Title
Comparative Community Genomics of the Gastrointestinal Microbiota

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Comparative community genomics of the gastrointestinal microbiota.

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The diverse community of gut microbes plays essential roles in human health, contributing to the digestive process, promoting gut maturation, modulating the immune system, and interacting with pathogens in several complex ways. We have initiated efforts to study the composition and coding capabilities of the gut microbial community at the metagenomic level.

Human fecal samples from two volunteers (mother and infant) were collected in 2004 and 2005. We have produced 4 different fosmid libraries, two from adult samples (2004 and 2005) and two from infant samples (2004, 1 month old and 2005, 11 moths old), each containing 50,000 clones. As a first step towards the characterization of these libraries, we are generating end-sequencing reads to investigate their general composition and coding capabilities. In addition, we are genetically and phenotypically screening the libraries in different ways. We have initiated multiplex PCR screenings with 16s rRNA primers and 11 primer sets directed towards universally conserved bacterial proteins, for phylogenetic analysis. In the same manner, we will also screen for different types of genes involved in microbe-host interactions. We are also performing phenotypic screenings to identify clones producing antibiotic molecules or antibiotic resistance activities. The information retrieved from these screenings will provide an ample biological background describing the gut microbial community.

In addition, we will perform comparative analyses with fosmid libraries from the gut microbiota of Indian infants at different months after birth, as a collaborative effort with Pune University in India.