16S rRNA Sequence Analysis of the Human Gut Microbiome

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Abstract

In the pilot study, we collected fecal samples from individuals of different ethnicity, geographic origin, and diets. For each sample, the V1-V3 region of the 16S rRNA gene was PCR amplified and then sequenced using the 454 sequencing technology. The raw data was filtered with quality control and the primers were removed. The microbial diversity within each sample was characterized using the QIIME (Quantitative Insights into Microbial Ecology) program, and through the RDP (Ribosomal Database Project) analysis. Samples from different individuals show different compositions in their microbiomes. However more samples are needed to elucidate the relative contribution of the diet, environment, and ethnicity to the microbiome in human digestive system.

Introduction

•The microbiome in human digestive system has increasingly been found to play an important role in human health.

•However, whether people of different ethnicity, geographical origin, and/or diet have different micriobiomes and how each of these factors affect the composition of the microbial community in human digestive system remain to be elucidated.

•We carried out a pilot study to address the above questions by analyzing the bacterial community in the digestive system of 5 individuals of different ethnicity, geographic origin, and diet using the metagenomic analysis of 16s rRNA gene sequence.

Materials & Methods

Fecal sample collection from 5 individuals

Genomic DNA extraction

PCR amplification for 16s rRNA gene

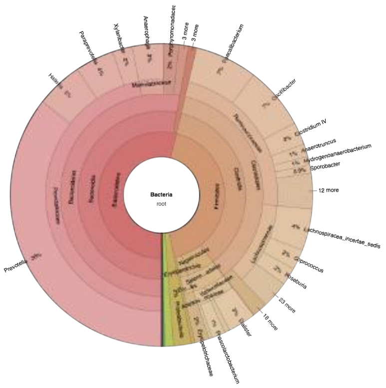
Sequencing with 454 technology

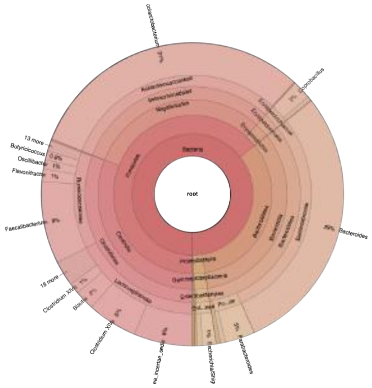
Quality control and primer removal

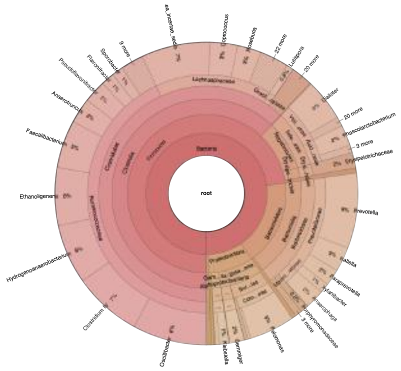
RDP analysis

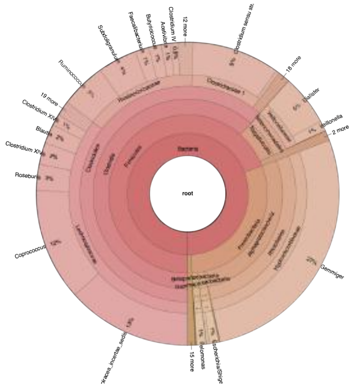
Visualization using Krona Tools

Results









Conclusion

1. Living environment seems to play an important role in the composition of human digestive system microbiome (S1 in comparison to others).
2. Different individuals have different types of bacteria as the dominant groups at lower taxonomic levels.
3. More samples need to be studied to examine the individual effect of ethnicity, diet, and gender and to verify the effect of living environment.

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