Characterization of the gut virome of South African infants using a viral metagenomics approach

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Background

A huge knowledge gap exists about the composition and diversity of the viruses colonizing the gastrointestinal tract of asymptomatic humans. A major drawback for this poor characterization of the human gut virome is due to lack of optimised methods for viral enrichment. A metagenomic study was performed to characterize and compare the enteric RNA virome of infants from South Africa.

Methodology

Faecal samples (n=12) were collected from four healthy infants at three different time points per participant (approximately 6, 24 and 36 weeks). Samples were enriched for viruses using the NetoVIR protocol. Sequencing was performed on an Illumina MiSeq platform (2x251 bp pairedend reads). Using an in-house analysis pipeline, quality-filtered reads were de novo assembled on MetaSPAdes. Contig annotation was done by BLAST search against the NCBI non-redundant database using DIAMOND.

Results

Diverse enteric viruses were detected in the faecal samples. Majority of the viral contigs belonged to Picornaviridae, including parechoviruses, echoviruses, coxsackieviruses, enteroviruses and polioviruses. Rotaviruses (belonging to Reoviridae) were present in 12 samples (100%). Since the study subjects were asymptomatic, the detection of rotavirus is thought to be derived from vaccine strains since it coincides with vaccination. Although wild-type polioviruses have been eradicated in most countries, their detection in this study could be associated with shedding of OPV. Astroviridae and Caliciviridae were the least predominant families. Few sequences matched to plant viruses which were likely introduced through diet. Some viruses of animal origin were also detected in two participants, suggesting potential interspecies transmission.

Conclusion

This study has lent credence to the practicability of viral metagenomics in human virome characterization, providing insights into viral community structure and diversity of enteric viruses.