

Metagenomic analysis of intestinal mucosa revealed an IBD-specific shift in the eukaryotic gut virome composition at early stages of gut inflammation.

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Disclosure of Conflicts of Interest:

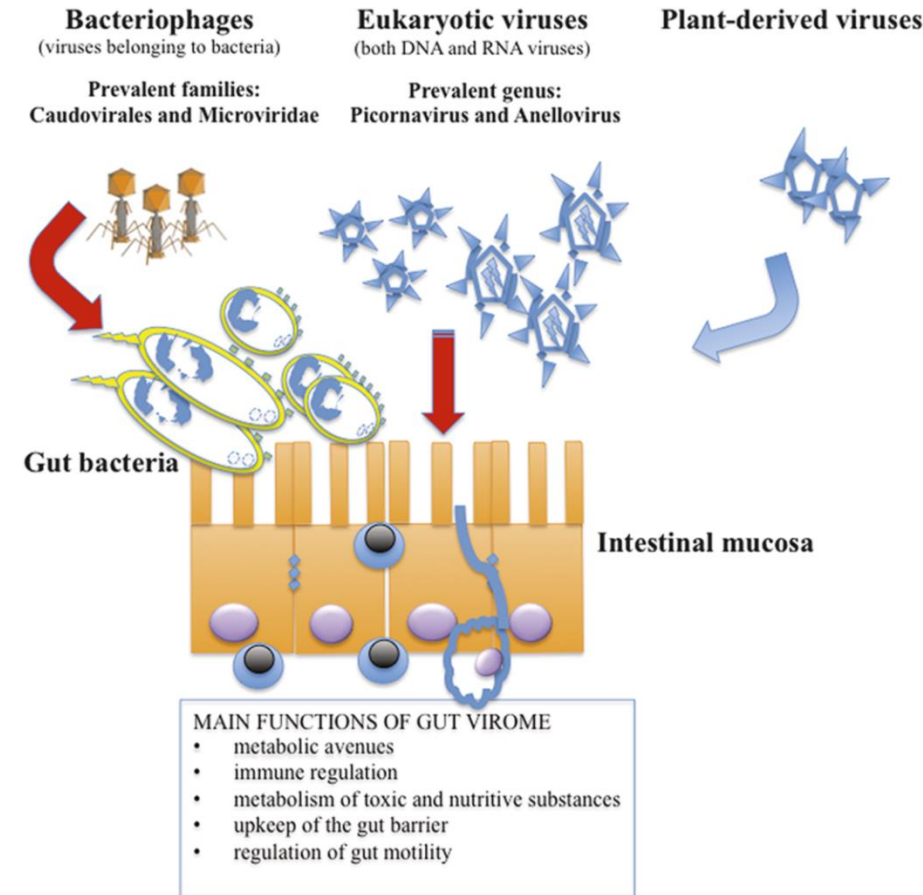
Conflict of interest:

The author has nothing to disclose

Background

- The human gut microbiota is made of bacteria and viruses.
- Intestinal communities of viruses compose the **human gut virome**.

May viral infections underlie IBD pathogenesis?



Study design

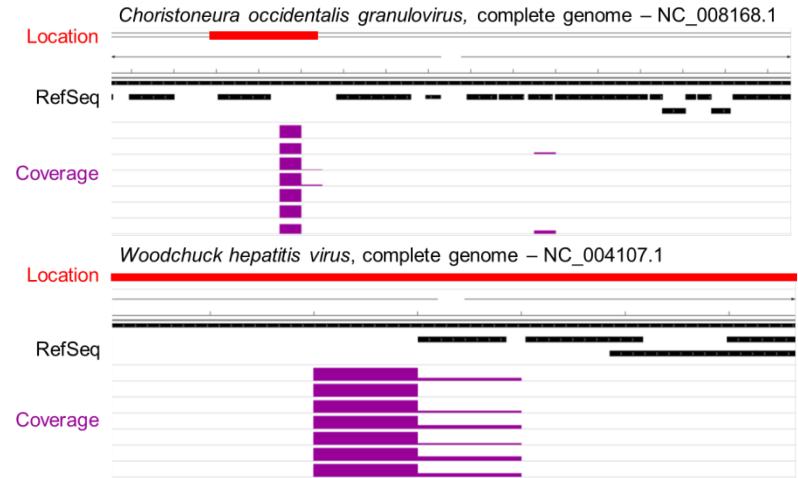
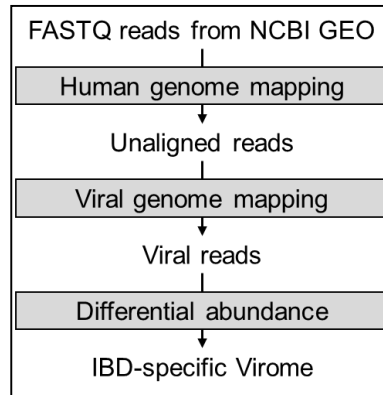
1. RNA-sequencing data mining from publicly available datasets (NCBI GEO):
 - patients with **treatment-naive, early-diagnosed** UC, CD and age-matched healthy controls.
 - Young patients (no more than 20 years-old subjects)
2. Metagenomics analysis of RNA-seq reads to identify eukaryotic viral entities in early stage of the disease.

Bioinformatic pipeline

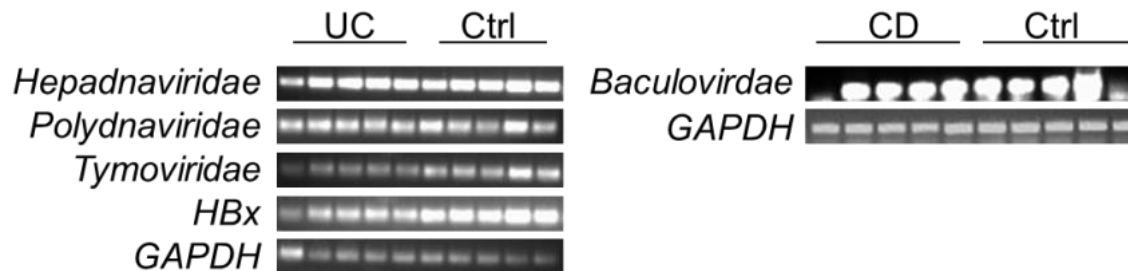
2. Metagenomic analysis

1. GSE5794 dataset

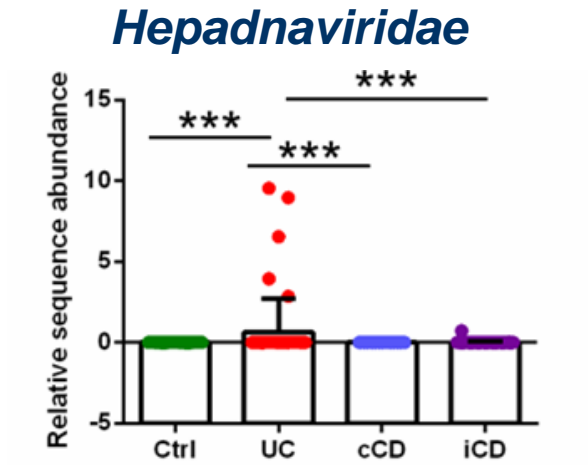
N=101 CD
N= 44 UC
N= 61 Healthy



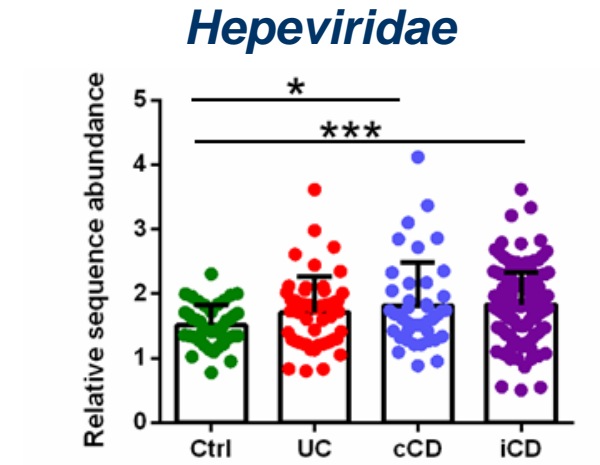
Viral transcripts were detected in IBD mucosa



Metagenomic analysis revealed a specific IBD gut virome composition

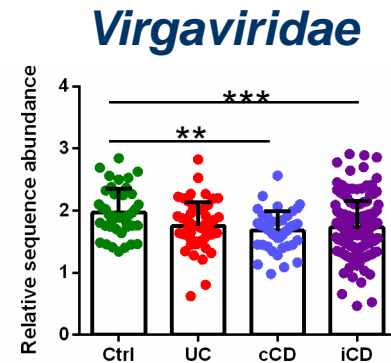
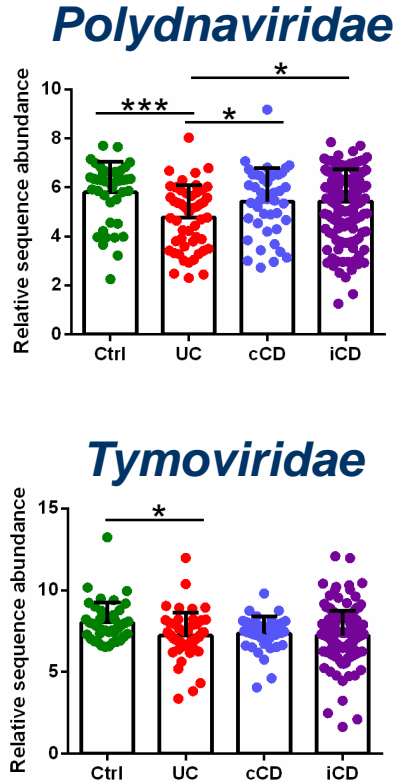


Hepadnaviridae family specifically colonizes UC gut mucosa



Hepeviridae family specifically colonizes CD gut mucosa

Metagenomic analysis revealed a specific IBD gut virome composition



Virgaviridae were reduced in CD gut mucosa

Polydnaviridae and *Tymoviridae* were reduced in UC gut mucosa

$P^{***} < 0.005$
 $p^{**} < 0.01$
 $P^* < 0.05$

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