



Indian Institute of Science
Centre for BioSystems Science and Engineering



Seminar

At 2:30 PM on 4th September 2018 (Tuesday)
CES Seminar Hall, 3rd Floor Biological Sciences Building

A novel bacterial microbiota quantification method at the single cell and single base level using our high dynamic range DNA molecular barcode and droplet system

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Abstract

Commensal microbiota affects the health of their hosts through bacteria-host interactions, and the dynamics between these interactions also contribute to the development of many diseases. To understand the mechanisms behind these effects of microbiota, characterization of the composition (species and number) of the bacterial microbiota is required. However, this is difficult with the current techniques.

We have developed a novel high throughput experimental method which enables one to identify 16S rRNA sequences of bacteria with single base accuracy independently of any database and to quantify each bacterium in a microbiota at the single cell level. These advantages allow us to measure the ratio of different bacteria directly and accurately, which is important information to understand bacteria-bacteria interactions. We applied this method for the microbiota analysis in different locations of the murine gut, and found many unregistered 16S rRNA sequences. The differences of population profile depending on different locations which we found may be related to the interactions between bacteria and with their host.

About the Speaker

Dr. Katsuyuki Shiroguchi received his PhD from the University of Tokyo working on motor proteins. For his post-doc, Katsuyuki studied single molecule biophysics at Waseda University in Tokyo, and developed quantitative digital RNA sequencing techniques at Harvard University, Cambridge. In 2012, Katsuyuki moved to Yokohama, Japan and started his independent research position at RIKEN. Currently, he is at the RIKEN Center for Biosystems Dynamics Research in Osaka, Japan.

