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Identification of molecular components of the host-microbiota-connectome by using "Omics Approaches"

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ABSTRACT

The host immune system plays an critical role in maintaining homeostasis with resident microbial communities, therefore ensuring that the complex symbiotic relationship is maintained. At the same time, resident microbiota contribute to host nutrition and energy balance and to the development or maintenance of a robust immune system. Dysbiosis of the microbiota is associated with various immunological disorders, including inflammatory bowel diseases (IBD). Both genetic and environmental factors are implicated in this disturbance; however, the relative contributions of these two factors, and the mechanism by which they interact remain unclear.

Recently, we started a project that aims to identify molecular components of the host-microbiota-connectome by taking advantage of common variation in – on the one hand – the genome, transcriptome and metabolome of the host, and – on the other hand – the composition of its gut microbiota. We will take advantage of the already established CEDAR cohort that provides integrated genetic (SNP genotypes) and transcriptome data (circulating immune cells subset, as well as samples from various anatomical locations in the intestine). We will further enrich the dataset in this cohort with metabolome (plasma), and gut microbiota data (16srRNA sampled at the ileum, colon, and rectum). The CEDAR cohort is composed of healthy individuals and is therefore more suitable to study effect of common risk variants than (IBD) patients, since analysis of samples from patients suffering from active inflammation may only give insight in ongoing patho-physiological processes, that are likely to mask the *primum movens* events. Next, we will study the overlap between the identified components of the HMC network identified and the ~160 GWAS-identified risk loci for IBD.

We anticipate to reveal novel connections between the microbiota and IBD by this integrative "omics" approach, thereby shedding new light on the pathogenesis of IBD. Latest results will be presented with respect to the microbiota composition of from different anatomical locations in the intestine using the V2 and V5-6 regions of the bacterial 16S rRNA.