YIRD 2019

3rd Young Investigator Research Day

8-9 August 2019, Kiel, Germany

Metaorganism research & career development

YIRD 2019
book of abstracts
&
detailed program

META ORIGIN AND FUNCTION OF ORGANISMS
COLLABORATIVE RESEARCH CENTRE 1182

Organized by :
Jinru He (CAU)
Cornelia Jaspers (GEOMAR)

YIRD 2019

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3rd Young Investigator Research Day

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Metaorganism research & career development

Career

1st day sessions:

Keynote speaker

Dr. Mary Beth Decker, Yale

- Personal development
- Proposal writing tips
- Funding opportunities:

NKS Nationale Kontaktstellen zum EU-Programm Horizont 2020

DFG Deutsche Forschungsgemeinschaft

DAAD Germany

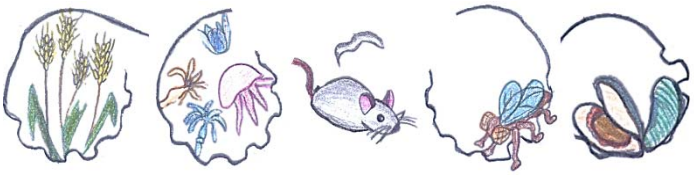
Science

2nd day sessions:

Keynote speaker

Prof. Paul Turner, Yale

- Metaorganism ecology & evolution
- Small scale host-microbe interaction
- Virus: Functional role & application



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Social

- *Networking BBQ*
- *Metaorganism PARTY*
- *Poster cross-talk*

Registration

until **10 July 2019**

No registration fee!
Social events included.

GEOMAR, Wischhofstrasse 1-3, 24148 Kiel, Germany

Organisers:

Cornelia Jaspers - GEOMAR
Jinru He - CAU

Email: yird2019@outlook.com

META ORIGIN AND FUNCTION OF ORGANISMS COLLABORATIVE RESEARCH CENTRE 1182

C|A|U

GEOMAR

Y I R D 2019

3rd Young Investigator Research Day

Program: 8-9 August 2019, Kiel, Germany

Metaorganism research & career development

Thursday 8.8.2019

10:00-11:00: Registration & coffee

11:00-11:15: Opening & welcome: General outline of funding opportunities

11:15-12:00: Keynote Dr. M.B. Decker (Yale University): Women in science, career options in the US

12:00-12:30: German Exchange Service short & long term funding opportunities (Deutscher Akademischer Austauschdienst – DAAD) Cordula Behrsing cancelled to be presented by Cornelia Jaspers

12:30-13:00: How to build up a career in science Prof. P. Turner (Yale University, USA)

13:00-14:00: Lunch

14:00-14:45: Application for individual fellowships e.g. Marie Skłodowska-Curie Alexandra Pohl (NKS MSC, DLR Projektträger)

14:45-15:30: Science management - DFG as employer Astrid Evers

15:30-15:45: Coffee

15:45-17:15: Personal development - SWOT analyses (Ute Jülly)

17:15-17:30: Break

17:30-17:40*:* Group picture by Christian Urban

17:40-18:00: How to utilize strengths and weaknesses for future development (Ute Jülly)

18:00-18:45: What's the secret behind a successful academic career? Discussion round with Prof T. Bosch (Christian-Albrechts-Universität)

19:00- open: Networking *Metaorganism science BBQ*

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Metaorganism research & career development

Friday 9.8.2019

08:45-09:00 Welcome

09:00-10:20 Metaorganism Ecology I

09:00-09:20 Mohamed-Amine Hassani

09:20-09:40 Ryszard Soluch

09:40-10:00 Jay Bathia

10:00-10:20 Fabian Nies

10:20-10:40 Poster Flash Mob I [4 min/each]

Florence Bansept, Lara Schmittmann, Christoph Giez, Barbara Pees, Kim-Sara Wagner

10:40-11:10 Coffee

11:10-12:30 Metaorganism Ecology II

11:10-11:30 Lucía Pita

11:30-11:50 Janina Lange

11:50-12:10 Julia Johnke

12:10-12:30 Michael Sieber

12:30-12:55 Poster Flash Mob II [4 min/each]

Georgios Marinos, Christine Blurton, Vaibhvi, Jakob von Frieling, Jelena Rajkov, Cornelia Jaspers

12:55-14:00 Lunch

14:00-15:40 Metaorganism Function

14:00-14:20 Román Zapién-Campos

14:20-14:40 Danielle Harris

14:40-15:00 Shauni Doms

15:00-15:20 Clinton Azuure

15:20-15:40 Felix Sommer

15:40-16:00 Metaorganism Discussion

16:00-16:15 YIRD2019 Award ceremony & Conclusion

16:30-18:00: Transport with ferry or bike to GEOMAR West shore building

18:00-18:05: Introduction by Prof. Thomas Bosch

18:05-19:00: Keynote Prof. Paul Turner (Yale) Virus and phage biodiversity: Potential in human therapy (all CRC members invited) to be held at GEOMAR West shore building

19:00-19:15: Award Ceremony of outstanding CRC Young Investigator Mentors

19:15-19:45: Reception with beer and wine

Y I R D 2019

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Metaorganism research & career development

Friday 9.8.2019

YIRD end

16:30-18:00: Transport with ferry or bike to GEOMAR West shore building

CRC 1182 Public lecture series (open to all)

18:00-18:05: Introduction by Prof. Thomas Bosch

18:05-19:00: Keynote Prof. Paul Turner (Yale) Virus and phage biodiversity: Potential in human therapy (all interested people welcome) to be held at GEOMAR West shore building

19:00-19:15: Award Ceremony of Outstanding CRC Young Investigator Mentors

19:15-19:45: Reception with beer and wine

CRC 1182 Event – only with registration (send mail to cjaspers@geomar.de)

20:00-open end: Networking Metaorganism Party (only for registered people)

Paul Tunrner

Virus and phage biodiversity: Potential in human therapy

Earth's biodiversity is numerically dominated by viruses that infect eukaryotes, and by phages which specifically use bacteria and archaea as hosts. Basic research on this teeming multitude yields new biological insights. In addition, these discoveries suggest that virus and phage biodiversity may be harnessed to solve difficult human problems. For example, the extreme genetic and species diversity of viruses is being used to develop oncolytic virotherapy, where tumor-destroying viruses provide alternative treatments against cancers. Also, the widespread failure of antibiotics predicts that human mortality from multidrug resistant bacterial infections will exceed cancer deaths in the coming decades, suggesting that classic phage therapy approaches should be reconsidered as possible solutions. This seminar concerns recent data on viruses and phages that are potentially useful in human therapy, especially success in bioprospecting for lytic phages that select against virulence and multidrug-resistance in target bacterial pathogens. Such phages bind to virulence-related proteins of bacteria and force evolutionary trade-offs: they kill the target bacteria, while selecting for these pathogens to evolve phage resistance by modifying (or losing) the virulence factor, causing bacterial pathogenicity to decrease, on average. Prime examples are phages that bind to bacterial proteins used in efflux (removal) of antibiotics from the cell; the phages kill susceptible bacterial cells while enriching for bacterial mutants that become re-sensitized to currently-failing antibiotics. Supportive data come from laboratory and animal studies, as well as from human cases where phages are used in emergencies to treat multidrug-resistant bacterial infections.

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List of Day 2 Talks

Metaorganism Ecology I		
09:00-09:20	The impact of domestication on the wheat microbiota	**Mohamed-Amine Hassani** Botanical Institute, CAU
09:20-09:40	*Pantoea agglomerans* colonization dynamics of the wheat roots upon germination	**Ryszard Soluch** Institute for General Microbiology, CAU
09:40-10:00	*Hydra viridissima*: A model for understanding a tripartite symbiosis	**Jay Bathia** Zoological Institute, CAU
10:00-10:20	Natural competence in cyanobacteria – More common than previously thought?	**Fabian Nies** Institute for General Microbiology, CAU

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List of Day 2 Talks

Metaorganism Ecology II		
11:10-11:30	Microbial recognition in marine sponges	**Lucía Pita** GEOMAR
11:30-11:50	Temperate bacteriophages: Key players in metaorganism maintenance	**Janina Lange** Zoological Institute, CAU
11:50-12:10	The effect of predatory bacteria on the *C. elegans* microbiome	**Julia Johnke** Zoological Institute, CAU
12:10-12:30	Phage-mediated competition between two members of the *Hydra vulgaris* microbiota	**Michael Sieber** MPI Plön

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List of Day 2 Talks

Metaorganism Function		
14:00-14:20	Stochastic colonization of microbe-free hosts: Consequences of ecological drift and a finite lifespan	**Román Zapién-Campos** MPI Plön
14:20-14:40	Microbiota speak: Using untargeted metabolomics to decode bacteria-host cross talk	**Danielle Harris** Zoological Institute, CAU
14:40-15:00	Identifying host genomic regions influencing microbial traits in mice	**Shauni Doms** MPI Plön
15:00-15:20	Association between the geographical distribution of *Mycobacterium tuberculosis* complex and HLA immune genes	**Clinton Azuure** MPI Plön
15:20-15:40	Targeting epithelial glycolysis through the microbiome as treatment for intestinal inflammation	**Felix Sommer** IKMB, CAU

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List of Posters

Poster Flash Mob I		
10:20-10:24	Evolution of bacterial life cycles in the early stages of host association	**Florence Bansept** MPI Plön
10:24-10:28	A new model on the runway of symbiosis: the breadcrumb sponge *Halichondria panicea* and its main symbiont	**Lara Schmittmann** GEOMAR
10:28-10:32	Are spontaneous contractions of the body wall shaping the microbiota in *Hydra*?	**Christoph Giez** Zoological Institute, CAU
10:32-10:36	Mechanistic and evolutionary basis of the effects of dietary protein restriction and malnutrition on immunocompetence in *Drosophila melanogaster*	**Vaibhvi** Zoological Institute, CAU
10:36-10:40	Sex-specific parental transfer of microbiota	**Kim-Sara Wagner** GEOMAR

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List of Posters

Poster Flash Mob II		
12:30-12:34	Metabolic modeling in metaorganisms	**Georgios Marinos** UKSH, CAU
12:34-12:38	Functional characterization of caenopore SPP-10 from *Caenorhabditis elegans*	**Christine Blurton** Zoological Institute, CAU
12:38-12:42	Effects of protein-restricted diets on the epithelia-microbe interactions in the intestinal tract of *Drosophila melanogaster*	**Jakob von Frieling** Zoological Institute, CAU
12:42-12:46	Tripartite species co-evolution under environmental change: Can prophages accelerate bacterial virulence evolution?	**Jelena Rajkov** GEOMAR
12:46-12:50	Metaorganism comb jelly: Microbiota differences of the comb jelly *Mnemiopsis leidyi* in native and invasive sub-populations	**Cornelia Jaspers** GEOMAR

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List of Posters

Other posters		
Day 2	*Hydra viridissima*: A model for understanding a tripartite symbiosis	**Jay Bathia** Zoological Institute, CAU
Day 2	The impact of domestication on the wheat microbiota	**Mohamed-Amine Hassani** Botanical Institute, CAU
Day 2	Role of antimicrobial proteins in shaping *Caenorhabditis elegans* microbial associations	**Barbara Pees** Zoological Institute, CAU
Day 2	Microbial recognition in marine sponges	**Lucía Pita** GEOMAR
Day 2	*Pantoea agglomerans* colonization dynamics of the wheat roots upon germination	**Ryszard Soluch** Institute for General Microbiology, CAU
Day 2	Protein energy malnutrition alters epithelia-microbiota interactions in the intestine with long-lasting effects on inflammation	**Felix Sommer** IKMB, CAU
Day 2	Stochastic inheritance of the microbiome	**Román Zapién-Campos** MPI Plön

---Abstract for Oral Presentation in YIRD2019---

The impact of domestication on the wheat microbiota

M. Amine Hassani[1,2], Ezgi Özkurt[1,2] , Heike Seybold[1,2], Eva H. Stukenbrock[1,2]

[1]Christian-Albrechts University of Kiel, Kiel, Germany

[2]Max Planck Institute for Evolutionary Biology, Plön, Germany

In nature, plants coexist with diverse microbial communities, such as archaea, bacteria and fungi[1]. The association between the plant and these microorganisms forms an ecological unit termed the holobiont[2]. Plant-associated microbes can have beneficial, neutral or deleterious impact on their host fitness[3,4]. It is therefore important to understand fundamental principles that govern the establishment of the plant microbiota toward better predicting dysbiosis-mediated diseases[5]. Most of the microbes that colonize plants are recruited from the surrendering environments[6] (air, soil) and/or vertically inherited[7] (seed microbiota). It is well-documented that abiotic factors[6] and host cues[1] are key determinants of the plant microbiota. However, the evolutionary processes that mediate microbiota co-adaptation to the host are not well understood. Plant domestication provides a framework to glean data on the dynamic of the plant microbiota over short evolutionary times, identify selective pressures that shape the microbiota of domesticated plant species and formulate precise hypothesis regarding host-microbiota co-evolution. The objectives of this research is 1) to study the role of domestication in altering the community structure and function of the wheat leaf- and root-associated microbiota (bacterial and fungal communities), 2) establish a bacterial and fungal culture collection representative of the wheat leaf- and root-associated microbiota of wild or domesticated wheat species and 3) decipher the interactions between the leaf microbiota of domesticated wheat and the fungal pathogen *Zymoseptoria tritici*. Our preliminary results show that wild and domesticated wheat species harbor distinct microbial communities and that infection by *Z. tritici* significantly alters the leaf-associated bacterial communities of the domesticated wheat.

References. [1]Müller et al. 2016. Annu. Rev. Genet., [2]Bordenstein et al. 2015. PLoS Biolo., [3]Hacquard et al. 2015. New Phytol., [4]Hacquard et al. 2015. Cell Host Microbe., [5]Carding et al. 2015. Microb Ecol Health Dis., [6]Bulgarelli et al. 2013. Annu Rev Plant Biol.

---Abstract for Oral Presentation in YIRD2019---

Pantoea agglomerans colonization dynamics of the wheat roots upon germination

Ryszard Soluch[1], Nils F. Hülter[1], Tal Dagan[1]

[1]Institute for General Microbiology, Kiel University, Germany

Background

Plants are colonized by a wide diversity of microbes that may play a role in plant adaptation to various environmental conditions and disease resistance. Members of the plant microbiota include bacteria that are recruited from the environment and vertically inherited bacteria. The main road for vertically inherited bacteria in plants is considered to be transmission via the seed. Wheat seeds have been reported to harbor bacteria, however, the wheat embryo has been reported to be germ-free hence the colonization routs of seed-borne bacteria remain poorly understudied.

Objectives

Here we study the colonization dynamics of one member of the wheat microbiota – Pantoea agglomerans (Pantoea) – which we isolated from wheat seeds.

Methods

We established a system to cultivate germ-free plants devoid their native microbiota. In addition, we equipped the Pantoea isolate with broad-host-range plasmid encoding kanamycin resistance and constitutively expressing a fluorescent protein (GFP or mCherry). We followed the process of Pantoea colonization of the roots by determining the number of Pantoea cells per plant root system over time.

Results

Our results demonstrate dynamics of bacterial density increase. Five days post germination, Pantoea population reaches a stable carrying capacity of 108 cells/gr. Experiments of priority effects in colonization show that early incoming colonizers have a numerical priority over late incoming colonizers already after 24h. Our results suggest that seed-borne bacteria have an advantage in root colonization in wheat. This data provides a fundament for future experiments on association between Pantoea agglomerans and wheat host.

Keywords: Metaorganism colonization, host colonization, plant symbiont, priority effects

---Abstract for Oral Presentation in YIRD2019---

Hydra viridissima: A model for understanding a tripartite symbiosis

Jay Bathia[1], Katja Schröder[1], Mayuko Hamada[2], Sebastian Fraune[3], Thomas Bosch[1]

[1]Zoologisches Institut, Christian Albrechts Universität, 24118 Kiel, Germany

[2]Okayama University, 700-8530 Okayama, Japan

[3]Zoologie und Organismische Interaktionen, Heinrich-Heine-Universität, 40225 Düsseldorf, Germany

Hydra viridissima is a fresh water polyp belonging to the phylum Cnidaria. It harbors endosymbiotic algae *Chlorella* in the endoderm. The interactions between the host and the algae are mainly metabolic in nature. The algae provides fixed carbon in the form of maltose and, in turn, the host provides the algae with the glutamine as a source of nitrogen. Moreover, there is a genomic loss of essential genes for nitrate and ammonium fixation in the algae, further strengthening the interdependence. We now take into account the third partner of the *Hydra viridissima* metaorganism: bacteria. We observed that upon co-housing of the symbiotic (hosts bearing the algae) and the aposymbiotic (hosts without the algae) animals, there is a diurnal shift in the microbiome composition of the symbiotic animals. During the dark phase, the microbiome of the symbiotic animals is similar to that of the aposymbiotic animals. Moreover, the disrupted diurnal cycle (constant darkness) also results in a higher resemblance of the microbiome of symbiotic animals to that of the aposymbiotic ones. However, upon mono housing, this effect is lost, indicating the selection pressure implied by the algae. To elucidate further the tripartite relationship, we compare the bacteria free symbiotic and aposymbiotic hosts with the controls and conventionalized animals. Our observations indicate that the absent microbiota has no effect on the fitness of symbiosis. However, more detailed and directed approaches might reveal the effect of the absent microbiota on the fitness of the symbiosis and hence provide a better understanding of the tripartite symbiosis.

---Abstract for Oral Presentation in YIRD2019---

Natural competence in cyanobacteria – More common than previously thought?

Fabian Nies[1]

[1]Institute for General Microbiology, Christian-Albrechts-University

Natural competence in cyanobacteria is mostly considered from an applied point of view to enable uncomplicated gene transfer. Also several relevant proteins have been identified by knock-out mutants in the model organism Synechocystis sp. PCC 6803, which are homolog to the natural competence machinery in other gram negative bacteria.

In the cyanobacterial phylum natural competence was often considered an exclusive trait of a small group of unicellular cyanobacteria. In our work we established a natural transformation protocol of the filamentous cyanobacterium Phormidium lacuna. Several strains of this organism have been isolated from rock pools in the North and Mediterranean Sea and their biotechnological potential has been characterized recently. Transformation was achieved by homologous recombination of a kanamycin resistance gene, flanked with endogenous sequences, into the genome. This is the first time natural transformation has been reported for a representative of the order Oscillatoriales and a member of subsection III.

Bioinformatic analysis predicts that the complete set of genes essential for natural competence is present in many species in the whole cyanobacterial phylum. This implies that natural competence is a more common trait among cyanobacteria than previously thought and might play a central role in the cyanobacterial physiology.

---Abstract for Oral Presentation in YIRD2019---

Microbial recognition in marine sponges

Lucía Pita[1], Marc Höppner[2], Marta Ribes[3], Ute Hentschel [1,4]

[1]GEOMAR Helmholtz Centre for Ocean Research, Kiel, Düsternbrooker Weg 20, 24105 Kiel, Germany
[2 4]Christian-Albrechts-University Kiel, Institute of Clinical Molecular Biology, Kiel, Germany
[3]Institute of Marine Science CSIC, Passeig Marítim de la Barceloneta 37-49, 08003 Barcelona, Spain
[4]Christian-Albrechts-University Kiel, Christian-Albrechts-Platz 4, 24118 Kiel

A common challenge for all animals is discriminating between microbes in order to maintain a specific microbiome, while also avoiding overgrowth, harmful infections, or energetically-expensive immune reaction to innocuous microbes. Sponges (phylum Porifera), as early-diverging animals, provide valuable insights in conserved mechanisms of animal-microbe interactions. They feed on bacteria from the seawater while filtering thousands of litres of water per day, yet they harbour complex species-specific microbial communities. However, sponge symbiosis research has largely focused on the microbial side, whereas the host perspective remains poorly explored. Here, we aim to characterize sponge mechanisms of microbial recognition. We performed two independent experiments in order to address the response of sponges to (i) microbial patterns (i.e. exposure to LPS and peptidoglycan vs sterile artificial seawater) and (ii) microbes (exposure to symbiont-enriched fraction vs bacterioplankton). Tissue samples were collected at different time points. We focused on two sponge species that represent a long-accepted dichotomy in sponge symbiosis: *Aplysina aerophoba* belongs to the group of high microbial abundance sponges (HMA), which harbour symbiotic communities in densities that are two to four orders of magnitude higher than those in low microbial abundance sponges (LMA) like *Dysidea avara*. In the first experiment, the response of sponges was assessed by differential gene expression analysis based on RNA-Seq data. The sponges responded by increased expression of a subset of relevant receptors (i.e., NLRs in *D. avara*, SRCR and GPCR in *A. aerophoba*) and the transduction of signal likely yielding apoptosis and phagocytosis processes. The differences between species relied on the activation of different set of receptors and pathways as well as the magnitude of the response, with higher number of differentially-expressed genes in the HMA than the LMA sponge. We proposed that these differences are due to conflicting signals from a different density of symbionts and a species-specific level of constitutive immunity. To our knowledge, this is the first study investigating the transcriptomic response of sponges to microbes. In our second experiment, sponges were exposed to either labelled *A. aerophoba* symbionts (fraction recovered by differential centrifugation) or labelled bacterioplankton and uptake of microbes was monitored by microscopy and flow cytometry. Whereas *A. aerophoba* could distinguish symbiont vs non-symbiotic bacteria and uptake only the free-living ones, *D. avara* take both types of microbes at similar rate. We are currently analysing RNA-Seq data derived from this experiment to tackle the molecular mechanisms involved. These studies are a first step towards understanding the role of sponge immunity in maintaining symbiosis and identifying orthologous genes that hint to conserved mechanisms of animal-microbe interactions based on experimental data.

---Abstract for Oral Presentation in YIRD2019---

Temperate bacteriophages: Key players in metaorganism maintenance

Janina Lange[1,2], Stephen Wandro[2], Stefan Friedel[2], Sebastian Fraune[3], Thomas Bosch[1], Katrine Whiteson[2], Tim Lachnit[1]

[1]Zoological Institute, Christian-Albrechts-University Kiel, 24118 Kiel, Germany

[2]Department of Molecular Biology and Biochemistry, University of California Irvine, Irvine, CA, United States

[3]Institute for Zoology and Organismic Interactions, Heinrich-Heine-University Düsseldorf, 40225 Düsseldorf, Germany

Every eukaryotic organism is associated with a complex microbial community and therewith considered a metaorganism. The bacterial community composition plays an important role in health and disease of their eukaryotic host. Considering that phages can shape whole bacterial communities and that bacteriophage-bacteria coevolution is crucial for ecology and evolution of microbial communities, researching and understanding phage-bacteria interactions is from enormous importance.

A perfect organism for studying bacteria-phage-host interactions is the freshwater polyp *Hydra*, because it features a host specific microbiome. We could demonstrate that the prophage of *Hydra*'s main colonizer *Curvibacter* (TJ1) is active on the eukaryotic host, influences the growth of other bacterial commensals and therewith ensures the high abundance of *Curvibacter*. However, constantly exposed to the phage, we could not observe evolution of resistance on *Hydra*. To evaluate the mechanisms behind this finding, we conducted an *in vitro* coevolution experiment with phage TJ1 and susceptible bacteria colonizer. We could show that after gaining resistance to the ancestral phage, the bacteria lose their ability to recolonize their host. This is caused by mutations in Fibronectin type III domain proteins and flagellum related genes, which reduce the ability to build biofilms or diminish the motility of resistant bacteria. These results give a hint to how temperate bacteriophages and bacteria can coexist on a eukaryotic host: High fitness costs in resistant strains result in favouring phage susceptibility over resistance on *Hydra*.

Keywords: metaorganism, bacteria-phage-host interactions, temperate phages, bacteria-phage coevolution, bacterial fitness

---Abstract for Oral Presentation in YIRD2019---

The effect of predatory bacteria on the *C. elegans* microbiome

Julia Johnke[1], Hinrich Schulenburg[1]

[1]Department of Evolutionary Ecology and Genetics, Zoological Institute, CAU Kiel, Am Botanischen Garten 1-9, 24118 Kiel, Germany

Microbial diversity has been shown to positively correlate with ecosystem stability, an observation that seems to expand to host-associated microbiomes. Therefore, factors contributing to microbial diversity are of great interest, especially as certain diseases have been linked to microbiome dysbiosis. A so far understudied group of candidates for microbiome restoration are *Bdellovibrio*- and like organisms (BALOs), which are obligate predators of Gram-negative bacteria. These bacteria can be considered as probiotic (they reduce dominant species, thereby promoting the growth of less abundant species) as well as antibiotic (they invade and lyse suitable bacteria).

By sampling natural *Caenorhabditis elegans* from a compost heap over time, we found that the majority of *C. elegans* microbiomes contain BALOs. Worms with BALOs possessed an overall more diverse bacterial microbiome. Additionally, a meta-analysis of microbiomes of a set of distinct hosts revealed that this association is universal.

In order to elucidate if BALOs are drivers of microbiome diversity we performed controlled laboratory experiments with the *C. elegans* minimal microbiome (CeMBio) and a newly isolated BALO. Communities decreased in richness over time, but this decrease was decelerated in the presence of the predatory bacterium.

Our results demonstrate that BALOs have a positive effect on microbial diversity and therefore represent promising candidates for the restoration of disturbed microbiomes.

Keywords: Bdellovibrio, predator-prey, microbiome, *C. elegans*

---Abstract for Oral Presentation in YIRD2019---

Phage-mediated competition between two members of the *Hydra vulgaris* microbiota

Michael Sieber[1]

[1]Max Planck Institute for Evolutionary Biology

The two commensal bacteria *Curvibacter* sp. and *Duganella* sp. protect their host, the fresh-water polyp *Hydra vulgaris*, from fungal infections, but only if both of them are present. Coexistence of the two bacteria is thus beneficial for *Hydra*. In vitro, however, *Duganella* appears to be the superior competitor due to its higher growth rate when both bacteria are grown separately. But, intriguingly, in co-culture their growth rates depend on the relative initial abundances of the two species, with *Duganella*'s growth rate suppressed when there is either a lot of *Curvibacter* present, or very little, but not at intermediate *Curvibacter* abundances. Using a mathematical model we show that the interplay between the lysogenic and lytic life cycles of an inducible *Curvibacter* prophage can explain the observed interaction between the two bacteria. This highlights the importance of taking lysogeny into account for understanding microbe–virus interactions and show the complex role phages can play in the interactions of their bacterial hosts.

---Abstract for Oral Presentation in YIRD2019---

Stochastic colonization of microbe-free hosts: consequences of ecological drift and a finite lifespan

Román Zapién-Campos[1], Michael Sieber[1], Arne Traulsen[1]

[1]Max Planck Institute for Evolutionary Biology, Plön, Germany

Macroorganisms are inhabited by microbial communities that change through the lifespan of an individual. One of the contributing factors is the colonization from the environment. Particularly interesting is the colonization of initially microbe-free hosts, as their microbiome depends entirely on microbes of external origin. We present a mathematical model of this process with a particular emphasis on the effect of ecological drift and a finite host lifespan. Our results indicate the host lifespan becomes especially relevant for short-living organisms (e.g. *Caenorhabditis elegans*, *Drosophila melanogaster*, and *Danio rerio*). In this case, alternative microbiome states (often called enterotypes), the coexistence of sterile and colonized hosts, and a reduced probability of colonization could be observed. These results unify multiple reported observations around colonization and suggest ecological drift might be influential during the formation of naturally occurring microbiomes.

Keywords: microbiome, host, colonization, mathematical modelling

---Abstract for Oral Presentation in YIRD2019---

Microbiota speak: Using untargeted metabolomics to decode bacteria-host cross talk

DMM. Harris[1,2], AM. Murillo[1,2], A. Klimovich[1], TJ. Demetrowitsch[3], J. Uhl[4], B. Kanawati[4], K. Schwarz[3], P. Schmitt-Kopplin[4], TCG. Bosch[1]

[1]Zoological Institute, Christian-Albrechts-Universität zu Kiel, Kiel, Germany

[2]Max Planck Institute for Evolutionary Biology, Plön, Germany

[3]Institute for Human Nutrition & Food Science, Department of Food Technology, Christian-Albrechts-Universität zu Kiel, Kiel, Germany

[4]Institute for Ecological Chemistry, BioGeoChemistry, and Analytics, Helmoltz Zentrum München, Germany

Host microbiota affect host health in a multitude of ways, although the biochemical means through which these interactions occur is not always clear. Previous work from our lab has demonstrated that the frequency of nervous system-dependent spontaneous body contractions of the freshwater polyp *Hydra vulgaris* are influenced by its conserved bacterial community, but the molecular mechanisms at play remain obscured. To address this, we employ an untargeted mass spectrometry-based approach. Medium conditioned with the *Hydra* microbial community nearly restores the contraction frequency of germ-free *Hydra* to levels of conventionally-raised *Hydra*, implying that the biochemical agent(s) influencing contraction frequency are secreted by the microbiota and are present in these extracts. To identify the chemicals in these complex extracts that have contraction-mediating bioactivity, we use a comparative approach, looking for microbial signals in conventionally-raised *Hydra* polyps that are not present in the germ-free polyps, and that are also present in the bioactive extracts. Because the bioactive extract was produced by microbes cultured in vitro, we further reasoned that the microbe(s) responsible for the bioactivity may produce the compound when monocultured in vitro. Therefore, we also investigate the metabolomes of the five main colonizers of *Hydra* (in monoculture and in co-culture). In sum, our approach uses *Hydra* as a model to decode the molecular conversation that occurs between resident bacteria and their host.

---Abstract for Oral Presentation in YIRD2019---

Identifying host genomic regions influencing microbial traits in mice

Shauni Doms[1], Hanna Fokt[1], Leslie M. Turner[1], John F. Baines[1]

[1]Max Planck Institute for Evolutionary Biology, Plön, Germany

Essentially all animals and plants are colonized by microorganisms, whereby different host species contain different microbial populations. These microbial communities form long-term relationships with their hosts. Understanding the genomic basis underlying these relationships would provide insight into the possible coevolution between hosts and their microbiota. In this study, we aim to identify host genomic regions that influence microbial traits in mice. For this, we have a unique panel of hybrids of two house mouse subspecies, the Eastern *Mus musculus musculus*, and the Western *Mus musculus domesticus*. We genotyped 320 second generation hybrid intercrossed mice and performed 16S rRNA profiling on both DNA and RNA level to represent the standing and the active communities, respectively. By performing QTL mapping, we identified a total of 16 and 12 unique host loci (DNA and RNA level, resp.) involving 41 bacterial taxa. Ten of these regions contained single genes. This resulted in a set of highly interesting candidate genes, including Sirtuin 5 and *Nckap5*. *Sirt5* is involved in the response to fasting and caloric restriction, and plays a role in insulin resistance and gut inflammation. *Nckap5* is the peripheral clock protein. In the peripheral clock, feeding time is the dominant *zeitgeber* and this mechanism is a known host-microbiota bi-directional interaction. These genes and others represent promising candidates for future functional validation.

---Abstract for Oral Presentation in YIRD2019---

Association between the geographical distribution of *Mycobacterium tuberculosis* complex and HLA immune genes

Clinton Azuure[1], Tobias Lenz[1]

[1]Evolutionary Immunogenomics group, MPI-Evolbio. Ploen,

Members of the *Mycobacterium tuberculosis* complex (MTBC) co-associate phylogenetically with distinct geographical regions and human populations, suggesting coevolution with their human host. *Mycobacterium africanum*, a member of MTBC is highly restricted to West Africa and is rarely identified outside of this region. Molecules of the human leukocyte antigen (HLA) play an important role in adaptive immunity and the frequency of HLA alleles differs significantly among different human populations, making it a prime candidate for coevolution with MTBC. Here we speculate that the distinct distribution of HLA polymorphism is contributing to the geographic restriction of *M. africanum* to West Africa. In order to test this hypothesis, we analyze geographical data of HLA allele frequencies in relation to *M. africanum* prevalence. We hope this study will illuminate our understanding of population-specific differences in disease susceptibility as well as mechanisms of coevolution between hosts and pathogens.

---Abstract for Oral Presentation in YIRD2019---

Targeting epithelial glycolysis through the microbiome as treatment for intestinal inflammation

J. Hamm[1], K. Klischies[1], N. Sommer[1], P. Rosenstiel[1], F. Sommer[1]

[1]Institute of Clinical Molecular Biology, Kiel University, Rosalind-Franklin-Str. 12, 24105 Kiel, Germany

Hexokinase (HK) catalyses the first step of glycolysis, a basic metabolic process generating energy from glucose. Dysregulation of HK is associated with inflammation and cancer and chemical inhibition of HK can ameliorate or even prevent disease development. The gut microbiota is an environmental factor that also affects host energy homeostasis, immune responses and cancer development. However, it is unclear whether the gut microbiota influences these physiological processes through modulation of HK and glycolysis. I showed previously that the microbiome modulates HK expression [1] and activity in intestinal epithelial cells (IECs). Now, I aim to test whether ablation of HK in the intestine protects from inflammation and prospectively colon cancer and whether modulation of HK through the microbiota could be a novel therapeutic option. To that end, we generated and phenotyped HK-IEC mice lacking HK specifically in IECs and subjected them to experimental models of intestinal inflammation (dextran sulfate sodium, DSS) or colitis-associated carcinogenesis (azoxymethane-DSS, AOM-DSS). We also analysed the microbiome composition using 16S amplicon sequencing and transcriptional responses using RNA sequencing. We investigated the regulatory function of specific bacteria on HK using gnotobiotic mouse models and *in vitro* stimulation experiments. Finally, we investigated HK expression in patients with intestinal inflammation and colon cancer. HK-IEC mice display metabolic and immunologic abnormalities already under baseline conditions and showed reduced susceptibility to intestinal inflammation. Susceptibility to colitis-associated carcinogenesis is currently being evaluated. We identified specific bacteria and metabolites, which modulate HK expression. Finally, we found that in humans HK is dysregulated during intestinal inflammation and in tumours of colon cancer patients. Taken together, our data points towards that inhibition of epithelial glycolysis protects from acute intestinal inflammation and potentially colitis-associated carcinogenesis. Thus, probiotic administration of HK-regulating bacteria or their modulation via prebiotics might serve as a novel non-invasive approach for inflammation and cancer therapy.

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Keywords: glycolysis, hexokinase, inflammation, cancer, microbiota

---Abstract for Poster Presentation in YIRD2019---

Evolution of bacterial life cycles in the early stages of host association

Florence Bansept[1], Nancy Obeng[2], Hinrich Schulenburg[2], Arne Traulsen[1]

[1]Max Planck Institute for Evolutionary Biology, Plön, Germany

[2]Zoological Institute, Kiel University, Germany

Microbial communities extend the host functional repertoire, thus making the host and its associated microbes a functional unit. We are only beginning to decipher how host and microbe fitnesses are intertwined: while it is now clear that the microbiota has a vast potential to affect the host physiology, less focus has been put to the microbial perspective, i.e. to understand what benefit or cost can retrieve bacteria from interacting with the host. In contrast with co-evolution hypotheses proposed to explain the emergence of such complex interactions, we propose here to focus on the steps leading a bacterium to transition from a free-living life-style to host association through biphasic life cycles. Mathematical modeling is in this context a powerful tool to assess the optimality of evolutionary strategies for bacteria. In a simple matrix population model, we show the existence of two different regimes: one where the effect of transmissibility from environment to host dominates, and a second where the within-host fitness matters most. Including more and more biological constraints to our models, we will be able to confront our results to strategies actually undertaken by bacterial populations in evolution experiments involving natural colonizers of *C. elegans*, forced either to switch from environment to host and back, or alternatively to evolve under comparable, yet completely host-free conditions.

Keywords: host association, evolution of life cycles, mathematical modeling

---Abstract for Poster Presentation in YIRD2019---

A new model on the runway of symbiosis: the breadcrumb sponge *Halichondria panicea* and its main symbiont

Lara Schmittmann[1], Kathrin Busch[1], Kristina Bayer[1], Björn Buchholz[1], Lucía Pita[1], Ute Hentschel[1,2]

[1]GEOMAR Helmholtz Centre for Ocean Research Kiel;

[2]Christian-Albrechts-University Kiel

Sponges (Porifera) as ancient metazoans have the longest record of interactions with microbes in the animal kingdom. Their associated bacterial communities are host species-specific and stable over space and time, which suggests recognition and differentiation of bacteria. While a growing body of -omics data has shed light on the composition and functional gene repertoire of bacterial symbionts, an experimental model is lacking that allows to understand the host side of the interaction. Therefore, we aim to develop the small and common breadcrumb sponge *Halichondria panicea* from the Baltic Sea as an experimentally tractable model system to study the response of the sponge-host towards different bacteria *in vivo*. This low microbial abundance sponge is characterized by a strikingly high abundance (40-80 %) of the bacterium *Candidatus* Halichondribacter symbioticus belonging to the family Rhodobacteraceae.

Both controlled outdoor experimental work on marine benthic communities and indoor experiments on the single species level are possible with *H. panicea*. We show that the sponge maintains its main symbiont under heat stress and after long-term cultivation in a flow-through aquaria system. In order to fully dissect the response of *H. panicea* towards different bacteria including *Candidatus* Halichondribacter symbioticus, we are establishing gnotobiotic sponge cultures for controlled inoculation of gnotobiotic sponges with bacterial mock communities. The specially designed culture units prevent contamination and allow a flow-through of sterile filtered artificial seawater. We are able to disrupt the symbiotic bacteria community after incubation with an antibiotic cocktail while reducing the main symbiont significantly. This novel gnotobiotic study system will pave the road towards a mechanistic understanding of host-microbe interactions within the sponge holobiont and incomparable possibilities for experimentation.

---Abstract for Poster Presentation in YIRD2019---

Are spontaneous contractions of the body wall shaping the microbiota in *Hydra*?

Christoph Giez[1], Janna Nawroth[2], Ann-Sophie Matt[1], Alexander Klimovich[1], Thomas Bosch[1]

[1]Zoological Institute, Christian-Albrechts University Kiel, Germany

[2]Emulate, Inc., USA

Spontaneous contractions are a ubiquitous phenomenon in the animal kingdom but their function is still not completely understood. They are found in the vertebrate intestine as well as in the early-branching metazoan *Hydra*. So far it is known that the spontaneous contractions are controlled by pacemaker cells which have a unique molecular signature. Recent findings also indicate that symbiotic bacteria are capable of modulating those spontaneous contractions. This is leading to the conclusion that bacteria are cross-talking with the pacemaker cell population. Here, we propose that in *Hydra*, an animal of early evolutionary emergence, the spontaneous contractions are shaping both the microbiota composition and their spatial distribution along the body column by continuously exchanging the fluid environment.

Keywords: Spontaneous contractions, host-microbe cross talk, fluid boundary layer

---Abstract for Poster Presentation in YIRD2019---

Mechanistic and evolutionary basis of the effects of dietary protein restriction and malnutrition on immunocompetence in *Drosophila melanogaster*

Vaibhvi[1,2], Thomas Roeder[1,2]

[1]Zoological Institute, CAU, Kiel, Germany

[2]Max Planck Institute for Evolutionary Biology, Plön, Germany

Dietary restriction (DR) or the decrease in the nutrient content of food without causing malnutrition, has been reported to increase the lifespan in a range of animals. At the evolutionary level, the most accepted theory given to explain this phenomenon is the disposable soma theory, according to which, when the resources are limited, the organism increases investment in somatic maintenance for the time being anticipating more resources in the future when reproductive investment can be resumed. However, unlike longevity, immunity, which is another important somatic trait, shows ambiguous results in response to DR. Possible reasons being the more complex nature of immunity and difficulty in quantitively measuring it because of the layer of components it consists of, that may not always be regulated the same way. What adds to the problem is the range of non-standardized diets used in various studies. To solve this, in this study, a chemically synthesized standardized holidic diet was used to study the effect of DR, in terms of protein content, on *Drosophila melanogaster* immunity. To differentiate the effects from malnutrition, an additional dietary regime with no protein was also studied. A range of immunity-related parameters were compared, including survivorship in response to different types of pathogens as well as severity of infection, basal and post-infection transcript levels of the antimicrobial peptides. Effect of duration of keeping on these diets on immune response and impact on the amplitude of circadian cycling in the organs responsible for major immune function were also looked at.

Keywords: Dietary Restriction, Protein Malnutrition, Immunity, Drosophila immunity, Innate immunity, Circadian rhythm, *Drosophila melanogaster*

---Abstract for Poster Presentation in YIRD2019---

Sex-specific parental transfer of microbiota

Kim-Sara Wagner[1], Isabel Tanger[1], Olivia Roth[1]

[1]GEOMAR Helmholtz Center for Ocean Research Kiel, Marine Evolutionary Ecology, Düsternbrooker Weg 20, 24105 Kiel, Germany

All living organisms are inhabited by a mutualistic microbial community, called the microbiota. The microbiota boosts the host's immune system, which in turn regulates the function of the microorganisms. A major pathway for immune priming in viviparous animals occurs via commensal bacteria that are transferred from parents to offspring during pregnancy, birth and breastfeeding. Although these processes are unique to the maternal body, evidence exists that fathers likewise influence the offspring microbiota and are thus involved in the transfer of immunity. With its unique reproductive strategy, the broad-nosed pipefish *Syngnathus typhle* combines female egg production with male pregnancy and therefore allows separating sex from parental investment. Describing initial microbial colonization permits to explore the sex-specific parental transfer of microbiota and its potential interaction with trans-generational immune priming. An earlier study suggested that female gonads and male brood pouches differ in their microbial community. However, which fraction of the microbiota is transferred to the offspring by whom, and what role the microbes play in shaping the offspring's immune system remains elusive.

In addition to previous descriptions of bacterial communities using next-generation sequencing, we will describe characteristic features and functions of associated microbes by culture-based experiments in combination with manipulation approaches. We currently investigate, which sex-specific microbes can be cultivated under laboratory conditions and which antibiotics these bacteria are sensitive to. A larger study will then transfer this knowledge to live pipefish to perform controlled depletion and manipulation of the sexspecific microbiota.

Keywords: microbiota, pipefish, male pregnancy, immunology, antibiotics

---Abstract for Poster Presentation in YIRD2019---

Metabolic Modeling in Metaorganisms

Georgios Marinos[1], Johannes Zimmermann[1], Silvio Waschina[1], Kristina Bayer[1], Martin T. Jahn[2], Beate M. Slaby[2], Peter Deines[3], Ute Hentsche[2], Christoph Kaleta[1]

[1]Medical Systems Biology Research Group – Institute of Experimental Medicine, UKSH Campus Kiel, CAU zu Kiel

[2]Marine Symbioses Research Unit – GEOMAR, Helmholtz Centre for Ocean Research Kiel

[3]Zoological Institute, CAU zu Kiel

Advances in Systems Biology have enabled the *in-silico* analysis of the metabolic capabilities of organisms through the reconstruction of their metabolic networks, based on the organisms' genome sequence. Importantly, these models can be used in context-specific simulations to explore their metabolic interactions with other organisms. Hence, an important application is the exploration of the metabolism of metaorganisms. The aim of our research is to predict host-bacteria and bacteria-bacteria interactions and to identify key molecules that characterize these relationships in various metaorganisms. Through an automatic pipeline (*GapSeq*), we constructed metabolic models of the bacteria starting from genomes or metagenomes, while conducting context-specific (e.g. nutrition, space, and time) computational experiments based on these models (software *MicrobiomeGS* [currently not published] and *BacArena*). Recent analyses revealed metabolic interactions among bacteria in sponges (*Aplysina aerophoba*), which led to a series of supplementation experiments *in-vivo*. In parallel, we have modeled and simulated the *in-vitro* growth in co-cultures of key bacteria occurring in the *Hydra* metaorganism. Taken together, our *in-silico* approach enables the prediction of ecological interactions between these bacteria, which can be compared with the interactions proposed by wet-lab experiments.

---Abstract for Poster Presentation in YIRD2019---

Functional characterization of caenopore SPP-10 from *Caenorhabditis elegans*

Christine Blurton[1], Lena Bluhm[1], Barbara Pees[1], Matthias Leippe[1]

[1]Comparative Immunobiology, Zoological Institute, Kiel University, Germany

Antimicrobial peptides (AMPs) in *Caenorhabditis elegans* are called caenopores and belong to the saposin-like proteins (SAPLIPs). Caenopores share structural similarities with amoebapore A, an ancient pore-forming AMP from *Entamoeba histolytica*, and are considered to have an antimicrobial and pore-forming activity. The *spp-10* gene encodes through alternative splicing for two or three saposin B-type domains, whose role as putative immune effectors in *C. elegans* has yet not been revealed.

Proteome analyses and a transgenic reporter strain verified a constitutive expression of SPP-10 and the presence of the two saposin B-type domains SPP-10a and SPP-10b. The population growth and reproduction rate of the *spp-10* mutant strain *spp-10* (*ok1585*), which lacks the sequence encoding for the two saposin B-type domains SPP-10a and SPP-10b, was significantly reduced. After the heterologous expression of the three saposin B-type domains of *spp-10* in *Escherichia coli*, we demonstrated a pore-forming activity for SPP-10a and SPP-10b towards artificial membranes composed of azolectin as well as bacterial membranes of viable Gram-positive *Bacillus megaterium*. Moreover, SPP-10a and SPP-10b showed a bactericidal effect against *B. megaterium* in a pH-dependent manner.

We confirmed the important role of SPP-10a and SPP-10b as immune effectors in *C. elegans* by demonstrating an antimicrobial and pore-forming activity. We are currently investigating a putative synergistic effect between both AMPs. Furthermore, we extend the phenotypic analyses by determining the larval developmental time of *spp-10* mutant strains, which may underline the crucial role of SPPs in *C. elegans*.

Keywords: *C. elegans*, antimicrobial proteins, caenopores

---Abstract for Poster Presentation in YIRD2019---

Effects of protein-restricted diets on the epithelia-microbe interactions in the intestinal tract of *Drosophila melanogaster*

Jakob von Frieling[1], Thomas Roeder[1]

[1]Zoological Institute, Kiel University

Nutritional uptake is tightly linked to the intestinal microbiota, which plays an important role in the regulation of energy balance, ontogeny, survival as well as in the development of metabolic diseases. Today, little is known about the function of the intestinal microbiota under chronic nutrient shortage, especially under protein-restricted malnutrition. Thus, we are using *Drosophila melanogaster* to investigate the effects of different protein-deprived diets on the gut microbiota and subsequent effects on the homeostasis of intestinal epithelial cell populations. On the molecular level, we examine the signaling of the Target of Rapamycin (TOR) pathway, a core component of the nutrient-responsive pathway, with regard to this different nutritional interventions and its association with the intestinal microbiota. We can show that long-term interventions of protein-restricted diets leads to substantial changes in the intestinal structure of the intestine and that the microbiota plays a central role in promoting growth and proliferation. Interestingly, the intestinal response to nutritional stressors as well as the growth promoting effects of the microbiota are absent in Tor deficient flies. Furthermore, the nutritional stressors and the intestinal microbiota have a marked impact on the transcriptional regulation of the host intestine.

---Abstract for Poster Presentation in YIRD2019---

Tripartite species co-evolution under environmental change: Can prophages accelerate bacterial virulence evolution?

Jelena Rajkov[1], Carolin C. Wendling[2], Olivia Roth[1]

[1]GEOMAR Helmholtz Center for Ocean Research Kiel, Germany

[2]Pathogen Ecology, Department of Environmental Systems Science, ETH Zürich, Switzerland

Accumulating evidence points to shifts in biotic interactions due to environmental change. However, empirical studies of complex types of interactions with multiple interaction partners are still missing. Here we use a natural tripartite system from the Baltic Sea: the broad-nosed pipefish *Syngnathus typhle*, opportunistic marine bacteria of the genus Vibrio, and their associated temperate phage, to study rapid adaptation. Previous studies suggest that lower salinity is one of the main factors leading to increased virulence of marine *Vibrio* bacteria, while environmental change can weaken host immune response, leading to poor defence against infectious diseases. Temperate bacteriophages are also known to alter bacterial virulence by integrating into the bacterial chromosome and transferring necessary virulence genes that can turn opportunistic bacteria into pathogens. Using two *in vivo* serial passage experiments, in which bacteria with and without a temperate phage are passed through the pipefish gut, we will investigate how the eukaryotic host can constrain or promote *Vibrio*-phage co-evolution and how this impacts *Vibrio* virulence. We will assess how these interactions change under a scenario of anthropogenic induced environmental change by conducting the experiment at different salinities. By separating the gut and the systemic passage we will assess if the virulence genes provided by the prophage enable *Vibrio* to cross the gut-blood barrier and cause systemic infection. The evaluation of this complex co-evolution will improve our knowledge on the impact of environmental change and the interaction with prophages on bacterial virulence.

Keywords: co-evolution, tripartite interaction, serial passage, virulence, *Vibrio*, prophage, pipefish

---Abstract for Poster Presentation in YIRD2019---

Metaorganism comb jelly: Microbiota differences of the comb jelly *Mnemiopsis leidyi* in native and invasive sub-populations

Cornelia Jaspers[1], Ruth A. Schmitz[2], Thorsten B.H. Reusch[1], Nancy Weiland-Bräuer[2]

[1]GEOMAR Helmholtz Centre for Ocean Research Kiel, Marine Evolutionary Ecology, Kiel, Germany

[2]Institute for General Microbiology, Christian-Albrechts-Universität zu Kiel, Kiel, Germany

The translocation of non-indigenous species around the world, especially in marine systems, is a matter of concern for biodiversity conservation and ecosystem functioning. While specific traits are often recognized to influence the success in the establishment of non-indigenous species, the impact of the associated microbial community for the fitness, performance and invasion success of basal marine metazoans remains vastly unknown. In this study, we compared bacterial composition patterns of the invasive ctenophore *Mnemiopsis leidyi* in different native and invasive sub-populations along with the genetic structure of the host (polymorphic microsatellite markers). Amplicon sequencing of the 16S rRNA gene (V1-V2 hypervariable regions) revealed that *M. leidyi* as representative of the phylum Ctenophora, the sister group to all metazoans, harbored a distinct microbiota compared to the ambient seawater, which significantly differed across two major tissues, namely epidermis and gastrodermis. Moreover, we identified significant differences in bacterial community compositions between native and invasive sub-populations of *M. leidyi* indicating, that the microbiota community is likely influenced by the genotypic background of the host.

---Abstract for Poster Presentation in YIRD2019---

Hydra viridissima: A model for understanding a tripartite symbiosis

Jay Bathia[1], Katja Schröder[1], Mayuko Hamada[2], Sebastian Fraune[3], Thomas Bosch[1]

[1]Zoologisches Institut, Christian Albrechts Universität, 24118 Kiel, Germany

[2]Okayama University, 700-8530 Okayama, Japan

[3]Zoologie und Organismische Interaktionen, Heinrich-Heine-Universität, 40225 Düsseldorf, Germany

Hydra viridissima is a fresh water polyp belonging to the phylum Cnidaria. It harbors endosymbiotic algae *Chlorella* in the endoderm. The interactions between the host and the algae are mainly metabolic in nature. The algae provides fixed carbon in the form of maltose and, in turn, the host provides the algae with the glutamine as a source of nitrogen. Moreover, there is a genomic loss of essential genes for nitrate and ammonium fixation in the algae, further strengthening the interdependence. We now take into account the third partner of the *Hydra viridissima* metaorganism: bacteria. We observed that upon co-housing of the symbiotic (hosts bearing the algae) and the aposymbiotic (hosts without the algae) animals, there is a diurnal shift in the microbiome composition of the symbiotic animals. During the dark phase, the microbiome of the symbiotic animals is similar to that of the aposymbiotic animals. Moreover, the disrupted diurnal cycle (constant darkness) also results in a higher resemblance of the microbiome of symbiotic animals to that of the aposymbiotic ones. However, upon mono housing, this effect is lost, indicating the selection pressure implied by the algae. To elucidate further the tripartite relationship, we compare the bacteria free symbiotic and aposymbiotic hosts with the controls and conventionalized animals. Our observations indicate that the absent microbiota has no effect on the fitness of symbiosis. However, more detailed and directed approaches might reveal the effect of the absent microbiota on the fitness of the symbiosis and hence provide a better understanding of the tripartite symbiosis.

---Abstract for Poster Presentation in YIRD2019---

The impact of domestication on the wheat microbiota

M. Amine Hassani[1,2], Ezgi Özkurt[1,2], Heike Seybold[1,2], Eva H. Stukenbrock[1,2]

[1]Christian-Albrechts University of Kiel, Kiel, Germany.

[2]Max Planck Institute for Evolutionary Biology, Plön, Germany.

In nature, plants coexist with diverse microbial communities, such as archaea, bacteria and fungi[1]. The association between the plant and these microorganisms forms an ecological unit termed the holobiont[2]. Plant-associated microbes can have beneficial, neutral or deleterious impact on their host fitness[3,4]. It is therefore important to understand fundamental principles that govern the establishment of the plant microbiota toward better predicting dysbiosis-mediated diseases[5]. Most of the microbes that colonize plants are recruited from the surrendering environments[6] (air, soil) and/or vertically inherited[7] (seed microbiota). It is well-documented that abiotic factors[6] and host cues[1] are key determinants of the plant microbiota. However, the evolutionary processes that mediate microbiota co-adaptation to the host are not well understood. Plant domestication provides a framework to glean data on the dynamic of the plant microbiota over short evolutionary times, identify selective pressures that shape the microbiota of domesticated plant species and formulate precise hypothesis regarding host-microbiota co-evolution. The objectives of this research is 1) to study the role of domestication in altering the community structure and function of the wheat leaf- and root-associated microbiota (bacterial and fungal communities), 2) establish a bacterial and fungal culture collection representative of the wheat leaf- and root-associated microbiota of wild or domesticated wheat species and 3) decipher the interactions between the leaf microbiota of domesticated wheat and the fungal pathogen *Zymoseptoria tritici*. Our preliminary results show that wild and domesticated wheat species harbor distinct microbial communities and that infection by *Z. tritici* significantly alters the leaf-associated bacterial communities of the domesticated wheat.

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---Abstract for Poster Presentation in YIRD2019---

Role of antimicrobial proteins in shaping *Caenorhabditis elegans* microbial associations

Barbara Pees[1], Carola Petersen[1], Christian Treitz[2], Andreas Tholey[2], Matthias Leippe[1]

[1]Comparative Immunobiology, Zoological Institute, Kiel University, Germany

[2]Systematic Proteome Research and Bioanalytics, Institute for Experimental Medicine, Kiel University, Germany

The identification of the native *C. elegans* microbiota and interacting host factors has only recently begun despite of the worm's microbe-rich natural habitat and its bacteriovorus lifestyle. Several protein families have been identified to be involved in digestion of food bacteria and in immune defenses against pathogenic bacteria. Yet, the interaction of host factors with microbiota bacteria has not been evaluated.

Hence, we aim at characterizing the role of antimicrobial proteins (AMPs) in shaping microbial associations with *C. elegans*. Comparative proteome analyses revealed that two families of AMPs, lysozymes (ILYS, LYS) and caenopores (SPP), were differently abundant in worms exposed to microbiota bacteria. Members of both protein families have previously been demonstrated to compromise bacterial cells walls. The expression of selected AMP encoding genes was primarily localized to the intestine of *C. elegans* as reporter strains could show. Further, in *ilys* knock-out mutants exposure to microbiota bacteria resulted in an increased bacterial colonization and also changes in fertility.

We are currently trying to knock-out whole gene clusters of both, caenopore and lysozyme genes, to understand the role of these clusters on microbiota bacteria *in vivo*. Additionally, we are characterizing recombinantly expressed ILYS and SPP proteins regarding their potential interaction with microbiota bacteria *in vitro*.

Our results may provide a first insight into the function of AMPs shaping microbial associations of bacteriovorus *C. elegans*.

Keywords: *C. elegans*, microbiota, antimicrobial proteins, lysozymes, caenopores

---Abstract for Poster Presentation in YIRD2019---

Microbial recognition in marine sponges

Lucía Pita[1], Marc Höppner[2], Marta Ribes[3] and Ute Hentschel [1,4]

[1]GEOMAR Helmholtz Centre for Ocean Research, Kiel, Düsternbrooker Weg 20, 24105 Kiel, Germany

[2 4]Christian-Albrechts-University Kiel, Institute of Clinical Molecular Biology, Kiel, Germany

[3]Institute of Marine Science CSIC, Passeig Marítim de la Barceloneta 37-49, 08003 Barcelona, Spain

[4]Christian-Albrechts-University Kiel, Christian-Albrechts-Platz 4, 24118 Kiel

A common challenge for all animals is discriminating between microbes. Sponges are early-diverging animals that feed on bacteria by constantly filtering seawater, yet they harbour specific microbial communities. We aim to characterize sponge mechanisms of microbial recognition. We adopt an experimental approach and evaluated the molecular response to microbial stimuli by RNA-Seq. We focused on two sponge species that represent a long-accepted dichotomy in sponge symbiosis: high microbial abundance sponges (HMA) harbour symbiotic communities in densities that are 2-to-4 orders of magnitude higher than in low microbial abundance sponges (LMA). Sponges responded by increased expression of immune receptors (i.e., NLRs in LMA, SRCR and GPCR in HMA) and the transduction of signal yielding apoptosis and phagocytosis. The differences between species relied on the activation of different set of receptors and pathways as well as the magnitude of the response, with higher number of differentially-expressed genes in the HMA than the LMA sponge. We proposed that these differences are due to higher conflicting signals from the symbionts in the HMA and higher level of constitutive immunity the LMA sponge. These studies allow us to identify conserved mechanisms of animal-microbe interactions.

Keywords: RNA-Seq; immune receptors; Porifera; microbial-associated molecular patterns

---Abstract for Poster Presentation in YIRD2019---

Pantoea agglomerans colonization dynamics of the wheat roots upon germination

Ryszard Soluch[1], Nils F. Hülter[1], Tal Dagan[1]

[1]Institute for General Microbiology, Kiel University, Germany

Background

Plants are colonized by a wide diversity of microbes that may play a role in plant adaptation to various environmental conditions and disease resistance. Members of the plant microbiota include bacteria that are recruited from the environment and vertically inherited bacteria. The main road for vertically inherited bacteria in plants is considered to be transmission via the seed. Wheat seeds have been reported to harbor bacteria, however, the wheat embryo has been reported to be germ-free hence the colonization routs of seed-borne bacteria remain poorly understudied.

Objectives

Here we study the colonization dynamics of one member of the wheat microbiota – *Pantoea agglomerans* (*Pantoea*) – which we isolated from wheat seeds.

Methods

We established a system to cultivate germ-free plants devoid their native microbiota. In addition, we equipped the *Pantoea* isolate with broad-host-range plasmid encoding kanamycin resistance and constitutively expressing a fluorescent protein (GFP or mCherry). We followed the process of *Pantoea* colonization of the roots by determining the number of *Pantoea* cells per plant root system over time.

Results

Our results demonstrate dynamics of bacterial density increase. Five days post germination, Pantoea population reaches a stable carrying capacity of 108 cells/gr. Experiments of priority effects in colonization show that early incoming colonizers have a numerical priority over late incoming colonizers already after 24h. Our results suggest that seed-borne bacteria have an advantage in root colonization in wheat. This data provides a fundament for future experiments on association between Pantoea agglomerans and wheat host.

Keywords: Metaorganism colonization, host colonization, plant symbiont, priority effects

---Abstract for Poster Presentation in YIRD2019---

Protein energy malnutrition alters epithelia-microbiota interactions in the intestine with long-lasting effects on inflammation

F. Sommer[1], Neha Mishra[1], J. Hamm[1], R. Häsler[1], L Thingholm[1], K. Klischies[1], N. Sommer[1], A. Franke[1], P. Rosenstiel[1]

[1]Institute of Clinical Molecular Biology, Kiel University, Rosalind-Franklin-Str. 12, 24105 Kiel, Germany

Maintaining health requires a homeostatic equilibrium between the microbial community and the intestinal epithelium that serves as the regulatory interface with the host. Nutritional stressors such as malnutrition, starvation or caloric restriction disturb this equilibrium and thus provoke changes in the function of the intestinal microbiota and intestinal mucosa. We aimed to elucidate the mechanisms underlying the complex tripartite interplay between microbiota, the intestinal epithelium and the environment (nutritional stressors). We therefore developed experimental protein energy malnutrition (PEM) models to investigate the effects of adult, postnatal and prenatal PEM on the microbiota and host physiology, in particular inflammatory susceptibility. We found that PEM induced drastic modifications of the host's gastrointestinal tract but also systemic immunity and metabolism. A single episode of PEM extensively changed the overall microbiota composition enriching for Gammaproteobacteria and Bacteroidaceae while depleting for Actinobacteria and Verrucomicrobia along with the functional metagenomic repertoire. The intestinal epithelial transcriptome was also largely reprogrammed in response to PEM. PEM-induced changes in the microbiota and epithelial transcriptome partially remained upon switching to control diet, indicating a "memory effect". Most important, the long lasting PEM-induced microbiome and transcriptome changes also altered the inflammatory susceptibility in an experimental colitis model *in vivo*. On-going experiments aim at determining whether PEM phenotypes are transmissible, for example from the mother to offspring or solely through the altered microbiome. Our data identified alterations in the microbiome and epithelial transcriptome as potential molecular mechanisms underlying the long lasting physiologic consequences of PEM, thus paving the way to develop probiotic therapeutic interventions for malnutrition.

Keywords: microbiome, protein energy malnutrition, inflammation

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Stochastic inheritance of the microbiome

Román Zapién-Campos[1], Michael Sieber[1], and Arne Traulsen[1]

[1]Max Planck Institute for Evolutionary Biology, Plön, Germany

Our current view of nature portraits a world where macroorganisms dwell in an ocean of microbes. Moreover, some of these microbes go beyond the transitory to establish themselves in or on hosts. Although this might be true for long periods of their life, for many hosts, a microbe-free stage during their prenatal development is the rule. The question of who are the first colonizers and whether these are obtained from the parents follows naturally. We have developed a mathematical model to study the microbial transfer from parents to offspring ("inheritance"). Our results indicate microbial inheritance could act as a support mechanism for hosts challenged by the environmental acquisition of low abundance microbial taxa, limited environmental colonization, or a short lifespan. Nonetheless, its effectiveness depends on the specific value of the parameters describing the host. In ecological and evolutionary terms, this suggests inheritance might become a reliable mechanism only for some host physiologies.

Keywords: microbiome, host, colonization, microbial inheritance, mathematical modelling

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COLLABORATIVE RESEARCH CENTRE 1182

3rd Young Investigator Research Day

List of Participants

Name	Institution	Email
Violeta Albacete	GEOMAR	violetaalbacete27@gmail.com
Clinton Azuure	MPI Plön	cazuure@yahoo.com
Florence Bansept	MPI Plön	bansept@evolbio.mpg.de
Jay Bathia	Kiel University	jbathia@zoologie.uni-kiel.de
Henry Berndt	Kiel University	henry.berndt@icloud.com
Lena Bluhm	Kiel University	stu205391@mail.uni-kiel.de
Christine Blurton	Kiel University	bloerten@gmail.com
Cynthia Maria Chibani	Kiel University	cchibani@ifam.uni-kiel.de
Peter Deines	Kiel University	pdeines@zoologie.uni-kiel.de
Shauni Doms	MPI Plön	doms@evolbio.mpg.de
Laura Ebeler	GEOMAR	lebeler@geomar.de
Yasmeen El-Rayyes	Kiel University	elrayyey@mcmaster.ca
Hanna Fokt	MPI Plön	fokt@evolbio.mpg.de
Christoph Giez	Kiel University	christoph-giez@web.de
Danielle Harris	Kiel University	dharris@zoologie.uni-kiel.de
Mohamed-Amine Hassani	Kiel University	ahassani@bot.uni-kiel.de
Jinru He	Kiel University	jhe@zoologie.uni-kiel.de
Melanie Heckwolf	GEOMAR	mheckwolf@geomar.de
Andreas Helbig	Kiel University	a.helbig@iem.uni-kiel.de
Florian Horn	other	horn@biochemie-des-menschen.de
Stéphanie Hornburg	Kiel University	michl@gma-buesum.de
Cornelia Jaspers	GEOMAR	coja@aqua.dtu.dk
Julia Johnke	Kiel University	jjohnke@zoologie.uni-kiel.de
Jana Krause	GEOMAR	jkrause@geomar.de
Hanna Kronfeld	Kiel University	hkronfeld@tierzucht.uni-kiel.de
Anne Kupczok	Kiel University	akupczok@ifam.uni-kiel.de
Tim Lachnit	Kiel University	tlachnit@zoologie.uni-kiel.de

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3rd Young Investigator Research Day

List of Participants

Name	Institution	Email
Janina Lange	Kiel University	jlange@zoologie.uni-kiel.de
Abuladze Mariam	Kiel University	stu219236@mail.uni-kiel.de
Georgios Marinos	UKSH Kiel	Georgios.Marinos@uksh.de
Véronique Merten	GEOMAR	vmerten@geomar.de
Fabian Nies	Kiel University	fabian.nies@web.de
Barbara Pees	Kiel University	bpees@zoologie.uni-kiel.de
Carola Petersen	Kiel University	cpetersen@zoologie.uni-kiel.de
Tatyana Pichugina	MPI Plön	pichugina@evolbio.mpg.de
Lucia Pita	GEOMAR	lpita@geomar.de
Daniela Prasse	Kiel University	dprasse@ifam.uni-kiel.de
Jelena Rajkov	GEOMAR	jrajkov@geomar.de
Malte Rühlemann	Kiel University	m.ruehlemann@ikmb.uni-kiel.de
AbdulGawaad Saboukh	Kiel University	stu213334@mail.uni-kiel.de
Lara Schmittmann	GEOMAR	lschmittmann@geomar.de
Arunabh Sharma	Kiel University	sharma@medinfo.uni-kiel.de
Michael Sieber	MPI Plön	sieber@evolbio.mpg.de
Sandra Sindt	Kiel University	sasi@tf.uni-kiel.de
Ryszard Soluch	Kiel University	rsoluch@ifam.uni-kiel.de
Felix Sommer	Kiel University	f.sommer@ikmb.uni-kiel.de
Navid Tahan Zadeh	Kiel University	Navid.t.p.m@gmail.com
Julia Tetens	Kiel University	juliatetens@tierzucht.uni-kiel.de
Vaibhvi Vaibhvi	Kiel University	vvaibhvi@zoologie.uni-kiel.de
Jakob von Frieling	Kiel University	jfrieling@zoologie.uni-kiel.de
Lara Vrbanec	MPI Plön	vrbanec@evolbio.mpg.de
Kim-Sara Wagner	GEOMAR	kwagner@geomar.de
Nancy Weiland-Bräuer	Kiel University	nweiland@ifam.uni-kiel.de
Román Zapién-Campos	MPI Plön	zapien@evolbio.mpg.de