

MICROBIOMES

Symbionts — in it for the long run

Research into the co-evolutionary history of hominids and their gut bacteria shows that multiple symbiotic associations arose in a common ancestor to all African great apes. Over the past 15 million years, these ancient symbionts have speciated in parallel ('co-speciation') with the nuclear and mitochondrial genomes of humans and African apes.

Communities of gut bacterial symbionts in mammals are necessary for development, immunity and health. Bacterial community profiles are influenced by genetics and evolutionary history, as well as by external factors, such as diet and antibiotics. However, little is known about the evolutionary origins of the bacterial lineages that exist in the human gut, including whether some lineages of gut bacteria have persisted in host hominid lineages over periods of time long enough to permit co-speciation.

To see whether the gut bacteria present in modern-day humans are descended from ancient bacterial symbionts that subsequently co-speciated with hominids, Moeller *et al.* first amplified a region of the DNA gyrase subunit B gene (*gyrB*) from

bacteria present in faecal samples from humans ($n = 16$), chimpanzees ($n = 47$), bonobos ($n = 24$) and gorillas ($n = 24$). This amplicon sequencing approach assays rapidly evolving protein-coding genes in bacterial genomes to profile gut microbiome diversity with high resolution (to enable the comparison of closely related bacterial lineages). Sets of primers were designed to target the *Bifidobacteriaceae*, *Bacteroidaceae* and *Lachnospiraceae* bacterial families, and a phylogenetic analysis was performed.

The *Bifidobacteriaceae* and *Bacteroidaceae* phylogenies of the hominid gut microbiomes closely mirrored the hominid evolutionary tree, although some differences were reported. For example, the team observed *Bacteroidaceae* strain divergence within the chimpanzee host lineage, loss of bacterial lineages from host populations, and a transfer of a *Bifidobacteriaceae* lineage from chimpanzees to gorillas.

Phylogenetic analysis of *Lachnospiraceae*, however, indicated that this bacterial family has been transferred between the hominids a number of times. The team propose that because *Lachnospiraceae* form spores

(and survive for long periods outside of their hosts) they are more easily passed between species.

As hominids evolved from a common ancestor into distinct species, the gut bacteria from this common ancestor evolved into distinct strains within each host; co-diversification and symbiotic associations between hominids and their gut bacteria have existed over hundreds of thousands of generations and across evolutionary timescales. Further work might reveal how far back into vertebrate history this co-diversification actually extends.

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ORIGINAL ARTICLE Moeller, A. H. *et al.*
Cospeciation of gut microbiota with hominids.
Science <http://dx.doi.org/10.1126/science.aaf3951> (2016)

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