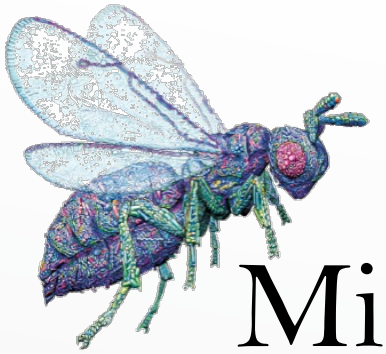


Mini-Symposium

MICROBIOTA

Free

Meet the speaker

Everyone welcome

14. November 2017
13:30 – 19:00
Bohnenkamp Haus

Sponsored by:

Universitätsgesellschaft Osnabrück e.V.

OMNILAB

Universität Osnabrück

SFB 944 Physiology & Dynamics of Cellular Microcompartments

PROGRAM

13:30 – 14:30 **Julia Vorholt**

The leaf microbiota: disassembling and rebuilding to explore plant microbe interactions

(Chair: Sabine Zachgo)

14:30 – 15:30 **Martin Kaltenpoth**

An inordinate fondness for symbionts: mutualists-provided defense, digestion, and desiccation tolerance in beetles

(Chair: Christian Kost)

15:30 – 16:00 **Coffee break** (Meet the speaker)

16:00 – 17:00 **Nicholas Youngblut**

Human genetic determinants of the microbiome

(Chair: Karlheinz Altendorf)

17:00 – 18:00 **Dirk Haller**

Intestinal microbiota – our Janus-faced companions

(Chair: Michael Hensel)

18:00 – 19:00 **Evening reception** (Meet the speaker)

PLANT microbiota

Julia Vorholt

The leaf microbiota: disassembling and rebuilding to explore plant microbe interactions

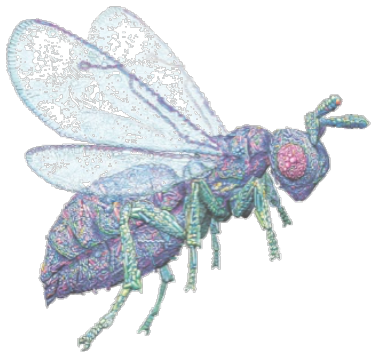
The aerial parts of the plants, which are dominated by leaves, represent one of the largest terrestrial habitats for microorganisms. This habitat, called the phyllosphere, is occupied by a diverse community of microorganisms, which is important for plant health and growth. Most of the phyllosphere inhabitants are not well investigated; however, there is a growing interest to study commensal bacteria to elucidate their interactions with the plants, among each other and to learn how they withstand the hostile conditions of their habitat. A predominance of Proteobacteria, Actinobacteria, and Bacteroidetes living in the phyllosphere of numerous plants has been revealed, while metagenomics and metaproteomics approaches gave insights into the general bacterial adaptation strategies to the phyllosphere. Recently, we conducted large-scale experiments to isolate *Arabidopsis thaliana* leaf bacteria as pure cultures. Individual plants as well as individual leaves were sampled at different European sites to determine their core leaf community and to establish a reference strain collection using flow cytometry and dilution series plating. After identifying approximately 3,000 isolates using a high-throughput DNA sequencing-based method we selected more than 200 representative strains belonging to 52 genera of the major phyllosphere phyla covering the majority of the culture-independent taxonomic diversity. Draft genomes of all selected isolates were generated. Recolonization experiments using synthetic communities in a gnotobiotic model system showed reproducible colonization patterns and represents a valuable starting point to identify mechanisms of community formation and function. Examination of plant responses to its microbiota revealed that the plant reacts differently to members of its natural phyllosphere microbiota. A subset of commensals increase expression of defense-related genes and thereby contribute to plant health and performance.

INSECT microbiota

Martin Kaltenpoth

An inordinate fondness for symbionts: mutualist-provided defense, digestion, and desiccation tolerance in beetles

Symbiotic associations with microbes are important driving forces of evolutionary innovation. The hyperdiverse insect order Coleoptera, the beetles, are associated with an astounding diversity of symbionts that provide a wide range of functional benefits to their hosts. Highlighting a few selected beetle-microbe associations, I will report on novel findings of symbiont-provided antibiotic defense, microbe-enabled digestion of plant material, and symbiont-mediated adaptation to the abiotic environment. These examples are intended to show the impact of symbionts on niche expansion and diversification in beetles, but also provide insights into life-style switches from parasitism to mutualism in bacteria as well as the process of extreme genome reduction beyond the well-known intracellular symbioses.



HUMAN microbiota

Nicholas Youngblut

Human genetic determinants of the microbiome

Recent genetic studies in mice and humans have revealed intriguing genetic associations with the composition of the gut microbiome. In a study of over one thousand twin pairs that were genotyped, we uncovered components of the microbiome whose abundances were partially determined by host genotype (e.g., heritable). Many of these heritable taxa have been validated in subsequent studies: of the hundreds of different types of bacteria and archaea present in the gut across individuals and even species, a select few are repeatedly shown to be heritable. Likewise, we uncovered associations between heritable taxa and genes related to diet, immunity, metabolism and olfaction. Here, I provide an overview of gene-microbe associations that are proving robust through cross-validation in similar studies. The human alleles that predict variation in the microbiome tend to be in genes or gene regions related to (i) changes in diet that are relatively recent in human cultural evolution, and (ii) to immunity in general, which is a rapidly evolving component of the host. Some of these instances show how the microbiome may compensate host genotype under specific selection pressures.

HUMAN microbiota

Dirk Haller

Intestinal microbiota – our Janus-faced companions

The intestinal microbiome is suggested to play an essential role in the regulation of human health and disease susceptibility. Human cohort studies demonstrated changes in gut microbiota composition and function in a variety of different pathologies including inflammatory bowel diseases (IBD), Type 1 diabetes, colon cancer, cardiovascular disease, obesity and Type 2 diabetes. Although metagenomic resolution and bioinformatic tools considerably improved, allowing even strain level analysis, the search for microbial risk patterns in human cohorts is often confounded by environmental factors (e.g. medication) and host status (e. g. disease relapse), questioning the prognostic and therapeutic value of the currently available information. Dysbiosis is considered as an alteration in microbiota community structure and/or function, capable of causing/driving a detrimental distortion of microbe-host homeostasis, nevertheless the functional impact of microbiome signatures on disease aetiology still remains elusive. In this presentation, I will focus on gut-related pathologies at the edge of inflammation and tumorigenesis describing microbiota transfer experiments in germfree mouse models for IBD and colon cancer. In this context, it is important to understand whether changes in microbial ecosystems are causally linked to the pathology and to what extend disease risk is predicable based on characteristic changes in community structure and/or function. In IBD, local changes in tissue integrity associated with focal areas of inflammation may result in the selection of a dysbiotic bacterial community associated with the propagation of a disease phenotype. In colonic tumorigenesis, changes in microbiota communities also occur independently of inflammatory mechanisms. However, causal mechanisms for the interaction of dysbiotic microbial communities in the gut and disease onset require additional clinical and experimental validation including clinical intervention and prospective cohort as well as gnotobiotic animal studies. In conclusion, microbe-host interactions in the intestine are suggested in the pathogenesis of chronic pathologies, but the mechanistic rational to support a pathophysiological role of this interface requires a critical reflection.