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Poster #59: Sulfate-Reducing Bacteria and Their Viral Fingerprints in the Gut Microbiome: Uncovering Adaptation and Disease Markers in Inflammatory Bowel Disease

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Inflammatory bowel diseases (IBD) arise from complex interactions between host genetics, immune dysregulation, and the gut microbiome. Sulfate-reducing bacteria, particularly the Desulfovibrionaceae family, are opportunistic pathobionts that are enriched in patients with IBD and contribute to epithelial damage by producing hydrogen sulfide and other metabolites. Like most gut microbes, these bacteria originate from environmental habitats and subsequently colonized and adapted to the gut. A critical open question is how these bacteria rewired their genetic and metabolic pathways to persist in such a complex and competitive ecosystem.

This project will use comparative genomics to investigate the evolution, gut adaptation, and pathogenic potential of Desulfovibrionaceae found within the human gut. Initially, we analysed publicly available genomes of the genus Desulfovibrio using an established bioinformatics pipeline to detect, filter, taxonomically classify, and characterise their prophages. The analysis showed numerous host-associated prophage clusters, whereby human-derived Desulfovibrio genomes contain more, generally shorter, prophages than environmental isolates. This indicates niche-specific pressures that select for diverse phage-host combinations.

To improve our understanding of bacterial adaptation and to support the development of novel diagnostic markers and therapeutic strategies for IBD, we will extend this analysis to the Desulfovibrionaceae family. We will focus on genetic differences and similarities between bacterial isolates from IBD patients and healthy controls and aim to identify prophage-associated signatures linked to IBD as well as to characterise their contribution to the gut environment by analysing the transcriptome, proteome, and metabolome.

Reference #1

Reference #2

Reference #3

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