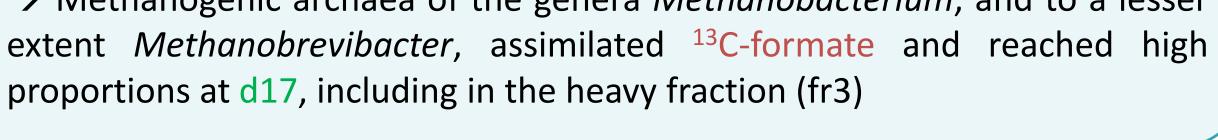
Context

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. 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.







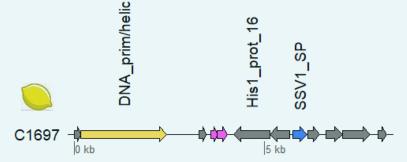


Bipartite network of 39 viral contigs predicted to have an archaeal host caudoviruses Siphovirus Myovirus → Most of the 39 viral contigs share genes with archaeal caudoviruses (e.g. C158) Other archaea-specific viruses Unclassified archaeal viruses Viral contigs with > Several of them share only few genes with genome maps shown in the poster previously known archaeal viruses (e.g. C1697) → Several of them share genes with viruses belonging to viral families specific to Archaea Bipartite network including the 39 viral contigs of interest and the genomes of previously known archaeal viruses





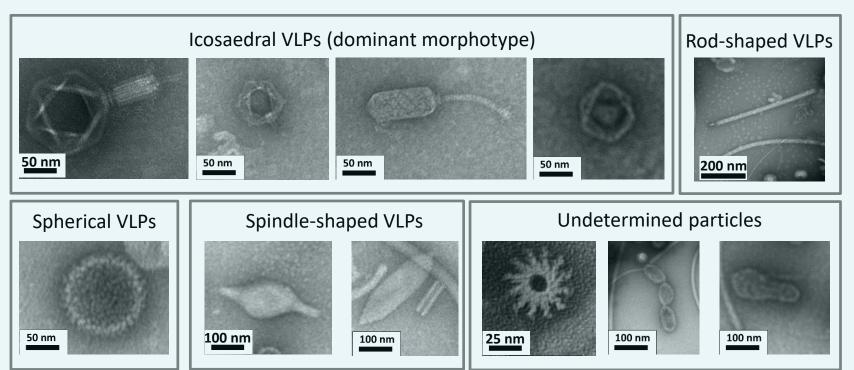
Caudovirus, complete genome, predicted host = 13 C-enriched *Methanobacterium*, based on gene content and k-mer composition - new family proposed: *Speroviridae* (abundance: RPKM \approx 263 at d17)



Spindle-shaped virus, partial genome, host = unenriched *Methanosarcina*, based on gene content and k-mer composition - likely represents a new family (abundance: RPKM \approx 9 at d17)

SSV1_SP: similar to the main structural protein of SSV1, a spindle-shaped virus (Fuselloviridae) indecting Sulfolobus solfataricus, an acidothemophilic archaeon His1_prot_16: similar to prot_16 of His1, a spindle-shaped virus (Halspiviridae) infecting Haloarcula hispanica, a halophilic archaeon

Virus-like particle (VLP) diversity



Transmission Electron Microscopy images

morphotypes was observed in the microcosms, including head-tailed, rod-shaped, spherical and spindle-shaped ones.
Spindle-shaped viruses are specific to Archaea.

→ A great diversity of

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, ...).















- 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.

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