Contribution ID: **61** Type: **Poster only**

Poster #61: Towards the human gut microbiome: expanding phage-plasmid detection with tyPPing

Monday, 5 October 2026 21:11 (1 minute)

Phage-plasmids (P-Ps) are temperate phages that replicate as plasmids during lysogeny while producing infectious virions upon induction. They are widespread and often carry important accessory functions, including virulence factors and antibiotic resistance genes. However, existing computational some tools define them often either as phages or plasmids, limiting our understanding of their diversity and ecological roles.

To address this, we previously developed tyPPing [1], a rapid and accurate pipeline for detecting distinct P-P types (e.g. P1, N15, SSU5) in both complete and draft genomes. tyPPing uses curated protein profiles, conservation patterns, and size ranges to predict P-Ps with confidence scores ranging from low-to-high. Moreover, we demonstrated experimentally that high confidence matches correspond to functional phages.

Nonetheless, despite being capable to detect P-Ps infecting clinically relevant pathogens (predominantly Enterobacteriaceae), tyPPing has been limited in detecting P-Ps in other environments, such as the human gut. Phages, and especially prophages, are increasingly recognized as shapers of the bacterial landscape in the gut microbiome. We therefore sought to extend tyPPing's detection range, and screened gut phage databases for P-Ps. We identified >1400 confident matches accounting for 2.6% of high-quality sequences (up to 8.4% when considering all matches). This high prevalence suggests a significant ecological function for P-Ps in the gut. Collectively, through the development of tyPPing 2.0, we aim to further elucidate the diversity and functions of P-Ps.

Reference #1

Ilchenko K, Bonnin RA, Rocha EPC, Pfeifer E. Efficient detection and typing of phage-plasmids. mBio. 2026

Reference #2

Reference #3

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Session Classification: Poster-Session