Gut virome and bacteriome of captive non-human primate species

Aonghus Lavelle[1,2], Cillean Thorne[3], Bernadette Crowley[3], Dave O'Leary[3], Sandra Molloy[4], Liam J. Fanning[1,3]

1.APC Microbiome Ireland, University College Cork, Ireland
2.Department of Anatomy & Neuroscience, University College Cork, Ireland
3.Department of Medicine, University College Cork, Ireland
4.Dublin Zoo, Phoenix park, Dublin 8, Ireland

Introduction

Non-human primates (NHP) are our closest genetic relatives and can provide insights into ancestral microbiomes and the impact of industrialisation and diet on the gut microbiome. While research has focused on the faecal bacteriome of NHPs, little is known about the structure of the faecal virome and how it relates to the bacteriome. We aimed to study the faecal bacteriome and virome of captive NHPs.

Methods

Faecal samples were retrieved from animal housing on a single day in Dublin Zoo. Four NHP species were targeted (Chimpanzees, Gibbons, Gorillas and Orangutans). Bacterial DNA was extracted using a standard approach and processed for amplicon sequencing of the V3-V4 region of the 16S rRNA gene. Following isolation of the virus-like particles (VLPs) from fecal samples with cesium-chloride gradient purification, shotgun metagenomics was performed on the virome fraction. Bioinformatic analysis was performed using the dada2 pipeline (bacteriome) and an in-house viral metagenomics pipeline.

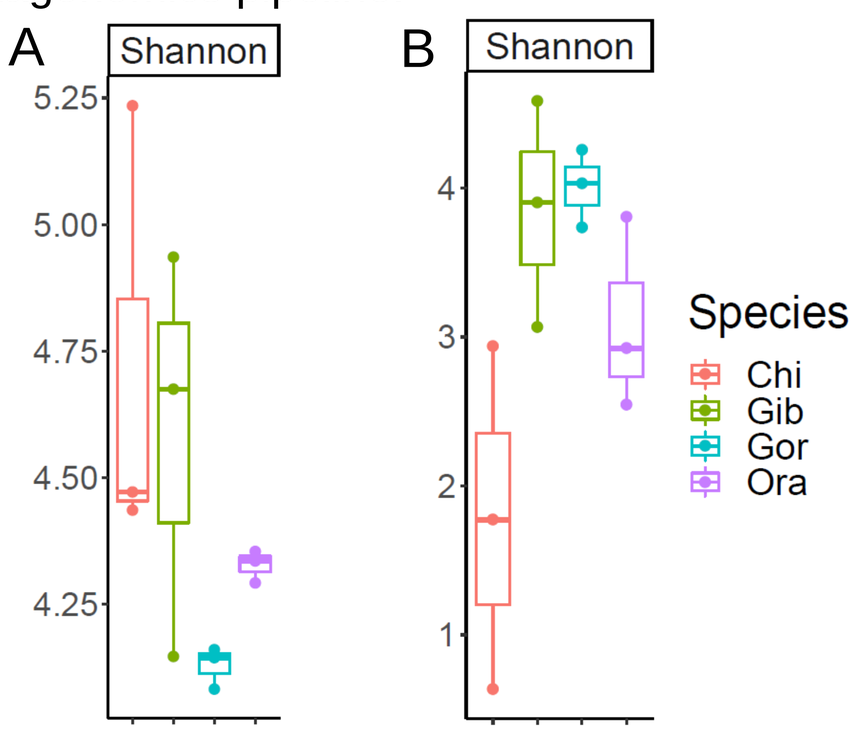
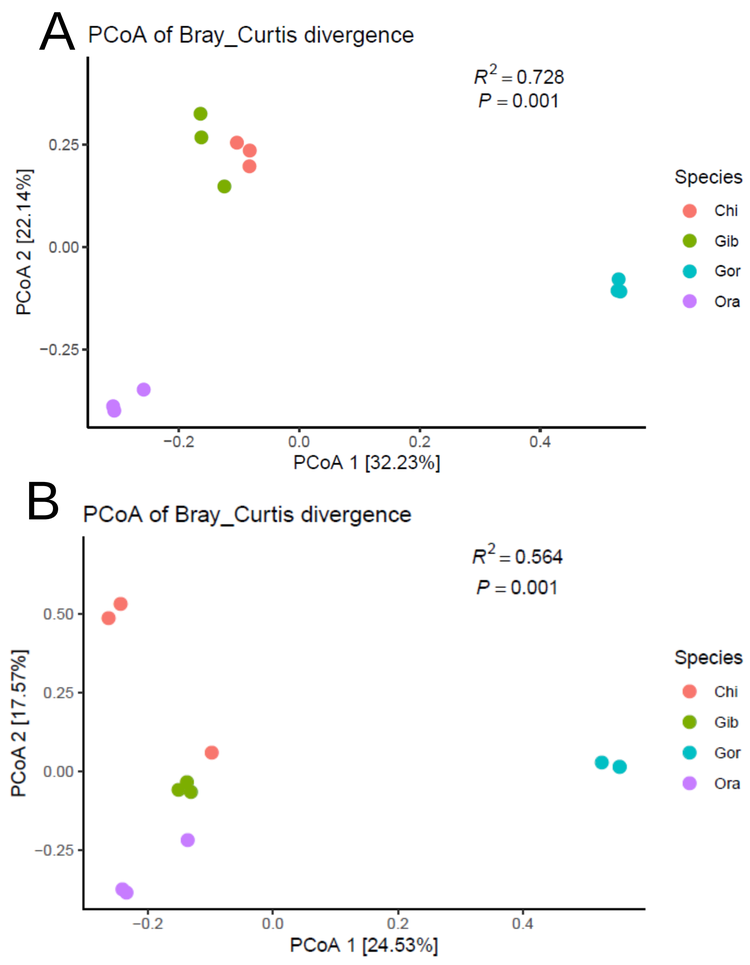


Fig. 1.: Alpha diversity for the faecal bacteriome (A) and virome (B). Virome diversity was lower in Gibbons.

Results

In total, 12 samples were analysed from the 4 different species (3 for each). There was no clear pattern in terms of bacterial diversity across the species, however Chimpanzees tended to have the lowest overall virome diversity.



Clear distinctions were evident between species for both the faecal bacteriome (Fig. 2A) and virome (Fig. 2B). While these differences could be due to species effects, it is more likely attributable to housing and diet.

Fig. 2.: Clear separation based on species was evident for both the faecal bacteriome (A) and the faecal virome (B).

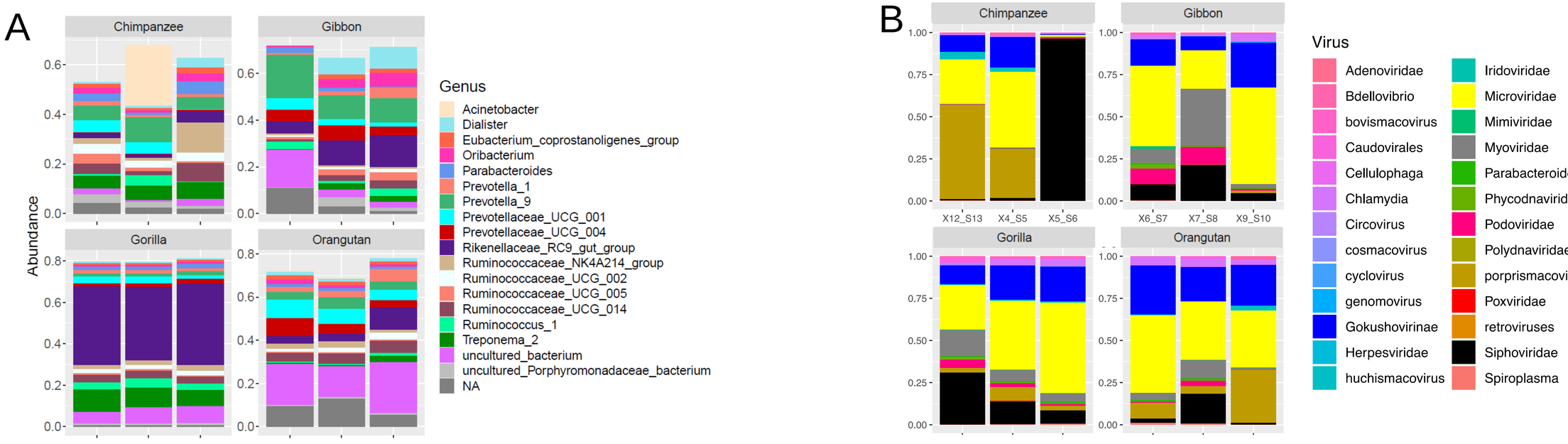


Fig. 3.: Taxonomic analysis suggest overlap with both humans and wild NHPs in terms of bacterial composition (A). In contrast, a very small proportion of virome reads could be assigned to any taxonomy (B), suggesting poorer representation in virome databases.

Discussion

This study demonstrates that captive NHPs develop an intermediate microbiome configuration between wild NHPs, enriched for enterotypes dominated by *Treponema* sp. and *Prevotella* sp. and human microbiomes, dominated by *Ruminococcaceae*. Most phage detected were not annotated, suggesting a large degree of novelty in the NHP phageome. Expanding this work to assess the impact of captivity and changes in mucosal immunity will be important.

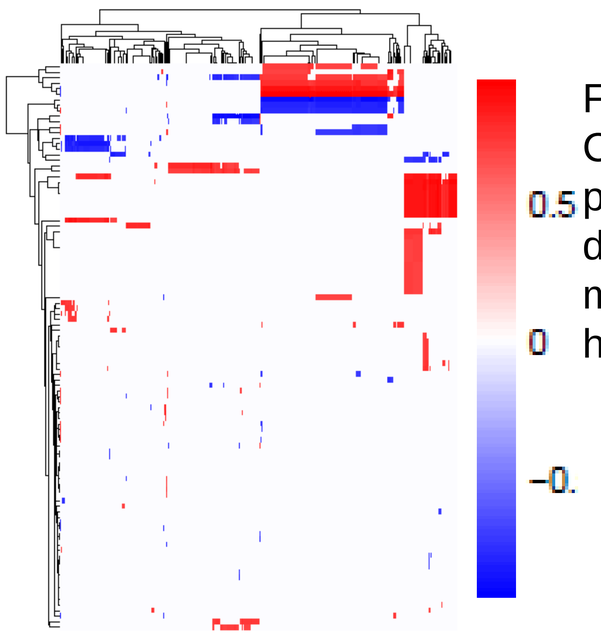


Fig. 4.: Correlations between phage and their host were detected although these may be confounded by housing

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