Previously unknown phages discovered in whole-community human gut metagenomes

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Video Byte

Keywords: phage, bacteriophage, dsDNA, gut microbiome, gut, Microbiome, taxonomy, sequence assembly, Caudovirales

Posted Date: October 14th, 2021

DOI: <https://doi.org/10.21203/rs.3.rs-968297/v1>

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Abstract

Our gut microbiomes are rich communities of bacteria, archaea, and viruses that play critical roles in our health. But although bacteria and archaea in the gut are well-characterized, the gut virome is less understood. A recent study sought to better understand a specific component of the gut virome. Double-stranded DNA bacteriophages (dsDNA phages) – viruses that infect bacteria – play pivotal roles in structuring the human gut microbiome. Using a new multilevel framework for taxonomic classification of viruses, researchers searched human gut metagenomes for phage hallmark genes. They identified 3,738 apparently complete phage genomes, representing 451 putative genera. Several of the genera were new, only distantly related to previously identified phages. Two of the candidate families – “Flandersviridae” and “Quimbyviridae” – included common members of the gut virome that infect ubiquitous gut bacteria, while the third family, “Gratiaviridae,” comprised less abundant phages. Comparative genomic analysis of the three families revealed unique functional features, including diversity generation, lipid biosynthesis, and host cell wall modification, and hundreds of the identified phages encoded catalases and iron-sequestering enzymes that could enhance cellular tolerance to reactive oxygen species. These results will help to facilitate taxonomic and functional classification of human gut viromes.