

Novel human-associated uncultured bacterial pathogens, environmental models, and what metagenomics data tell us

Cleber Ouverney

San Jose State University, USA

The diversity of prokaryotes associated with humans has been dominated by uncultured species (not isolated in pure culture). For instance, nearly 80% of the human gut and 68% of the human oral microbes are thought to be uncultured; some of which have been associated with human oral, digestive, vaginal, and cardiovascular diseases. The prevalence of uncultured pathogens is expected to continue to increase within the near future. In fact, public databases such as GenBank have nearly quadrupled the number of *candidate* phyla (those made entirely of uncultured organisms) since the 1980s and currently lists many new lineages of unclassified Bacteria and Archaea. Because detection of uncultured organisms has been limited to the 16S rDNA gene sequence, little is known about the function (e.g. pathogenicity) they play in humans. Nonetheless whole genomes of uncultured bacteria have been acquired through microfluidics, flow cytometry combined with fluorescence *in situ* hybridization, large-insert libraries (BAC/COSMID/FOSMID), and direct sequencing of genomic DNA. Access to human samples, however, imposes limitations to reproducible data and alternative models have been proposed. This talk will discuss the various methods used to find and acquire the whole genome of the human-associated uncultured bacteria TM7, what its genome tells us, and how environmental strains of TM7 can serve as potential model organisms to help us determine the role uncultured bacteria play in humans.

Biography

Cleber Ouverney completed his Ph.D. at University of Southern California, where he applied culture-independent molecular techniques to characterize complex microbial communities in marine systems. As a postdoc at Stanford University Medical School, he continued studying complex microbial communities, but of pathogens associated with the human oral cavity. He has proposed protocols to measure bacteria metabolic activity *in situ* without the need of cultivation. He is currently an Associate Professor at San Jose State University, where he combines environmental and medical microbiology to better understand the role of human pathogens by the use of environmental models.