



# 第2回若手セミナー

テニュアトラック普及・定着事業

(共催：第349回つくば分子生命科学セミナー)

演題：Enterotypes of human gut microbiome

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日時：2012年6月8日(金) 17:00-18:30

会場：医学学群棟4A103室

要旨：

Microbiota in the human intestine is composed of 100 trillion bacterial cells, which number is 10 times larger than the number of cells in the human body. They construct a complicated eco-system inside of our gut and definitely affect our health conditions.

Here, I introduce our recent works for human gut microbiome, to focus on its phylogenetic diversity and functional compositions. We sequenced metagenomes derived from fecal samples of 22 individuals (Danish, French, Italian and Spanish), and combined them with publically available data of 17 individuals (Japanese and American). 4 samples are removed because of an unusual low Bacteroidetes fraction and suspicious of technical errors. Finally, we investigated 33 individuals.

Cluster analysis using similarity of phylogenetic profiles by mapping metagenomic sequence reads to 1511 reference genomes revealed that the 33 samples formed three distinct clusters, that we called "enterotypes". Each of these three enterotypes are identifiable by the variation in the levels of one of three genera: Bacteroides (enterotype 1), Prevotella (enterotype 2) and Ruminococcus (enterotype 3). The same analysis on two larger published gut microbiome data sets of different origins (16S pyrosequencing data from 154 American individuals and Illumina-based metagenomics data from 85 Danish individuals) shows that these data sets could also be represented best by three clusters. In addition to phylogenetic composition, each enterotype also has distinct features in functional aspects, for example, each enterotype has different biosynthesis ability of vitamins.

Together, we identified the existence of enterotypes in human gut microbiome. Our current knowledge still does not answer the majority of the enterotypes-induced questions, for example, temporal stability, association with metadata (e.g. BMI, age etc), effects of digestion or drug intakes and so on. There are several issues needed understand human microbiome deeply, suggesting further analyses must be required in this growing field.

参考文献 (Nature 473, 174--180 (12 May 2011), Nature 464, 59-65 (4 March 2010))

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