

Recent genomic changes in the human gut microbiome

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Most modern metagenomic studies include only functional and taxonomic profiling while very expensive metagenomic data contain much more information about the genomes of organisms in the analyzed community. We developed a bioinformatic approach for reconstruction phylogenetic trees and gene content of individual gut bacterial species. This approach was applied to 514 gut metagenomic samples from subjects of four countries: Russia, USA, Denmark and China. Russian cohort was presented by healthy people as well as patients with chronic obstructive pulmonary disease under antibiotic therapy. Reconstructed phylogenetic trees were used for detection of mutational hotspots in dominant bacterial species. Many of these hotspots were localized in antibiotic target genes and genes associated with metal resistance. We also classified a large subset of bacterial genes into particular classes based on their phylogenetic characteristics and coverage features . These classes can reflect recent genomic changes in dominant bacterial species.