# RIKEN SEMINAR

## 4th Epigenetics Seminar Series 2017
## 4th Symbiosis Seminar Series 2017

**Title**

### Microbial fermentation products shape host immune system through epigenetic modifications

Human intestinal microbiota is a complex community composed of more than 500 species. The total genes of gut microbiota outnumber our genes by more than 100-fold. Many of these microbial genes are involved in main metabolic pathways such as carbon metabolism and amino acid synthesis. Using the abundant genes, commensal microbiota actively perform microbial fermentation and produce a diversity of metabolites. Certain microbial metabolites regulate barrier functions as well as mucosal immunity. For instance, butyrate mainly produced by bacterial species belonging to Clostridiales cluster IV and XIVa plays a critical role in development of intestinal regulatory T (Treg) cells in response to bacterial colonization early in life. Butyrate facilitates induction of Foxp3, the master transcription factor of Treg cells, by enhancing histone acetylation of regulatory regions of the gene though inhibition of histone deacetylase (HDAC). We recently observed that the microbial metabolite play a key role in preventing the onset of CIA through regulating germinal center B cell reaction and autoantibody production. Our observations suggest that butyrate regulates not only local inflammation in the gut, but also systemic autoimmune response

**Speaker**


## Prof. Koji Hase

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**Language : English**

**Date/Time : Tue, June 27 / 17:00-18:00**

**Location : Main Office Bldg. Koryu-to Hall, Yokohama**

- Live telecast from Yokohama Main
  - <Wako: 408 Seminar Room, Chemical Biology Bldg. >
  - <Kobe: N701-703 Seminar Room, Building A>
  - <Tsukuba: Moriwaki Hall>


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