



# Programme and abstracts

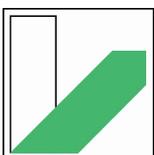
14<sup>th</sup> to 16<sup>th</sup> March 2019

[Bayreuth](#), Germany

Organized by the  
Reproductive and Ecological Immunology Group, Animal  
Population Ecology, Animal Ecology I, [University of Bayreuth](#)

## Organising committee

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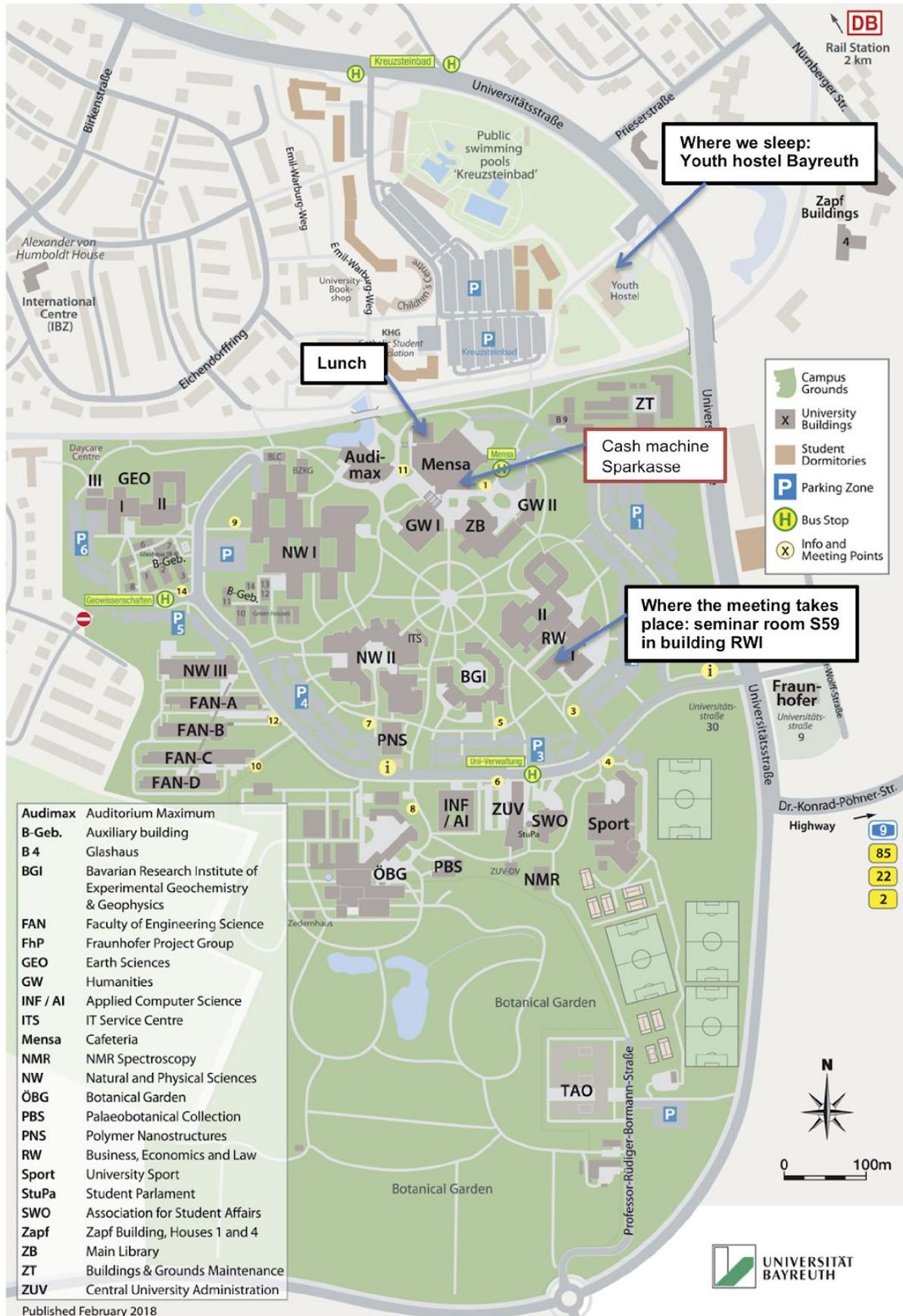


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and Environmental Research

# Venue



# Programme

<u>Thursday</u> , 14.03.2019	
Time	
11:00	Arrival
14:00	Meet & Greet
14:55	Opening words
15:00	<b>1:</b> Martin Těšický et al.: Effect of ageing on immunity, antioxidant enzymes and markers of oxidative stress in great tits ( <i>Parus major</i> )
15:30	<b>2:</b> Margy A. Esparza Mora et al.: Social immunity is plastic: identity and life cycle of pathogen shapes collective defense
16:00	<b>3:</b> Jamie Parker et al.: Convergent evolution of immunological tolerance in male pregnancy
16:30	<b>4:</b> Nithya Kuttiyarthu Veetil et al.: Evolution of neuroimmunological effects of mycoplasmal conjunctivitis in house finch ( <i>Haemorhous mexicanus</i> )
17:00	<b>5:</b> S. Krausová et al.: How the Barn Swallow escaped from parasites?
18:30	Dinner
19:30	Invited talk <b>Tim Janicke:</b> Sex-specific sexual selection across the animal kingdom: evolutionary causes and consequences

## Friday, 15.03.2019

Time	
08:00	Breakfast
09:20	Opening
09:30	<b>6:</b> Jana Křemenová: Age determination in individual wild-caught <i>Cimex lectularius</i> using pteridine concentration
10:00	<b>7:</b> Christian Massino: Ecological speciation and sperm biology in populations of the common bed bug
10:30	<b>8:</b> Barbara Eckel et al.: The role of spermathecal secretory cells for female fertility in <i>Drosophila melanogaster</i>
11:00	Coffee break
11:30	<b>9:</b> Ruijian Guo: How age interacts with mitonuclear epistasis to affect sperm metabolism in <i>Drosophila melanogaster</i>
12:00	<b>10:</b> Arpita Nath: Exploring DNA double strand breaks and their effects on recombination
13:00	Lunch
15:00	<b>11:</b> Christine Manthey et al.: Gut microbiota changes throughout development
15:30	<b>12:</b> Véronique Paris: Microbiota turnover and host immunity throughout insect metamorphosis
16:00	<b>13:</b> Henry Goehlich: Temperate phages go viral at reduced salinity levels
16:30	<u>Poster and discussion session</u>
18:30	Dinner
19:30	Invited talk <b>Olivia Roth:</b> Evolution of male pregnancy requires remodeling of adaptive immunity

## Saturday, 16.03.2019

Time	
08:00	Breakfast
09:20	Opening
09:30	<a href="#">14</a> : Florent Manzi et al.: Temperature and host diet jointly influence the spread and intensity of disease in a <i>Daphnia</i> -fungal parasite system
10:00	<a href="#">15</a> : Agnes Piecyk et al.: Helminth immune modulation in sticklebacks
10:30	<a href="#">16</a> : Baydaa El Shazely: Fitness costs of antimicrobial peptide resistance
11:00	Coffee break
11:30	<a href="#">17</a> : Beatriz Acuña Hidalgo et al.: Infection dose and bacterial persistence in <i>Drosophila melanogaster</i>
12:00	<a href="#">18</a> : Luís Silva et al.: Dynamics of insect tolerance to bacterial infections
12:30	<a href="#">19</a> : Yicong Liu et al.: Collateral sensitivity of antimicrobial peptide-resistant <i>Staphylococcus aureus</i> to conventional antibiotics
13:00	Departure

# Thursday, 14.03.2019

1 in *Ecological immunity*: [Seminar room S59](#), 14.03.2019, 15:00-15:25

## Effect of ageing on immunity, antioxidant enzymes and markers of oxidative stress in great tits (*Parus major*)

MARTIN TĚŠICKÝ<sup>1</sup>, OLDŘICH TOMÁŠEK<sup>1,2</sup>, TEREZA KRAJZINGROVÁ<sup>1</sup>, HANA VELOVÁ<sup>1</sup>, JANA SVOBODOVÁ<sup>1</sup>, PETRA BAUEROVÁ<sup>3</sup>, HANA PINKASOVÁ<sup>1</sup>, TOMÁŠ ALBRECHT<sup>1,3</sup> & MICHAL VINKLER<sup>1</sup>

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In senescence, physiological function and reproductive success typically decrease with age whereas the probability of mortality increases. While the symptoms of ageing are well described in human and domestic animals, our knowledge of ageing in free-living birds is still limited. Due to higher level of antioxidants in blood, higher resistance against oxidative stress and higher longevity compared to mammals of similar size, small passerines could serve as a good biomedical model for studying longevity. In 2011-2018, we studied a free-living population of great tits (*Parus major*) breeding in nest boxes in a forest fragment at outskirts of Prague, Czech Republic. We collected datasets of 204 birds of known age (cohort dataset) and 153 repeatedly captured birds (longitudinal dataset). The main aim of this study is, therefore, to describe the effect of ageing on biologically relevant traits involving (1) immunity (differential and absolute white blood cell count, oxidative burst), antioxidant capacity (superoxide dismutase, glutathione peroxidase and thiol concentration in blood), and several markers of oxidative damage (isoprostane, leukotriene, nitrotyrosine, deoxyguanosines concentration, etc.). We describe symptoms of ageing in great tits and the crosstalk between immunity, antioxidant level and markers of oxidative stress.

2 in *Ecological immunity*: Seminar room S59, 14.03.2019, 15:30-15:55

## Social immunity is plastic: identity and life cycle of pathogen shapes collective defense

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Social insects nesting in soil environments are in constant contact with entomopathogens and have evolved disease resistance mechanisms within a colony to prevent the occurrence and spread of infectious diseases. Among these mechanisms: mutual grooming reduces the cuticular load of pathogens, and burial of cadavers and cannibalism can prevent pathogens from replicating within the group. Termite species can be a good non-Hymenopteran eusocial model for studying the evolution and function of animal immunity and sociality. In this project, I aimed to understand how different entomopathogenic strategies are defended against by their social insect hosts. Specifically, I tested the following hypothesis: the rate and type of social immune responses within termite mini-colonies are driven by key stepwise pathogen infection process. We infected the eastern subterranean termite *Reticulitermes flavipes* with the entomopathogenic fungus *Metarhizium anisopliae* by injection of  $5 \times 10^8$  blastospores/mL (alive blastospores and heat-killed blastospores) and Ringer as a control, then isolated at different stages of infection: 2, 8, 12 and 15 hours: times chosen based on the timing of events in the infectious process. Subsequently, each *M. anisopliae*-infected or control termite was reintroduced to a healthy nestmates group and behavioural responses were recorded. As expected, termites groomed pathogen-infected individuals significantly more than controls; however, grooming was not

different in alive blastospores and heat-killed blastospores treatments. Significantly, we found that cannibalism became prevalent in both treatments (alive blastospores and heat-killed blastospores) but increased rapidly and was more intense at 15 h after injection with alive blastospores and when termites were close to dead, this highlights the importance of host condition as a cue for social hygienic behaviour. Our study reveals that the internal infection is triggering cannibalism as a main response. Specifically, we show how the host appears to emit sickness cues that targets for its own sacrifice demonstrating that termites have independently evolved to both identify and destructively respond to sickness.

Keywords: termites, social immunity, host-cues, pathogen-cues

3 in *Ecological immunity*: Seminar room S59, 14.03.2019, 16:00-16:25

### **Convergent evolution of immunological tolerance in male pregnancy**

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Syngnathids (pipefish and seahorses) are an enigmatic example for the evolution of parental investment due to their unique male pregnancy that is displayed in a variety of forms ranging from external pregnancy (Nerophinae) to two different fully internal gestations (*Syngnathus* and *Hippocampus*). Extensive mammalian pregnancy studies have highlighted that adaptive immune system expression changes and gene silencing were key to tolerating semi-allogeneic embryonic growth. These were thus integral for the evolution of pregnancy. However, the loss or heavy modification of the MHC II adaptive immune pathway in *Syngnathus* and *Hippocampus*, respectively, suggests that selection for male pregnancy in syngnathids resulted in adaptations that go beyond expression changes. In order to discern whether the unique paternal pregnancy could only have evolved due to the loss of the MHC II pathway, its key function of self/nonself recognition needs to be understood. Intraspecies fin grafts will be used to examine immunological tolerances and expression of genes involved in allorecognition, across syngnathid species with and without the MHC II pathway. In addition, single cell expression analyses will be used to examine the repercussions of these gene losses on immune system function and the potential loss of related specific immune cell lines within the Syngnathiforme lineage. Lastly, to gain insight into immune and pregnancy gene expression changes and highlight co-opted genes specific to paternal pregnancy, RNA-seq will be utilised across multiple syngnathid brooding types. Further comparisons can be used to help determine whether similarly co-opted genes have evolved convergently among viviparous species across other phyla.

4 in *Ecological immunity*: Seminar room S59, 14.03.2019, 16:30-16:55

### **Evolution of neuroimmunological effects of mycoplasmal conjunctivitis in house finch (*Haemorrhous mexicanus*)**

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Host-pathogen coadaptation is one of the most rapid evolutionary processes in the living world. Particularly interesting are cases of recent host switches in pathogens followed by accelerated evolution of host immunity and pathogen virulence which are highly relevant for our insight into the mechanisms of the mutual coadaptation. This project conducted in collaboration with our US partners aims at revealing the evolutionary adaptations in the interaction of house finch with *Mycoplasma gallisepticum*, a unique research model system. We will focus on changes in gene expression (RNA-seq and RT-qPCR) in brain and peripheral lymphoid organ (conjunctiva), two

sites recognised to be affected by the interaction with pathogen. Using the research material transported to Czech Republic, in the first year we plan to extract RNA from 120 samples representing 60 house finch individuals from 4 different populations (Virginia, Iowa, Arizona and Hawaii) and perform the initial RNA-seq run. Furthermore, we will analyse expression of a key cytokine (IL1B). We will also analyse the sickness behaviour in the experimental individuals. In the second year we will finish the transcriptome analysis and select appropriate candidate genes for the RT-qPCR analysis that will be conducted in the third year of the project. We expect our results to importantly contribute to the understanding of the evolution of physiological mechanisms linking immune function to animal behaviour.

5 in *Host-parasite interaction*: Seminar room S59, 14.03.2019, 17:00-17:30

### **How the Barn Swallow escaped from parasites?**

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Host range shifts can be associated with a loss of former parasites and subsequent acquisition of novel parasites from the new location. In species that undergo regular migrations the range shift comprises the invasions into a new breeding area or changes in migration behaviour. Migratory species face a risk of infection at winter grounds by parasites of resident species, hence the change of migration behaviour may result in a decrease of the parasite load and consequently reduction of the cost of migration. We studied distribution and prevalence of *Plasmodium* and *Haemoproteus* haemosporidian parasites using nested PCR and sequencing of cytochrome b in 2196 Barn Swallows from a wide range covering all six subspecies and their hybrids. We have found zero parasite prevalence in the subspecies exhibiting essentially no migration behaviour. The prevalence in subspecies regularly exhibiting long-distance migration ranged from 11 to 19 %. We have detected 37 (9 *Haemoproteus*, 28 *Plasmodium*) parasite lineages whose distribution tightly mirror the host phylogeography. Parasite lineages from the North American Barn Swallows *Hirundo rustica erythrogaster* differ from the lineages in the other Barn Swallow subspecies and were very similar or identical with lineages formerly described from other American birds. The American parasite lineages were not detected in *Hirundo rustica tytleri* which colonised northeast Asia from the North America. Our analysis suggests that both the shift of the breeding sites and reduction of migration resulted in parasite loss during the Barn Swallow evolutionary history.

INVITED TALK: Seminar room 59, 19:30-20:30

### **Sex-specific sexual selection across the animal kingdom: evolutionary causes and consequences**

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The presumably most fundamental concept in sexual selection research posits that competition for mating partners and their gametes is generally stronger among males compared to females. Surprisingly, this so-called Darwin-Bateman paradigm has rarely been tested at a global scale, which more recently gave rise to alternative ideas arguing that sex differences in the strength of sexual selection are random or entirely driven by environmental factors. Moreover, many of the predicted evolutionary causes and consequences of stronger sexual selection males are still poorly understood. In my talk I will present a data-driven synthesis of our current knowledge on the sex difference in sexual selection. More specifically, I will (i) discuss the role of anisogamy as an evolutionary precursor for the observed sex differences, (ii) explore the importance of the

operational sex ratio and other environmental conditions for generating inter-specific variation in sexual selection, and (iii) point to some evolutionary consequences of sex-specific sexual selection such as sexual dimorphism, sex differences in immunity, and species richness.

Keywords:

anisogamy; immunity; meta-analysis; operational sex ratio; sexual selection; species richness

## Friday, 15.03.2019

6 in Open session: [Seminar room S59](#), 15.03.2019, 9:30-9:55

### Age determination in individual wild-caught *Cimex lectularius* using pteridine concentration

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The individual age for different insect species can be determined by the concentration of pteridines in the eye. The female age and with it the changing ability to keep viable sperm seems to be an important parameter in the study of ecological speciation and reproductive isolation of two host lines of bedbugs (*C. lectularius*) parasitizing humans and bats. No studies have yet been conducted to determine the age of the bed bug and there are still some methodological inconsistencies in determining the age we had to deal with, i.e. the selection of pteridine standards and extraction method, the presence of light during extraction, before we could proceed to compile a calibration curve for the dependence of pteridines on age. After optimizing the extraction and measurement of pteridine concentrations, we developed new methodological protocol. Of the five tested pteridine standards, Leucopterin showed the highest consistency within the age cohort and seems to be most appropriate for determining the age of bedbugs in wild populations.

7 in Reproduction: Seminar room S59, 15.03.2019, 10:00-10:25

### Ecological speciation and sperm biology in populations of the common bed bug

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The research field of speciation is a long-studied field. Speciation is a process whereby a reproduction barrier is established between different populations. In ecological speciation populations diverge because of adaptations in response to diverging natural selection pressures. A crucial is how these adaptations cause a reproductive barrier. Most studies focussed on adaptations that act before mating e.g. behavioural isolation and male competition. Here I will focus on postmating prezygotic isolation using human- and bat-associated host races of the common bedbug *Cimex lectularius*. Previously it was shown that sperm metabolism is altered inside the female sperm storage organs. I will measure sperm function in relation to male diet using fluorescence lifetime imaging microscopy (FLIM) and I will provide an overview of this technology as well.

## The role of spermathecal secretory cells for female fertility in *Drosophila melanogaster*

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Females of virtually any internally fertilising species store viable sperm, lasting from days to years, in their reproductive tract or in specialised organs. *Drosophila melanogaster* females store sperm for at least 14 days after mating. They possess two types of storage organs. The paired spermathecae serve for long-term sperm storage, while the seminal receptacle is used for short-term sperm storage. The spermathecae are surrounded by cells with secretory function, whose products as a whole are required for proper sperm storage in spermathecae and seminal receptacle. While little is known about individual secretory products, several components of the spermathecal secretions have been suggested to support sperm viability (and hence, female fertility), including aquaporins, antioxidants, antimicrobials and metabolic enzymes. We use the GAL4/UAS system to investigate the function of secretory cells around the spermatheca and test for the effect of spermathecal secretions on female sperm storage and fertility. We examine females that have their spermathecal secretions enhanced and completely disrupted. We further assess the impact of single secretions, for instance antioxidants, on sperm storage and fertility.

## Age but not genetic factors affect sperm metabolic rate in *Drosophila melanogaster*

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Sperm function is essential to male fertilization as only normal and functional sperm can deliver genetic information successfully to the next generation. Recently, there are increasing evidence for mitochondrial and mitonuclear effects on sperm traits and reproductive aging across species. We constructed mitonuclear introgression lines of *Drosophila melanogaster* from three geographically different populations and examined males at two ages. This design allowed us to separate the independent effects of mitochondrial and nuclear genomes and male age on sperm metabolic rate, a dynamic sperm trait. Neither mitochondrial nor mitonuclear interaction effects were present in sperm metabolic rate. However, old males possessed a higher sperm metabolic rate in relative to young males, and the effect was found to function independently of any genetic factors. Moreover, disruption of population-specific coevolved mitonuclear genotypes did not result in reduction in sperm metabolic rate, as might be predicted under a scenario of mitonuclear coadaptation. These results provide us a deeper understanding of contribution of mitonuclear epistasis to sperm function in general and dynamic sperm metabolic rate specifically.

## Exploring DNA double strand breaks and their effects on recombination

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Recombination is a dominant evolutionary force with strong implication for bacterial adaptation to antibiotic stress and genome innovation. Certain antibiotics such as quinolones increase the recombination frequency. Other classes of antimicrobials though do not lead to increase in recombination frequency. What explains this difference? We found that the only antibiotics that can induce DNA double strand-breaks (DSBs) lead to increase in recombination rate in the model bacterium *Escherichia coli*. We tested several classes, but only quinolones, mitomycin C and bleomycin induced DSBs. The induction of DSBs by bleomycin strongly depends on intracellular iron levels. The removal of intracellular iron decreases both, DSBs and recombination rate. Our results shed light on the mechanisms underlying antibiotic-induced recombination but also on how recombination can enable innovations in bacterial evolution.

## Gut microbiota changes throughout development

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Complete metamorphosis is a key trait explaining the incredible diversity of the holometabolous insects, the most diverse taxon on earth. Complete metamorphosis radically transforms the insect body, leading to distinct larval and adult life stages separated by a pupa. The pupal stage generates several problems. Most importantly the renewal of the gut during complete metamorphosis creates a dilemma. Either the host must eradicate and subsequently re-establish the gut microbiota from the environment, or it must maintain its microbiota while preventing opportunistic microbes from infecting the hemocoel. In other words, holometabolism, provides the unique opportunity for an organism to drive an almost complete change between the larval and adult gut microbiota, increasing the opportunity to exploit advantages of niche shifts or to reduce growing populations of pathogenic bacteria which would otherwise persist in the adult host. Systematic studies of changes in the gut microbiota during insect development are rare, but some examples lend support to the notion that complete metamorphosis facilitates change of the gut microbiota. Whether such results reflect a general pattern or are specific to the study systems remains to be tested. Here we compare the changes in the gut microbiota throughout development in holo- and hemimetabolous insects. We sampled 18 different species from seven major insect orders across the life stages and study systematically the changes in both the abundance and diversity of the gut microbiota. Our specific prediction is that hemimetabolous taxa will show a linear increase in both total bacterial counts and alpha-diversity across development. In contrast we predict that holometabolous taxa will show a significant reduction in both total bacterial counts and alpha-diversity at the onset of the pupal stage.

## Microbiota turnover and host immunity throughout insect metamorphosis

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Metamorphosis is one of the most widely used life-history strategies found in the animal kingdom and considered to be a key trait explaining the incredible diversity of holometabolous insects. Complete metamorphosis entails a radical re-organization of the anatomy including the entire dissolution of most organs which are then rebuilt. The myriad relationships with beneficial microorganisms in the gut are thought to play an important role for diversification and the evolutionary success of insects. Consequently, the renewal of the gut in the pupal stage creates a dilemma for the insect host. Either the host must eradicate and subsequently re-establish the gut microbiota from the environment, or it must maintain its microbiota while preventing opportunistic microbes from infecting the hemocoel. The insect's immune system seems to play a big role in mediating the interaction between the host and the microbiota in both, hemi- and holometabolous insects. In numerous orders of holometabolous insects, a rapid induction of bactericidal activity in the gut can be observed at the onset of pupation. In order to understand whether the immune control of the microbiota turnover in insects is a general feature, we quantified immune effector gene expressions in the gut of hemi- and holometabolous insects during the final moult. We also determined whether a RNAi mediated suppression of the induced immune effectors permits a greater number of bacterial taxa to persist from the larval to the adult stage. By this, we will be able to get a better idea about how the host gut immune system shapes the diversity and abundance of the microbiota throughout metamorphosis.

## Temperate phages go viral at reduced salinity levels

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Whereas lytic phages kill their bacterial host, temperate phages can be friend and enemy due to their dual life history. They integrate as prophages into the bacterial genome and provide the bacterial host with beneficial genes enhancing its fitness. However, upon a shift of environmental conditions towards unfavourable for the bacterial host, they switch back to the lytic cycle and thereby kill their host. The Baltic Sea is predicted to decrease in salinity by 5 PSU at the end of this century. We aimed to investigate the consequence of this ocean salinity drop on the interaction between opportunistic *Vibrio* bacteria and temperate phages. We used 32 *Vibrio* strains isolated from the Kielfjord region and infected them with their inherent temperate phages at ambient salinity conditions (15 PSU) and at future salinity levels (11 and 7 PSU). Under a scenario of future salinity conditions, lytic infections spread, and bacterial resistance was diminished. In a subsequent evolution experiment we assessed the impact of a salinity shift on bacterial resistance evolution and propagation of temperate phages in *Vibrio* populations. At future low saline conditions, the evolution and fixation of bacterial resistance against phage infection was slowed down by 50 %. Bacteria carrying the co-evolving phage remained twice as long in the bacterial population at reduced salinity conditions before being outcompeted by phage resistant mutants. A shift in salinity seems to impair bacterial growth and increases the impact of temperate phages on bacterial populations, which may feed back into altered pathogenicity when *Vibrio* bacteria infect their final eukaryotic host in a scenario of environmental change.

## Evolution of male pregnancy requires remodeling of adaptive immunity

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Vertebrate pregnancy has evolved multiple times independently from fishes to mammals with drastic morphological, physiological and immunological adaptations. In mammalian pregnancy, the immune system suppresses both Major Histocompatibility Complex (MHC) pathways to prevent semi-allogeneic embryo rejection. The unique gradient from external fertilisation to distinct forms of male pregnancy in syngnathids (pipefishes and seahorses) allows for in-depth characterization of their genomic trajectories. Within this family immunological tolerance is facilitated by impairment and progressive loss(es) of key genes of the MHC class II pathway. Remodelling of the adaptive immune system of seahorses and pipefishes has taken distinct evolutionary routes. The pipefish genera have lost the entire MHC II pathway, coupled with reorganizations of the MHC I gene repertoire towards non-inflammatory immune responses during male pregnancy. This indicates unexpected flexibility in vertebrate immune systems and underlines that evolution can take multiple routes to achieve the goal of immunological tolerance.

## Saturday, 16.03.2019

14 in *Host-parasite interaction*: [Seminar room S59](#), 16.03.2019, 9:30-9:55

### Temperature and host diet jointly influence the spread and intensity of disease in a *Daphnia*-fungal parasite system

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Climate change has the potential to shape the future of infectious diseases. By elevating the mean temperature of freshwater bodies and shifting the community composition of primary producers (i.e. phytoplankton), global warming can influence the metabolism of waterborne parasites and affect the immune response of defending hosts. Previous experimental studies have demonstrated the respective effects of water temperature or food quality on infection outcomes, using *Daphnia* and their microparasites as model systems. Few attempts have been made, however, to combine both stressors in experimental settings. In order to understand how these factors interact at the host-parasite interface, we exposed two *Daphnia* genotypes to a fully factorial design with varying levels of temperature, food quality (PUFA content and toxin production) and infected them with the yeast *Metschnikowia bicuspidata*. Low-quality host diets strongly reduced the parasite's ability to produce spores, while temperature effects on virulence and infectivity were strictly clone-dependent. *Daphnia* fed with cyanobacteria also had greatly reduced fecundity and survival. We discuss these results with regard to climate change and how it may directly or indirectly influence the spread of disease in freshwater environments.

### Helminth immune modulation in sticklebacks

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The vertebrate immune system co-evolved with helminth parasites. A decrease of helminth infections due to increased hygienic standards has been linked to an increase of autoimmune and inflammatory disorders in human populations. Helminth therapy, the controlled infection of patients with worm parasites, their ova, or their products is already applied in clinical settings. However, the evolutionary ecology and specificity of host-helminth associations is poorly understood. Here, we aimed to determine the effects of host and parasite genotypes, their interaction, and the temporal component in helminth infections of sticklebacks (*Gasterosteus aculeatus*). Different types of sticklebacks and their specific cestodes *Schistocephalus solidus* were used in experimental infections. The different types (high resistance & low resistance against *S. solidus*; high virulence & low virulence in *G. aculeatus*) came from populations with divergent co-evolutionary backgrounds and ecologies. *S. solidus*' immune modulatory effects were analysed at three distinct time points through (i) co-infection with another parasite species and (ii) immune gene expression. Our data demonstrate that host and parasite genotype influenced the infection phenotype and that interaction effects depended on the temporal component. The parasite type, the parasite developmental status, and the co-evolutionary background influenced host immune gene expression and co-infection probabilities. Our study gives answers to the questions how and why epidemiological traits of host-parasite associations vary among populations. The evolutionary and ecological perspectives need to be incorporated in future investigations of premises and consequences of helminth therapy.

### Fitness costs of antimicrobial peptide resistance

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Bacteria evolve a number of resistance mechanisms against antimicrobial peptides (AMPs). The fitness costs of evolving AMP resistance in a pathogen influence the persistence or the loss of the evolved resistance mutation. So far, the link between evolutionary processes observed *in vitro* and survival of the resulting bacteria *in vivo* is very limited. In our study, we infected the mealworm beetle *Tenebrio molitor* with *Staphylococcus aureus* that were evolved *in vitro* in the presence of one or two antimicrobial peptides from *T. molitor*. The results showed that the host immune effectors cleared the mutant resistant strains as efficient as the sensitive controls. The bacterial loads of AMP-resistant *S. aureus* segregate by mutation. Thus, the type of the mutation determines the efficacy of the microbial clearance. Some mutations evolved through selection against AMP have low or no detectable fitness cost. Our study showed that Tenecin resistant strains are resistant against phagocytosis. This might be due to reduced recognition by the *Tenebrio* immune system as altering the cell wall structure and net charge are common strategies to secure AMP resistance. The evolved differences in resistance against AMPs and phagocytosis did not translate into changes in virulence. AMP resistance, while a prerequisite for an infection in vertebrates, does not provide a survival advantage to *S. aureus* in a host environment that is dominated by AMPs.

## The effects of age and fungal infection on the activity of the ant *Myrmica scabrinodis*

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When fighting an infection, hosts do not always succeed in eliminating the pathogen. In the case of insects, it has been shown that bacteria can persist in the hemolymph of their hosts for at least a month. The outcome of infection (i.e. elimination or persistence of the infection) seems to be highly variable, although the underlying reasons behind this variability remain poorly understood. Here, we aimed to understand two factors that may contribute to pathogen clearance: pathogen dose and species. Using different bacterial species varying in virulence levels, we infected *Drosophila melanogaster* with different pathogen doses and followed the infection during the acute and chronic phases. We then evaluated how pathogen load influences the outcome of infection and we determined whether there is a dose threshold, below which the host immune system is capable of clearing the infection. Moreover, by characterizing the infection for each of the bacteria species, we determined the infection parameters for the subsequent experiments where we will test the effectiveness of immune priming against persistent pathogens.

## Dynamics of insect tolerance to bacterial infections

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Hosts are able to avoid or limit parasitic infections through two major counter-strategies: via resistance, which inhibits or controls the pathogen; or through tolerance, which limits the negative fitness impact of the pathogen on the host. Tolerant hosts may live longer (defined as mortality-tolerance) or produce more offspring than non-tolerant hosts (defined as fecundity-tolerance) for a given bacterial load. Upon an infection, different pathogens elicit different host immune strategies. These strategies are expected to change during infection progression. Using an outbred fruit fly population and a range of bacterial pathogens, we test how these defence strategies vary over the time-course of infection depending on the bacteria and inoculation dose. This characterization will establish the baseline resistance and fecundity-tolerance for the subsequent selection line experiment where we will test how selection for host fecundity-tolerance affects host resistance, and vice-versa.

## Collateral sensitivity of antimicrobial peptide- *Staphylococcus aureus* to conventional antibiotics

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Antimicrobial peptides (AMPs), important effectors of multicellular organism innate immune system, have been proposed as candidates for new antibiotic drugs to tackle the issue of drug resistance. However, AMPs resistance can also evolve. Here we explore if AMP-resistant variants of the human pathogen *Staphylococcus aureus* to different peptides show collateral sensitivity, i.e. because of their resistance to AMPs show increased susceptibility to conventional antibiotics. We selected three strains where we evolved AMP resistance and their parental variant. We found that pexiganan-resistant strains showed collateral sensitivity to some important Beta-lactam

antibiotics, while melittin-resistant strains showed increased resistance to aminoglycoside antibiotics. Although some resistant variant showed a slightly increased minimal inhibitory concentration, killing curves indicated that they are more susceptible to fast killing.

## Poster session

Seminar room S59, Friday, 15.03.2015, 16:30-18:30

P1

### Comparative analysis of formic acid ingestion behavior in Formicine ants

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Living in social colonies makes individuals vulnerable for pathogens, due to the high relatedness and physical contact among individuals. Further, trophallaxis may promote the spread of pathogens during food sharing. So, the question remains how ants protect themselves and each other against pathogen pressure. It was found that workers of the formicine ant *Camponotus floridanus* practices tip grooming behavior to lower the pH value in their crop and therefore prevent pathogen transmission within the colony during trophallaxis.

To test whether this behavior is widespread in formicine ants, we investigated six further formicine ant species belonging to the genera *Camponotus*, *Lasius* and *Formica*. We found tip grooming behavior in all species with an increased frequency after food uptake. We found a decreasing pH value (minimum pH=2) in the crop content of ants over the time of 48 hours. Moreover, we measured limited in vitro growth of the intestinal bacteria *Asaia* at pH of 3, which suggest reducing of these bacteria due to tip grooming behavior. Additionally, a possible protease function of the low pH of formic acid or another component could be shown, using a Bradford assay.

P2

### Sexual transmission of environmental bacteria in the common bedbug *Cimex lectularius*

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Animals have intimate associations with bacteria that are found in the environment or even on host surfaces. However, we have a limited understanding of the occurrence and frequency of transmission of environmental bacteria between host individuals. During mating environmental bacteria on the cuticular parts of the reproductive organs could be exchanged between mating partners and even enter their host through genital openings and copulatory wounds. Once inside the host such bacteria could cause infections or even kill sperm. From two metagenomic studies we have indications that sexual transmission of environmental bacteria occurs in both directions between sexes. To verify this, we investigated the frequency and direction of sexual transmission of bacteria between the sexes of the common bedbug *Cimex lectularius* using GFP-labelled bacteria (*Asaia* sp.). We tested if sexual transmission of bacteria occurs from the male intromittent organ to the female ectospermalege, the cuticular part of the female paragenital organ called the spermalege, and vice versa by applying bacteria to the respective male or female organ. We observed that bacteria are transmitted from male to female as well as from female to male. A large proportion of bacteria transmitted from male to female was located where the male punctured the female. Female to male transmission manifested in a high proportion of bacteria at the base and the tip of the intromittent organ. Our results show that sexual transmission of environmental

bacteria works in both directions, at least for the cuticular parts of the reproductive organs. Therefore, the next steps will be to investigate the frequency of transmission to the internal reproductive organs in both sexes and how the immune system deals with the potential threat. By identifying the transmission dynamics and the effects of environmental bacteria on reproduction we gain important information on their role in shaping the evolution of reproductive traits.

P3

### **Effects of microplastic-particles on terrestrial organisms and their microbiota**

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Pollution in the environment with microplastic (MP) is an urgent problem that is currently receiving worldwide attention. A negative impact, e.g. weight loss of organisms which fed on MP, mainly in aquatic ecosystems, has already been shown. However, until now not much is known about the influence of MP particles on soil organisms. In my PhD project I am investigating the direct and indirect effects of the environmentally most relevant MPs (PE, PP, PS, PA, PET, PVC and PLA) on the ground-dwelling compost worm *Eisenia fetida* and the carpenter ant *Camponotus floridanus*. Not only are we examining the impacts of homogeneous particles on these organisms but also the influence of different particle sizes, concentrations, and different plastic morphologies (fibre, fragments or spherical shape). Direct effects on *E. fetida* and *C. floridanus* will be studied by measuring different life-history traits and histological alterations or damages, such as in the gut tissue. To explore the mechanisms behind the observed effects we will look at the transcriptome and proteome to characterize potential stress and immune reactions. Also, the MP particles can indirectly affect the activity and diversity of the organisms gut microbiome. In regard of this, we will analyze the metatranscriptome and decipher possible enzymatic activities.

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# General information

## Posters

Poster will be displayed in the Seminar room S59 throughout the meeting. Each poster has a unique number starting with P given in the abstract booklet. On the poster panels you will find those numbers and you should put your poster next to this number. Please put your poster as soon as possible after your arrival.

## Poster session

The poster session will start directly after the last talk on the second day. Therefore, we urge the poster presenters to proceed quickly to their posters. To ease the pain of thirst and hunger for all attendees due to the lack of a break drinks and snacks will be provided at the poster session.

## WLAN-access

On the university campus internet access is available via eduroam.

## Meals

If you have any special dietary requirements or meal preferences and did not indicate so at the online registration: no worries! Please tell either me or Sara and we will sort you out.

## Travel

To organise your trip, have a look at the following links:

Travel to Bayreuth by [train](#) or less CO<sub>2</sub>-friendly by [coach](#) or [car](#).

[Public transport](#) in and around Bayreuth

## Parking

Unfortunately, parking on the University Campus is for free and there is a lot of space.

## Questions

If you have any questions, please ask me or Sara.

We thank the Bavarian-Czech Academic Agency for the support of our meeting

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vysokoškolská agentura

