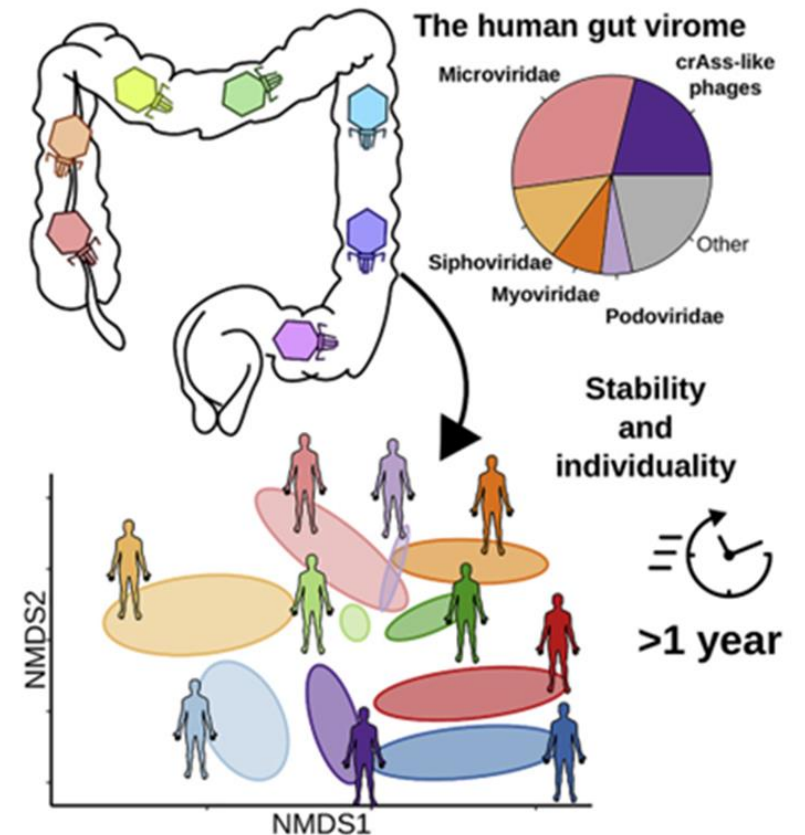


Case Study: Characterising the healthy human virome

One of the main challenges in microbiome research is to identify those microbial species, strains or genes that define a healthy individual. To date scientific research has looked primarily at changes in the bacteriome in health and disease but natural predators of bacteria are their cognate viruses, bacteriophages. Their numbers are thought to be similar to bacteria in the gut so the role of bacteriophages in shaping the microbiota needed to be explored.

Here we wanted to investigate the composition and diversity of the gut virome in a group of healthy individuals. In doing so we could understand healthy baselines and develop robust protocols for future studies exploring the microbiome.



Study Product/Sampling	Faecal Samples were taken monthly over one year
Primary endpoint	Longitudinal profile of faecal virus diversity
Study Duration	1 year

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Scientific outcomes

The human gut virome is highly individual and stable for up to 1 year. A stable and predominant fraction of viruses persistent in the gut and are personal to each individual. In fact only two viruses were shared among 5 or more people. Persistent bacteriophages can be linked to highly predominant groups of gut bacteria. Two families of bacteriophages, CrAss-like and Microviridae predominate and persist in the gut, something that may not have been predicted given their mode of replication.

Other outputs

Computational (bioinformatic) tools specific for virome research and analysis were developed as a result of this study. Experimental procedures in the lab were defined and created to allow better characterisation of faecal viruses.

Publication Title: The Human Gut Virome Is Highly Diverse, Stable, and Individual Specific

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The Clinical Research Ethics Committee approved the study related to this work which was entitled APC055 - Exploring the Gut Virome and Bacteriophages in Inflammatory Bowel Disease.”

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