



## Phage–bacteria interactions and the phageome of apricot trees: exploring viral roles in plant health and disease

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- **Date and Time:** Tuesday, November 18, 2025, 15:00 CEST
- **Webinar Link:** Scan the QR to join the mailing list. The webinar link will be sent by email.



**Abstract:** Synthetic pesticides remain central to pest control, but environmental concerns and resistance are driving the search for sustainable alternatives. Insect-associated microbiomes offer untapped potential for developing targeted biological control strategies. Here we investigated the microbiome of the potato leafhopper (*Empoasca fabae*), a major agricultural pest, using metagenomic sequencing of wild specimens from alfalfa fields in southern Québec. After removing host DNA, we assembled 34 metagenome-assembled genomes (MAGs), including 12 high-quality genomes. Key taxa included *Pseudomonas*, *Acinetobacter*, *Symbiopectobacterium*, and several Enterobacteriaceae (*Pantoea*, *Kosakonia*, *Enterobacter*). Functional annotation revealed biosynthetic gene clusters (BGCs) linked to antimicrobial and signaling compounds, particularly in *Pseudomonas*. Enterobacteriaceae were enriched in pathways for sugar metabolism, possibly supporting insect nutrition. We also detected 17 prophages, primarily in Enterobacteriaceae, some with intact structural and regulatory genes, including CI repressors, indicative of active lysogenic cycles. These findings highlight microbial symbionts and phages as promising targets for biocontrol. By manipulating the leafhopper microbiome, disrupting key symbionts, enhancing antagonistic strains, or activating latent phages, it may be possible to reduce pest fitness or vector competence. This work sets the foundation for microbiome-based pest control approaches, contributing to more sustainable agriculture.

### Speaker's Bio:

Dr. Clara Torres-Barceló is a researcher at INRAE's Plant Health Institute Montpellier (PHIM), pioneering the use of bacteriophages to manipulate plant-associated microbial communities for crop protection. Her interdisciplinary approach combines evolutionary biology, community ecology, and molecular microbiology to develop phage-based therapeutics against key agricultural pathogens, including *Pseudomonas syringae*, *Erwinia amylovora* (fire blight), and *Ralstonia solanacearum* (bacterial wilt). Her research journey began with a Ph.D. in evolutionary virology at the University of València, followed by postdoctoral work at Oxford University studying antibiotic resistance evolution. She explored phage-antibiotic interactions at the Institute of Evolutionary Sciences of Montpellier (2013-2015) and developed phage biocontrol applications during fieldwork in Reunion and Mauritius Islands (2018).

