Gut Microbiome Dynamics: Metagenomic Exploration of Composition, Function, and Disease Association

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ABSTRACT

The human gut microbiome plays a crucial role in digestion, immunity, and metabolism, with its composition influenced by age, lifestyle, diet, and geography. This study employs metagenomic sequencing data to analyze microbial communities in the large intestine across different age groups and regions. Metagenomic datasets from the MGnify database and the European Nucleotide Archive (ENA) project PRJEB3079 were used for comparative analysis. Bioinformatics tools, including FastQC for quality assessment, Trim Galore for sequence trimming, and Kraken2 for taxonomic classification, were utilized on the Galaxy platform. Visualization through Kraken PieChart and Krona charts provided an interactive representation of microbial diversity. Results showed microbial richness increasing with age, with Firmicutes and Bacteroidetes as dominant phyla and Actinobacteria playing a significant role. *Frankia alni*, an environmental bacterium, was detected, possibly indicating contamination or an unrecognized gut-associated strain. Additionally, the presence of Levivirus and fungal communities highlighted microbiome complexity. This study underscores the value of integrating public metagenomic datasets with computational tools for microbiome research, offering insights into microbial diversity, personalized medicine, and probiotic therapies.

Keywords: human gut, microbiome, metagenomics, computational biology