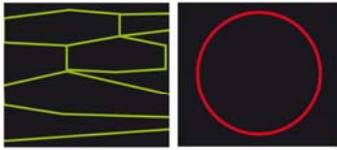


**CRC 670**



CELL-AUTONOMOUS IMMUNITY



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## **Seminar**

**Tuesday, June 17<sup>th</sup>, 2014, 11 a.m.**

**Dr. Felix Sommer**

Institute of Molecular and Clinical Medicine, Gothenburg University

**Establishment and selection of our second  
genome: microbial effects on host physiology**

**Host:**

Prof. Dr. Manolis Pasparakis, Institute for Genetics, University of Cologne

**Venue:**

CECAD Research Center, Joseph-Stelzmann-Str. 26, 50931 Köln

Lecture hall ground floor

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## Dr. Felix Sommer

### Establishment and selection of our second genome: microbial effects on host physiology

Recent technological advances in detecting individual microbial species have revolutionized our understanding of an individual organism. All living beings are closely associated with a huge variety of microbes, most of which are bacteria and reside within the gastrointestinal tract. These microbiota have diverse and immense effects on host physiology<sup>1</sup>. However, the vast numbers of intestinal bacteria represent a substantial threat. Furthermore, the gastrointestinal tract is a very dynamic habitat and the composition of the microbiota can change very rapidly. Host physiology, however, depends on a stable microbiota that provides suitable biochemical properties. Thus, host-microbial interaction has to be tightly regulated on a cross-species level. Collectively, my research projects aim to get insides into the molecular regulation of host-microbial homeostasis and the effects on host physiology. The main findings were:

1. The glycosylation pattern of the intestinal mucus layer has selection effects on microbiota composition and thereby contributes to intestinal inflammation and tissue architecture<sup>2</sup>.
2. Expression of the innate immunity component DUOX2 is specifically induced by the microbiota through two different signaling pathways in the ileum and colon epithelium with implications for gut inflammation<sup>3</sup>.
3. The microbiota elicits global but site-specific responses in the intestinal epithelium and employs distinct regulatory networks to modulate the host's transcriptome<sup>4</sup>.

Together, these findings demonstrate the diverse effects of the resident microbiota for host physiology and this knowledge might ultimately be used to develop novel therapies for the treatment of several diseases, e.g. chronic intestinal inflammation or the metabolic syndrome.

#### References:

1. Sommer F, Backhed F. The gut microbiota - masters of host development and physiology. *Nat Rev Microbiol* 2013; **11**(4): 227-238.
2. Sommer F, Adam N, Johansson MEV, Xia L, Hansson GC, Bäckhed F. Altered Mucus Glycosylation in Core 1 O-Glycan-Deficient Mice Affects Microbiota Composition and Intestinal Architecture. *PLoS One* 2014; **9**(1): e85254.
3. Sommer F, Bäckhed F. The gut microbiota engages different signaling pathways to induce Duox2 expression in the ileum and colon epithelium. *Mucosal Immunol.*, 1st revision.
4. Sommer F, Nookaew I, Adam N, Fogelstrand P, Bäckhed F. Site-specific programming of the host epithelial transcriptome by the gut microbiota. *Genome Res*, in review.