

Cospeciation of Gut Microbiota with Hominids

Andrew H. Moeller, Alejandro Caro-Quintero, Deus Mjungu, Alexander V. Georgiev, Elizabeth V. Lonsdorf, Martin N. Muller, Anne E. Pusey, Martine Peeters, Beatrice H. Hahn, Howard Ochman

Adapted by Skyler Hallinan

Introduction

Many types of bacteria have symbiotic relationships with humans. The various species of gut bacteria provide many critical functions, such as the inhibition of pathogens. The community of bacteria in a given individual, the microbiome, is based on diet, geography, and, “host genetics and evolutionary history.” Bacterial communities are formed anew in each the progeny of each generation, and adapt to changes over time within their host. It is unclear if the bacteria and host hominid cospeciate, which is when both groups diverge from an ancestor into two new distinct species in response to each other. Three common gut bacteria families, Bifidobacteriaceae, Bacteroidaceae, and Lachnospiraceae, were investigated for this study. They were from hominid species of humans, gorillas, chimpanzees, and bonobos.

Question

Do lineages of gut bacteria persist within host lineages over time? Specifically, are gut bacteria residing within present-day humans descended from ancestral bacterial symbionts that cospeciated with humans and the African apes?

Methods

- Researchers obtained samples of feces from wild bonobos, gorillas, and chimpanzees from their natural habitats, and samples from humans living in Connecticut, USA.
- Researchers used specific gene tracking software and programs. They used amplicon sequencing, an approach to analyze genetic variation in a genome, to examine strain diversity in the microbiota of the Bifidobacteriaceae, Bacteroidaceae, and Lachnospiraceae bacteria families. They amplified the variable region subunit B gene (gyrB), from the DNA gyrase.
- Primers designed to target one of the three families of the select bacteria families, and relative frequencies were recorded.
- Phylogenetic maximum-likelihood trees, the most likely phylogeny based on the data, were created separately for each family. They were based on the data from aligning sequences through the tool ClustalW, and analyzing nucleotide substitutions.

From left to right, Bifidobacteriaceae, Bacteroidaceae, and Lachnospiraceae that were examined and tested for in fecal samples.

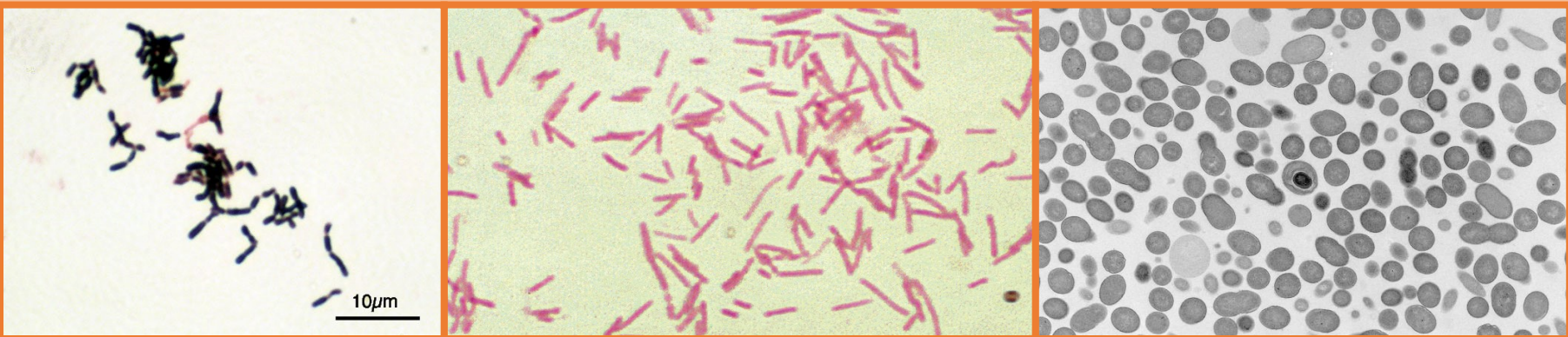


Figure 1

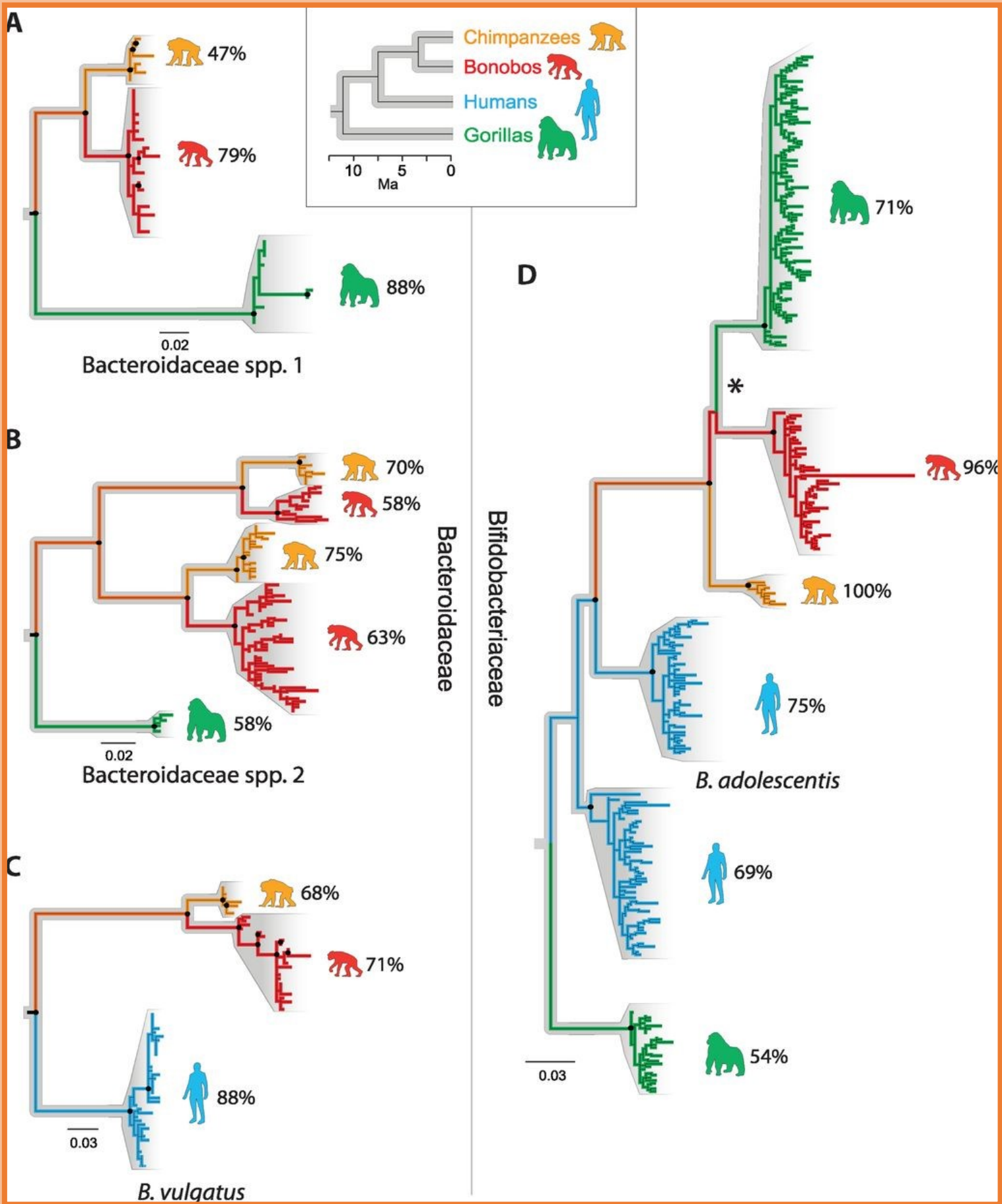


Figure 1 shows the maximum likelihood phylogenetic trees of these species. Colors indicate where the host species was recovered from, and percentages are the percentage of host individuals that had these clades.

Figure 2

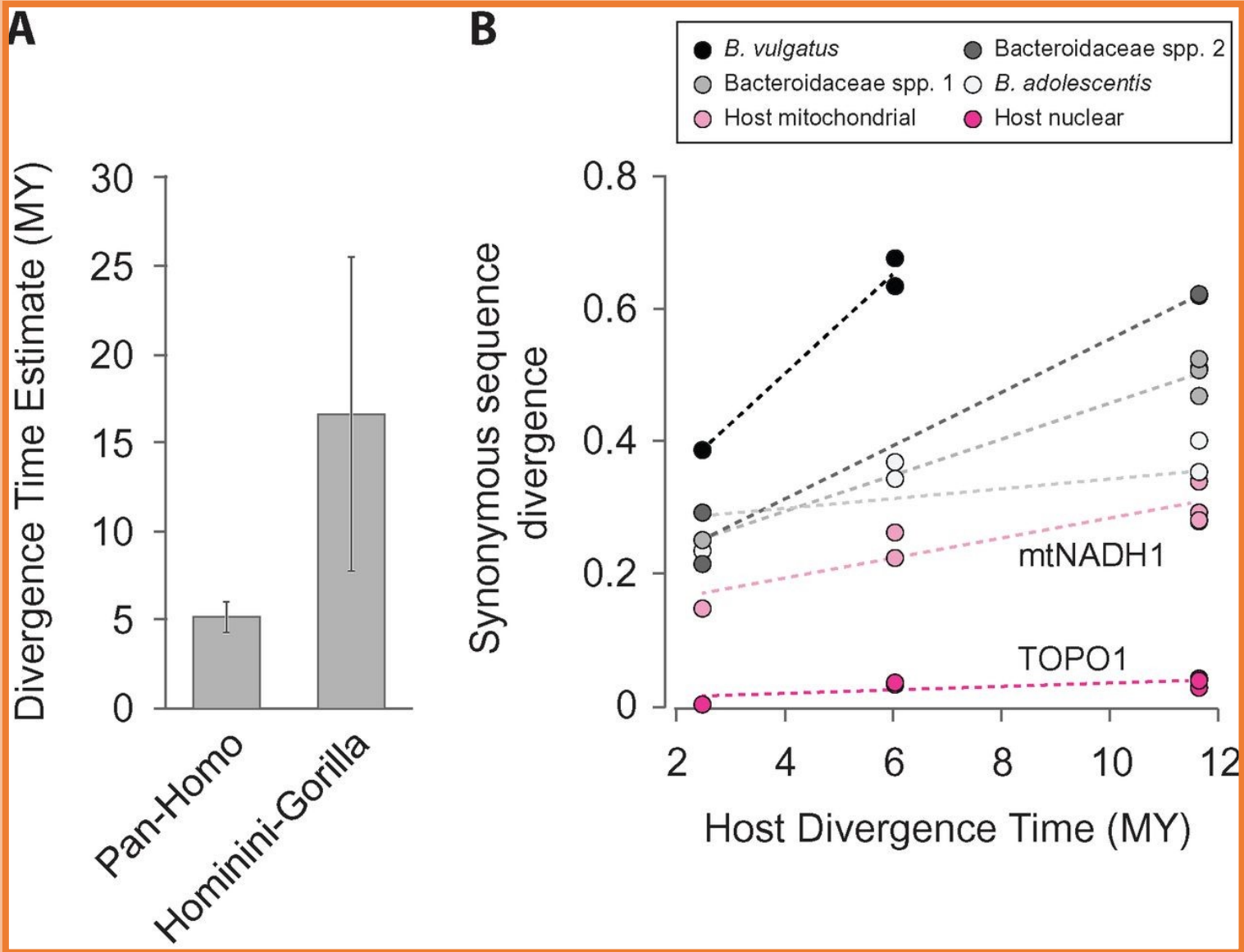


Figure 2A shows, in millions of year, the divergence time estimate for hominid species from estimations with bacteria. Figure 2B shows the relative rates of synonymous diversion from the different bacteria, specifically in the gyrB gene on in the DNA gyrase.

Data and Analysis

For Bacteroidaceae, there was a definitive pattern of cospeciation with host lineages. Figure 1A and 1B show a clear divergence of the bacteria in correspondence to hominid divergence. Figure 1A indicates that 88% of gorillas sampled had a new species of bacteria, while 79% of bonobos had a speciated version of this bacteria. Figures 1A and 1B also indicate that this bacterial lineage was nowhere to be found in humans. The conclusive statement within this group was that bacterial strains had diversified within their respective host species. There were similar results of cospeciation for the second family of bacteria, the Bifidobacteriaceae. Figure 1D shows how the bacteria diverged chronologically with gorillas, then humans, then chimpanzees, bonobos, and gorillas. 100% of chimpanzees surveyed had and 96% of bonobos had a modified strand of this bacteria. The third family of bacteria, Lachnospiraceae, had contrasting results. Results showed that it was common in all species. There were likely transfer events between host species, which have modified them. Results indicate that because this family is spore forming, and can survive outside of the traditional gut, it may be able to disperse and transfer among host species, which would limit the role of cospeciation within the bacteria family and hominids.

Conclusion

There were definitive results showing cospeciation of bacteria with hominid hosts. Additionally, using their phylogeny data in 2A and 2B, researchers estimated when specific hominid species diverged. For example, they dated the split of humans and chimpanzees to be 5.3 million years ago., which is close to estimates based on mitochondrial genomes. This is significant because it contributes another piece of evidence to date the divergence of ancient species. Also, based on phylogenetic tree estimates, the researchers were able to come up with estimates of the molecular evolution rates of different bacteria. In the presence of a pathogen, they found that bacteria had a higher molecular evolution rate. Finally, they found that genes within bacteria symbionts evolve faster than host genes, which could be used in future studies to estimate biogeographical relationships between species.

In a small additional study, researchers tested for cospeciating gut bacteria in human populations. They found a large difference in the diversity between African populations and people in the United States. The U.S. had a large loss of bacterial lineages in comparison to the people tested in Africa. This might have an implication in future research to simply compare diversity of gut microbiota in various groups of humans around the world. Finally, some implications that this report might have is that it shows the diversification of bacteria is possible in all vertebrates, and that hominid species are not the only ones.

Works Cited

Moeller, A., Caro-Quintero, A., Mjungu, D., Georgiev, A., Lonsdorf, E., Muller, M., . . . Ochman, H. (2016). Cospeciation of gut microbiota with hominids. *Sci* (New York, N.Y.), 353(6297), 380-2.

Amplicon Sequencing. (n.d.). Retrieved October 10, 2017, from <https://www.illumina.com/techniques/sequencing/dna-sequencing/targeted-resequencing/amplicon-sequencing.html>