



## Editorial

# Unveiling the gut virome in human health and diseases

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Due to the advances in high-throughput sequencing technologies, the gut virome is increasingly being perceived as one important component of the gut microbiome, where the number of viral biological entities is believed to far outcompetes that of the bacterial populations [1,2]. The human virome are primarily composed of bacteriophages, animal-cell viruses, endogenous retroviruses and viruses causing persistent and latent infections. Collectively they contains a more diverse genetic entity than the gut bacteria [3,4]. While the composition of them in the gut is precipitately being revealed, their roles in human health remain largely unexplored. It is undeniable that certain gut viruses are deleterious to human health. Interestingly, enteric viruses however, in some cases, can recapitulate the beneficial effects of commensal bacteria through different mechanisms, including modulating the innate and adaptive immunity of the host [5-7].

A healthy human gut virome are predominated by bacteriophages, temperate dsDNA *Caudovirales* and ssDNA *Microviridae* that latently infect their bacterial hosts and when under stress generate progenies that may infect and kill other bacteria [8-11]. In the absence of disease, gut bacteriophage exhibit significant diversity between individuals and are temporally stable [8,10]. Bacteriophages can adhere to host mucus providing a non-host-derived immunity, keeping gut bacteria in check [12]. Fecal microbiota transplantation (FMT) in *Clostridium difficile* infection has demonstrated that when more phage taxa were transferred from donor to recipient, a favourable treatment outcome was observed, and that donor fecal bacteriophage richness may be influential to treatment response [13], indicating the significance of gut phageome in human health. In addition, people are now realizing new therapeutics strategies complementary to antibiotics, using phages, though the results are still staggering [14].

A number of studies have shown gut viral dysbiosis in diseases [2,15,16], particularly bacteriophages. Nonetheless, it remains unknown disease-specific alterations in the gut virome in a vast array of diseases. Alterations in bacteriophage composition might have impact on the bacterial microbiota ecology. Bacteriophages are primary drivers of bacterial fitness and diversity in different ecosystems [17]. Lysis of bacteria is associated with a release of lipids, nucleic acids, and proteins that serve as pathogen-associated molecular patterns (PAMPs) that trigger inflammatory responses to induce cytokines, cellular infiltration, and tissue damage. The gut microbiome are sensitive to bacteriophage invasion, leading to changes in the abundance of specific intestinal bacterial species [18]. In the gastrointestinal tract, bacteriophages are responsible for the horizontal transfer of genetic elements among bacterial populations, including those for antibiotic resistance and disease pathogenesis [18-20].

Human virome evolve rapidly due to varying conditions and stresses conferred by both the host and the environment [3,8,21-23]. Currently, we know little about the functions and roles of gut virobiota in human health and diseases, further experimental explorations of interactions of virobiota-host and virobiota-other components of the gut microbiota are warranted. Such studies hold the promise of yielding insightful understandings on the complex relationships between human physiology and the microbial communities, and hence lay the basis for devising new strategies for improving human health.

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