

GENOME: THE GIS SPEAKER SERIES

Codiversification of Gut Microbiota with Human

18 January (Wednesday) · 4pm (SGT, GMT+8)

Online – via Zoom



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The gut microbiomes of human populations worldwide have many core microbial species in common. However, within a species, some strains can show remarkable population specificity. The question is whether such specificity arises from a shared evolutionary history (codiversification) between humans and their microbes. To test for codiversification of host and microbiota, we analyzed paired gut metagenomes and human genomes for 1225 individuals in Europe, Asia, and Africa, including mothers and their children. Between and within countries, a parallel evolutionary history was evident for humans and their gut microbes. Moreover, species displaying the strongest codiversification independently evolved traits characteristic of host dependency, including reduced genomes and oxygen and temperature sensitivity. These findings all point to the importance of understanding the potential role of population-specific microbial strains in microbiome-mediated disease phenotypes.

Ruth Ley performs basic research into the ecology and evolution of the human gut microbiome. She is the Director of the Department of Microbiome Science at the Max Planck Institute for Biology in Tübingen, Germany, since 2016. She is the Manager Director of the Max Planck Institute for Biology in Tübingen. Ley received a BA in Integrative Biology from the University of California at Berkeley, and a Ph.D. in Ecology and Evolutionary Biology at the University of Colorado, Boulder. Her post-doctoral work was with Dr. Norman Pace at CU Boulder, and Dr. Jeffrey Gordon at Washington University School of Medicine. From 2008-2016, Ley was Assistant and Associate Professor at Cornell University in the Departments of Microbiology and Molecular Biology and Genetics.