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GUT MICROBIOTA

The gut virome and bacterial microbiome—the early years

The human gut microbiota in infancy is highly dynamic, with marked changes in the composition of bacteria, viruses and bacteriophages with age, according to new data published in *Nature Medicine.*

The gut microbiota has been well-studied, but research has largely focused on gut bacteria with evidence on the gut virome only just emerging. "The bacterial microbiome is established early in life and alterations are associated with a variety of human diseases," notes author Lori Holtz. "Our understanding of the human virome lags behind."

Holtz and colleagues collected stool samples from four healthy twin pairs (one monozygotic twin pair, three dizygotic twin pairs) at six time points from birth to 2 years of age (0, 3, 6, 12, 18 and 24 months). Total nucleic acid was extracted from the stool samples and two complementary amplification methods (multiple displacement amplification and sequence-independent DNA and RNA amplification) were performed before sequencing to detect both DNA and RNA viruses; bacterial 16S ribosomal RNA gene sequencing was also performed.

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The researchers found that, from birth, the eukaryotic virome and bacterial microbiota expanded over the next 2 years becoming richer with increasing diversity in different microorganisms. The most commonly detected viruses included enterovirus, parechovirus and anellovirus, and, as was expected, the predominant bacterial microflora shifted from Firmicutes (at 0 months), to Proteobacteria (at 3 and 6 months), to Bacteriodetes (after 12 months). The opposite trend was observed for bacteriophages, the composition of which contracts and shifts over the same time period (shifting from Caudovirales to predominantly Microviridae).

Also, the virome and gut microbiota was more similar between co-twins than between unrelated infants. The investigators also found evidence that suggests the bacteria–bacteriophage relationship in the infant gut is indeed a predator–prey relationship, consistent with the Lotka-Volterra prey model.

"We hypothesize that bacteriophage diversity is high at birth, but the low bacterial population cannot support this," explains Holtz. "So, the bacteriophage population contracts because there is not the proper host". Further work will expand the study to include a larger cohort of infants and to examine the effect of environmental factors (for instance, birth method, antibiotic exposure or diet).

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Original article Lim, E. S. *et al.* Early life dynamics of the human gut virome and bacterial microbiome in infants. *Nat. Med.* doi:10.1038/nm.3950