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Poster #60: Antibiotics and diet modulate phage-bacteria interactions in the gut microbiome

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The gut microbiome is vital for human health. While most studies focus on bacteria, roles of gut phages remain poorly understood. Our team aim to decipher how phage-bacteria interactions are shaped by diet and antibiotics, strong modulators of gut bacterial composition. To achieve this, we integrate metagenomics with longitudinal samples of *in-vitro* gut models and clinical cohorts.

Previously, we analyzed the impact of 3rd-generation cephalosporins on a healthy cohort. Beyond a 15–20% reduction in diversity (bacteria and phages), the treatment triggered the dominance of specific bacterial species reported to encode resistance genes. Interestingly, we also detected blooms of virulent phages. We propose that "Kill the Winner"dynamics generate abundant phages that act as perturbation markers. Consistently, we found dominant phages to be significantly enriched in a cohort undergoing chronic antibiotic treatment in comparison to healthy individuals. To explore those ecological dynamics, we will conduct *in-vitro* studies, where sampling frequency and host factors do not limit resolution.

We are now analysing a dataset from a collaborative project using advanced in vitro gut models to study diet effects. As 70-80% of gut bacteria carry prophages, we hypothesize that diet components modulate microbiota and prophage dynamics. Across >400 bacterial species, we identified 197 high-quality prophages (>90% completeness), of which approximately 50% were found active in at least one condition, many showing diet-associated activation patterns.

Collectively, our findings highlight that virulent and temperate gut phages shape microbiota diversity and resilience, paving the way for targeted interventions while underscoring the need for well-designed follow-up studies.

Reference #1

Reference #2

Reference #3

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