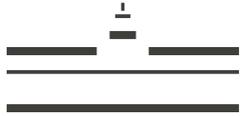


2019 JOINT SYMPOSIUM

27 - 28 May 2019 | University of Münster

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RTG 2220
EvoPAD



2019 Joint Symposium

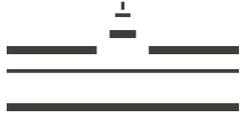
MÜNSTER GRADUATE SCHOOL OF EVOLUTION
RESEARCH TRAINING GROUP EvoPAD
TRANSREGIO COLLABORATIVE RESEARCH CENTRE NC³

ABSTRACT BOOK

27 - 28 May 2019

University of Münster





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MÜNSTER GRADUATE SCHOOL OF EVOLUTION

Prof. Dr. Jürgen Gadau

Speaker of the MGSE

Dr. Kristina Wensing

MGSE Coordinator

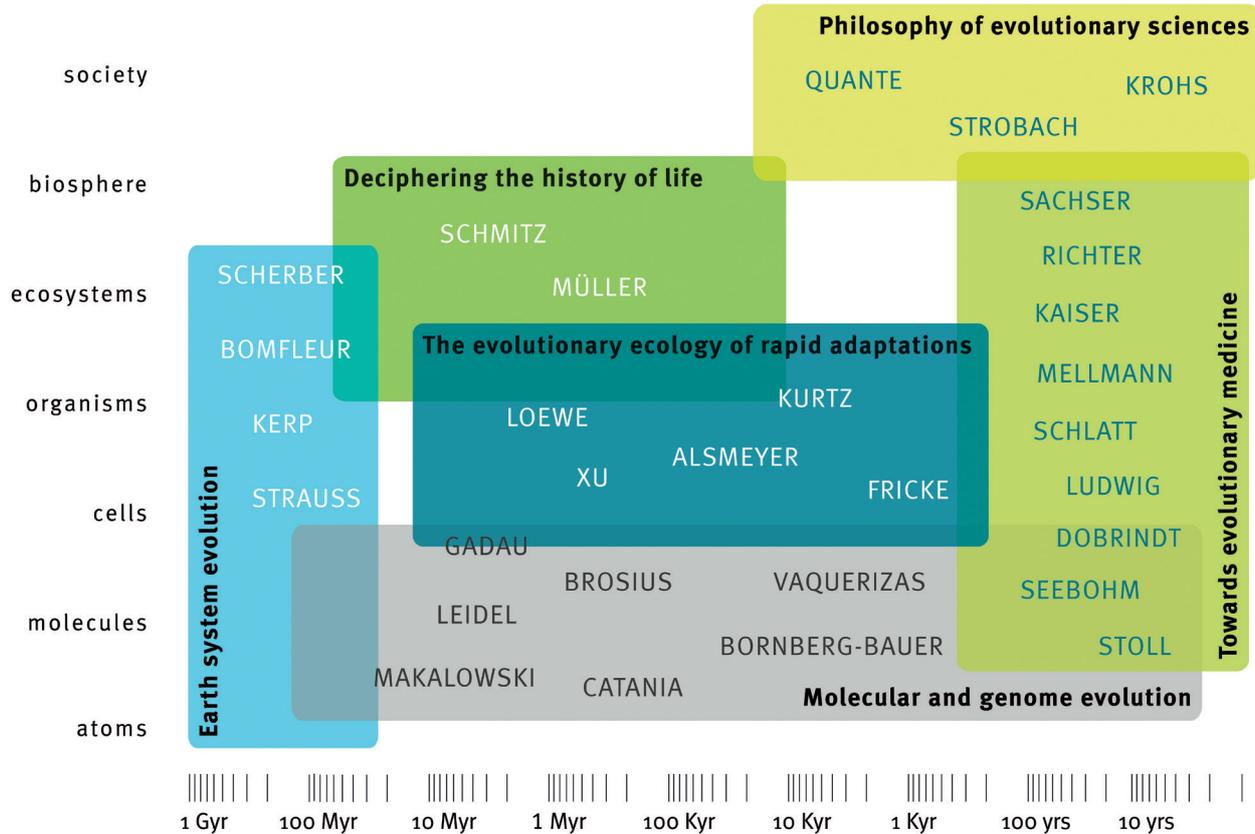
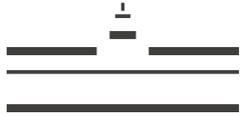
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The **Münster Graduate School of Evolution (MGSE)** is an interdisciplinary association of researchers at the University of Münster bridging the Faculties of Biology, Medicine, Geosciences, Mathematics, and Philosophy.

The MGSE provides a structured study program for doctoral students of different faculties in the general field of evolution. The doctoral students of the MGSE address a broad range of questions, from the evolution of earth to the philosophy of evolutionary theory. MGSE students benefit from one another because similar general principles act across disciplines, thus allowing common theoretical approaches and experimental testing at different levels.

Currently, 30 research group leaders from the different faculties and the Max Planck Institute for Biomedicine contribute to the MGSE. 25 doctoral students carry out their PhD projects within the framework of the MGSE.





Prof. Dr. Joachim Kurtz
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The rapid evolution of pathogens and the rising rates of cardiovascular diseases and psychiatric disorders, pose major challenges to human health. Moreover, the distinction between health and disease may depend on individual life history and its interaction with the environment.

The Research Training Group EvoPAD (**E**volutionary **P**rocesses in **A**daptation and **D**isease) is an interdisciplinary PhD programme which integrates biological, medical, and philosophical research at the University of Münster with the core idea to use the theory of evolution to understand processes leading to adaptation and disease. It is funded by the German Research Foundation (DFG) and started in April 2017.

Currently, 13 doctoral students and 5 associated doctoral students conduct their PhD studies within the EvoPAD framework. With its broad overarching scientific portfolio, the MGSE serves as umbrella organisation for EvoPAD, providing additional expertise and support. The PhD students of EvoPAD are associated to the MGSE.

Individuals differ. This seemingly trivial statement has nevertheless led to paradigm shifts, as behavioural biology, ecology and evolutionary biology have seen a marked change in key concepts over the last years.

Researchers from Bielefeld University, the University Münster and the University of Jena joined forces in a transregio collaborative research centre (CRC-TRR) to redefine the niche concept on the individual level. By doing so, the CRC-TRR aims to gain a comprehensive understanding of how individual phenotypes interact with their environment and what the ensuing consequences for ecological and evolutionary processes are. The main hypothesis is that across taxa, the interaction between the individualised phenotype and the environment results in individualised niches via three mechanisms of adjustment and adaptation: **Niche choice**, **niche conformance** and **niche construction** (NC³). The CRC-TRR is funded by the German Research Foundation (DFG) and started in January 2018.



Prof. Dr. Oliver Krüger
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2019 JOINT SYMPOSIUM - VENUE

Schloss (Schlossplatz 2)

The 2019 Joint Symposium takes place in the main building of the University of Münster, the iconic *Schloss*. All talks take place in the main auditorium and posters are displayed in the foyer.

Coffee breaks are served in the foyer of the Schloss. On Tuesday, lunch is served in the foyer.



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Schlossgarten Café (Schlossgarten 4)

The conference dinner takes place in the Schlossgarten Café. The restaurant is located in the heart of the park area behind the Schloss next to the Botanical Garden. The buffet opens at 19.00.

On Thursday, we offer all participants the possibility to have lunch at the canteen **“Mensa am Aasee”**. You find a food voucher for a meal at your choice including a non-alcoholic drink attached to your name tag.



© Schloßgarten Café

JOINT SYMPOSIUM - PROGRAMME

Monday, 27 May 2019

08.45 Registration

Foyer, Schloss

09.30 - 10.00 Introduction

Auditorium, Schloss

09.30 Welcome address by Prorektor Michael Quante

09.45 Welcome address by the Speaker of the MGSE,
Jürgen Gadau

10.00 - 11.00 Keynote lecture

Auditorium Schloss

Chair: Joachim Kurtz

Michael E. Hochberg

University of Montpellier, Santa Fe Institute

Phage therapy through the lens of evolutionary
medicine

11.00 - 11.30 Coffee break

Foyer, Schloss

11.30 - 12.30 Talks

Auditorium, Schloss

Chair: Jürgen Gadau

11.30 Joachim Kurtz

Institute for Evolution and Biodiversity, WWU

Plasticity and evolution of innate immune defence

12.00 Ulrich Dobrindt

Institute of Hygiene, WWU

Genome plasticity and its impact on bacterial
adaptation: lessons from uropathogenic *Escherichia*
coli

12.30 - 14.00 Lunch break

Mensa am Aasee

14.00 - 15.45 Talks

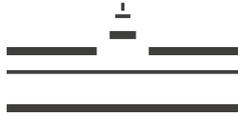
Auditorium Schloss

Chair: Claudia Fricke

14.00 Marco Chittò

Institute of Hygiene, WWU

SOS-response inducing antibiotics stimulate
integrase expression and excision of pathogenicity
islands in uropathogenic *E. coli* strain 536



- 14.15 Nadja Haarmann
Institute of Hygiene, WWU
RNA-seq analysis reveals a dramatic effect of the pAA plasmid on EHEC O104:H4 flagellar expression
- 14.30 Daniel Dowling
Institute for Evolution and Biodiversity, WWU
The evolution of putative novel protein-coding genes in primates
- 14.45 Christoph Scherber
Institute of Landscape Ecology, WWU
Humans as the world's greatest evolutionary force: Conserving biodiversity in human-modified landscapes
- 15.15 Steven Ramm
Department of Evolutionary Biology, Bielefeld University
Seminal fluid-mediated fitness effects: plasticity and evolution of a multivariate trait

15.45 - 16.15 Coffee break

Foyer, Schloss

16.15 - 17.15 Talks

Auditorium, Schloss

Chair: Ulrich Krohs

- 16.15 Ozan Atınok
Department of Philosophy, WWU
From passive plasticity to active plasticity: A shift in the role of plasticity in the evolutionary processes
- 16.30 Jasmin Kurafeiski
Institute for Evolution and Biodiversity, WWU
Specificity, promiscuity, and epistasis in regulatory interactions
- 16.45 April Snøfrid Kleppe
Institute for Evolution and Biodiversity, WWU
Biological errors - do they even exist?
- 17.00 François Pellet
Department of Philosophy, WWU
Plasticity and evolution: Towards a new theory

JOINT SYMPOSIUM - PROGRAMME

17.15 - 18.15 Keynote lecture

Auditorium, Schloss

Chair: Jürgen Gadau

Sara E. Brownell

Arizona State University

Using cultural competence to effectively teach evolution to religious students

18.30 Poster session with fingerfood

Foyer, Schloss

Tuesday, 28 May 2019

09.30 - 11.30 Keynote lectures

Auditorium, Schloss

Chair: Jürgen Gadau

- 09.30 Johanna Mappes
University of Jyväskylä
Diversity in warning signals: Paradox or paradigm?
- 10.30 Jacobus (Koos) Boomsma
University of Copenhagen
Understanding the evolution of social insect colonies from first Hamiltonian principles

11.30 - 12.00 Coffee break

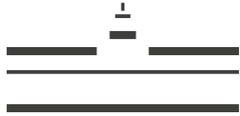
Foyer, Schloss

12.00 - 12.45 Talks

Auditorium, Schloss

Chair: Anna Bucharova

- 12.00 Christian Lampei
Institute of Landscape Ecology, WWU
Multiple simultaneous treatments change plant response from adaptive parental effects to within-generation plasticity, in *Arabidopsis thaliana*



12.30 Malte Conrady
Institute of Landscape Ecology, WWU
Rapid evolution in novel environment: a multispecies approach

12.45 - 14.00 Lunch break

Foyer, Schloss

14.00 - 15.00 Talks

Auditorium, Schloss

Chair: Norbert Sachser

14.00 Oliver Krüger
Department of Animal Behaviour, Bielefeld University
An integrative conceptual framework across behaviour, ecology and evolution: individualised niches

14.30 Holger Schielzeth
Institute of Ecology and Evolution, University of Jena
A rethink of ecological niches

15.00 - 15.30 Coffee break

Foyer, Schloss

15.30 - 16.45 Talks

Auditorium, Schloss

Chair: Oliver Krüger

15.30 Meinolf Ottensmann
Department of Animal Behaviour, Bielefeld University
Habitat imprinting in Common Buzzards (*Buteo buteo*): Factors explaining nest-site selection, dispersal and age of first reproduction

15.45 Elina Takola
Institute of Ecology and Evolution, University of Jena
How novel is new? Revisiting the novel object paradigm

16.00 Rose Trappes
Department of Philosophy, Bielefeld University
What is niche construction constructing?

16.15 Pia Oswald
Department of Animal Behaviour, Bielefeld University
Size matters: Risk-taking activity of fire salamander larvae (*Salamanca salamandra*) is affected by size rather than by origin

16.30 Alexandra Mutwill
Department of Behavioural Biology, WWU
Adaptive Reshaping of Neuroendocrine Profiles
in Adulthood

17.15 - 18.15 Public talk

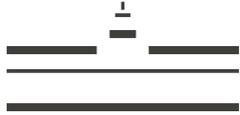
Auditorium, Schloss

Chair: Sylvia Kaiser

17.15 Norbert Sachser
Department of Behavioural Biology, WWU
Das Denken, Fühlen und Verhalten der Tiere -
Neue Erkenntnisse der Verhaltensbiologie

18.30 Dinner

Schloßgarten Café (Schlossgarten 4)



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KEYNOTE LECTURES (IN CHRONOLOGICAL ORDER)

PHAGE THERAPY THROUGH THE LENS OF EVOLUTIONARY MEDICINE

One of the great health challenges of the 21st century is chemotherapeutic resistance. The list of diseases concerned is large and growing, because of the increased proximity of humans to each other and with wildlife. But just as importantly, progress in sanitation and health care mean that people are living to older ages and therefore are more susceptible to disease. I examine some of the features of the chemotherapeutic puzzle and how evolutionary approaches provide robust solutions. Specifically, I focus on the application of viruses to combat bacterial pathogens, and show how ecological and evolutionary information can help guide therapies and control resistance.

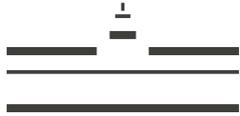
KEYNOTE LECTURE

Michael E. Hochberg

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USING CULTURAL COMPETENCE TO EFFECTIVELY TEACH EVOLUTION TO RELIGIOUS STUDENTS

KEYNOTE LECTURE

Sara E. Brownell

School of Life Sciences
Arizona State University

Students' religious beliefs have been identified as a major barrier to accepting evolution and lack of acceptance of evolution is a challenge for those who teach evolution. Nationwide interviews with instructors teaching evolution and Judeo-Christian students learning evolution revealed that cultural competence, the ability of people from one culture to effectively communicate with those from another culture, could be a useful framework for evolution education. From these interviews and the prior literature in evolution education, we created a new instructional framework for teaching evolution called "Religious Cultural Competence in Evolution Education (ReCCEE)". Further, our studies in undergraduate biology classrooms indicate that using ReCCEE can increase students' acceptance of evolution, decrease students' perceived conflict between religious beliefs and evolution, and create more inclusive college biology classrooms.

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DIVERSITY IN WARNING SIGNALS: PARADOX OR PARADIGM?

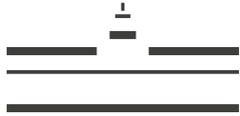
Animal coloration is a model system for understanding evolution because coloration is involved in individual survival and reproduction. Moreover, coloration is easy to observe and accessible for experimental manipulation. I will discuss how recent technological developments have advanced our understanding of how colour patterns can be measured, and how different animals can see them. This mechanistic approach is, however, not sufficient if we ignore the animals' natural environment and relevant selective agents shaping animal coloration. I will use the aposematic, polymorphic wood tiger moth (*Arctia plantaginis*) as an example of how variation in chemical defence, predator community structure and microhabitat conditions select wing coloration and maintain colour polymorphism. Polymorphism in aposematic warning signals is puzzling because efficient predator learning should fix the most common signal as a result of positive frequency dependent selection. This prediction is a commonly accepted paradigm and indeed numerous times shown to be true in mathematical models and controlled laboratory settings, yet polymorphism is common among aposematic animals. I will discuss conditions that drive diversity in warning signals and highlight the need of identifying suitable and diverse study systems.

KEYNOTE LECTURE

Johanna Mappes

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Environmental Sciences
University of Jyväskylä

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KEYNOTE LECTURE

Jacobus (Koos) Boomsma

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In our century of data-driven biology it is too little appreciated that biology has an encompassing theory of adaptation. This theory emerged after William D. Hamilton and George C. Williams independently established the ‘gene’s eye view of adaptation in the 1960s. Hamilton’s version, known as inclusive fitness or kin selection theory, explained reproductive altruism as a logical consequence of the expression of selfish genes, a metaphor coined by Richard Dawkins.

The logic is summarized in Hamilton’s rule, a simple inequality saying that any gene inducing reproductive altruism (helping someone else to reproduce) would spread if $br_s > cr_o$. Here, cr_o is the gene-level opportunity-cost of not having offspring to which one is related by r_o (usually 0.5), and br_s is the benefit in gene copies passed on to future generations via the offspring of siblings (or lesser kin) to which one is related by r_s . Inclusive fitness theory makes many testable predictions of the kind of social traits that could generally evolve (and of those that could not possibly evolve) and these predictions have been confirmed with very high consistency in animals, plants, fungi and microbes.

Social insects have been prominent testbeds for inclusive fitness theory because their workers remain often or always unmated, which leads to forms of sterility that only make sense if relatives benefit. In insect societies workers are only conditionally unmated, but permanent unmatedness was a necessary condition for evolving beyond society, i.e. for the origin of superorganismal colonies characterized by what Darwin coined ‘neuters’. I will discuss the causal mechanisms that have induced evolutionary transitions from society to superorganism and highlight the close analogies with reproductive altruism among somatic cells in multicellular organisms.

DAS DENKEN, FÜHLEN UND VERHALTEN DER TIERE - NEUE ERKENNTNISSE DER VERHALTENSBILOGIE

In den letzten Jahren hat eine Revolution des wissenschaftlichen Tierbildes stattgefunden. Heute wissen wir: Tiere mancher Arten können denken, sie erkennen sich im Spiegel und bei ihnen sind zumindest Ansätze von Ich-Bewusstsein vorhanden. Tiere mancher Arten haben Emotionen, die denen des Menschen bis in verblüffende Details vergleichbar sind. Auch Tiere sind keine Spielbälle ihrer Instinkte, die starr auf Schlüsselreize antworten. Vielmehr wird ihr Verhalten entscheidend durch Umwelteinflüsse, Sozialisation und Lernprozesse geprägt. Als Folge kommt es auch bei den Tieren zur Ausbildung unverwechselbarer Charaktere, so dass in der Verhaltensbiologie mittlerweile von Tierpersönlichkeiten gesprochen wird. Und auch in einem weiteren Aspekt hat sich das Bild von den Tieren entscheidend verändert: Früher waren Biologen der Meinung, dass sich Tiere zum Wohle der Art verhalten und eine Hemmung besteht, Artgenossen zu töten. Heute wissen wir, dass dem nicht so ist. Tiere unternehmen alles, um mit maximaler Effizienz ihre eigenen Gene in die nächste Generation weiterzugeben. Wenn sie dieses Ziel am besten erreichen, indem sie anderen helfen und mit ihnen kooperieren, so tun sie es. Wenn sie dieses Ziel aber durch Nötigung, Aggression oder das Töten von Artgenossen erreichen, dann werden sie sich entsprechend verhalten.

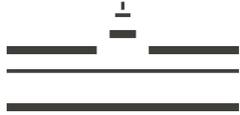
PUBLIC TALK

Norbert Sachser

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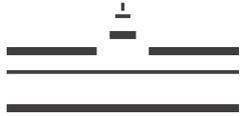
TALKS (IN CHRONOLOGICAL ORDER)

Immune defences show an enormous degree of phenotypic plasticity. In the vertebrate adaptive (or acquired) immune system, immune memory provides enhanced and often highly specific protection that is ‘learned’ from previous exposures. However, also innate immune systems are phenotypically highly plastic. For example, ‘trained immunity’ as a form of memory provided by cells of the vertebrate innate immune system is currently intensively debated. In invertebrates, an accumulating number of studies demonstrate forms of acquired immunity, such as immune priming in insects, which can even be specific. Currently, we still know little about the degree of plasticity as well as the evolution of basic characteristics of these forms of immunity. In my talk, I will provide a brief overview of the current evidence for such forms of immune memory throughout the animal kingdom, and then focus on our main model organism, the Red Flour Beetle *Tribolium castaneum*. Using experimental evolution approaches, we also tested whether the ability to show phenotypically plastic immunity, and in particular the specificity of these reactions, can evolve rapidly. The observed phenotypic differences between the evolved populations were mirrored in the transcriptomic responses. These revealed an involvement of metabolic and transcription-modifying genes and might point towards parallels with vertebrate trained immunity.

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GENOME PLASTICITY AND ITS IMPACT ON BACTERIAL ADAPTATION: LESSONS FROM UROPATHOGENIC *ESCHERICHIA COLI*

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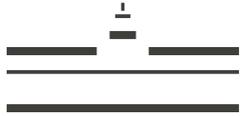
SOS-RESPONSE INDUCING ANTIBIOTICS STIMULATE INTEGRASE EXPRESSION AND EXCISION OF PATHOGENICITY ISLANDS IN UROPATHOGENIC *E. COLI* STRAIN 536

The genome of uropathogenic *Escherichia coli* (UPEC) strain 536 contains six chromosomal pathogenicity islands (PAIs) that differ in their genetic stability. Each of the PAIs carries virulence genes that contribute to bacterial pathogenesis and/or provide a survival advantage in the host. In order to learn more about fundamental mechanisms involved in bacterial genome plasticity and genome evolution by the acquisition and loss of genomic regions, we conducted a series of experiments in which the stability of the six PAIs and the activity of the associated P4-like integrases were analyzed when testing subinhibitory concentration of different classes of antibiotics. We constructed two YFP-based reporter systems; with the first system we measured the stability of the six PAIs, with the second system we measured the promoter activity of the associated integrases. Our data indicate that the stability of the islands is correlated with the expression of the integrases and that subinhibitory concentration of SOS-response inducing antibiotics induce the expression of the integrases, suggesting that the excision mechanisms of PAIs is mainly regulated by the regulation of the expression of the island-associated integrase. The observation that SOS-response inducing antibiotics lead to the activation of the integrases and subsequent loss of the respective islands is similar to the mechanism adopted by bacteriophages, supporting the phage origin hypothesis of PAIs.

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The 2011 enterohemorrhagic *Escherichia coli* (EHEC) O104:H4 outbreak strain carries both a chromosomally integrated Shiga toxin 2a encoding bacteriophage and an enteroaggregative *Escherichia coli* (EAEC)-specific virulence pAA plasmid. Our group reported that EHEC O104:H4 can sporadically lose pAA in the course of illness and that pAA loss is associated with a significantly reduced correlation of HUS development in patients, which speaks for an attenuated virulence of the pAA-negative (pAA⁻) strain.

Here, using RNA-seq we analyzed the whole transcriptome of the pAA⁻ strain and wild type EHEC O104:H4, in order to screen for factors and mechanisms, which contribute to virulence and fitness.

FliC protein levels were analysed with semi-quantitative Western blot. Computational screening for AggR binding sites was performed with FIMO.

Gene ontology analysis showed that the most abundant class of downregulated genes in the pAA⁻ strain were genes involved in motility and chemotaxis. These dramatic transcriptome differences were reflected by non-detectable FliC on the protein level. Interestingly, genes throughout the whole flagellar transcriptional hierarchy were found downregulated, suggesting the differential regulation of the FlhDC master regulator as a trigger for the effect. A computational analysis revealed two high scoring binding sites of the pAA-encoded virulence transcriptional regulator AggR in the proximity of the flhD coding region. Our study indicated a dramatic effect of the pAA plasmid on EHEC O104:H4 host gene expression and in particular in flagellar synthesis. In addition to motility, flagella are playing an important role as virulence factors in EAEC and EHEC O104:H4.

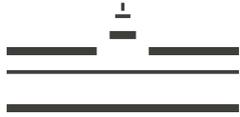
THE EVOLUTION OF PUTATIVE NOVEL PROTEIN-CODING GENES IN PRIMATES

Novel protein-coding genes can contribute to lineage-specific adaptations or integrate with per-existing gene networks and acquire essential functions. Numerous mechanisms have been proposed to explain the origin of such novel genes such as highly divergent paralogs, domestication of transposable elements, or *de novo* emergence from ancestrally non-coding DNA. A number of recent studies suggest that almost the entire genome is transcribed into RNA and can serve as the basis for the formation of novel *de novo* genes. Small transcribed open reading frames (ORFs) have also been shown to be associated with ribosomes indicating that genomes may harbour vast quantities of small novel proteins. Most of these translated ORFs are likely non-functional but a small fraction may benefit the organism and acquire functions and become genuine protein-coding genes. The structural properties of these novel ORFs and how they gain functions and evolve over time are little understood. Here, using transcriptomic data from human and other primates we trace structural evolution of novel transcribed ORFs over 90 million years of evolution. We find thousands of ORFs transcribed from intronic and intergenic regions. By comparing ORFs of different ages we find that these novel ORFs do not appear to undergo a period of structural maturation with their lengths remaining short over millions of years and physicochemical such as intrinsic structural disorder and aggregation propensity being similar to more ancient protein-coding genes. We also find evidence of purifying selection acting upon conserved primate-restricted ORFs indicating that they code for small function proteins.

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Humans modify landscapes in many ways, from direct habitat conversion to indirect effects of various global change drivers. The recent publication of the IPBES report on biodiversity and ecosystem services shows that there is a pressing need to find solutions that „work“ to conserve biodiversity while maintaining ecosystem service provisioning. Here, I will report on decade-long results from a variety of experiments on (i) consequences of biodiversity change and (ii) measures to conserve biodiversity in human-modified landscapes. Results show that (i) biodiversity loss at multiple trophic levels has far-reaching consequences for ecosystem processes and (ii) large-scale enhancement of biodiversity is possible by altering intensive production systems

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SEMINAL FLUID-MEDIATED FITNESS EFFECTS: PLASTICITY AND EVOLUTION OF A MULTIVARIATE TRAIT

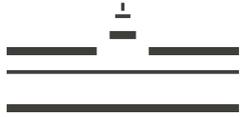
Seminal fluid proteins (SFPs) are crucial mediators of sexual selection and sexual conflict, since they are uniquely positioned to influence female reproductive physiology and behaviour after mating. However, the complexity, functional redundancy and rapid evolution of seminal fluid means that identifying which seminal fluid proteins induce specific physiological or behavioural responses in mating partners is not straightforward, and predicting their evolutionary trajectories is further complicated by the multivariate nature of this secretion.

I will here report on our recent efforts to understand the function and evolution of seminal fluid in the free-living, simultaneously hermaphroditic flatworm *Macrostomum lignano*. I will focus on 1) our use of quantitative genetics combined with molecular tools to identify novel seminal fluid-mediated effects and 2) experiments designed to partition genetic and environmental sources of multivariate variation in seminal fluid expression, which have revealed evidence of genotype-environment-interactions linked to sperm competitive ability and thus fitness.

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Discussions revolving around plasticity and evolution generally regard plasticity as an evolutionary novelty that can enable organisms to adapt better to their environments. However, in these discussions plasticity is generally seen as the end result of an evolutionary process rather than a collection of possible evolutionary processes that result in evolutionary change. I argue that instead of seeing plasticity as a parameter in the mapping problem where organism has a passive role, as Pigliucci (2001) does, following recent trends in evolutionary research that uses more complex selection mechanisms where plasticity can be the bearer of the evolutionary processes is much more productive (Jablonka, 2012).

The old black boxed structure of the organism as a passive reactor to the environment and the selection seemed to be losing ground mostly due to the evolutionary processes that were simply seen as plasticity before (Lind & Spagopoulou, 2018). In addition to that, while epigenetics, niche construction and similar processes of evolution are gaining increasing roles in evolutionary understanding, to what extend plasticity can still be meaningful is a pressing question. On one hand, the return of plasticity might end up being redundant due to the difficulty of finding common elements in the manifold of evolutionary processes that sprung from counting as common themes of plasticity. Against that, I claim that the common element in plasticity is becoming the centrality of organismic responses to the conditions of selection in the evolutionary processes.

SPECIFICITY, PROMISCUITY, AND EPISTASIS IN REGULATORY INTERACTIONS

Transcription factor binding interactions are a nuanced mechanism controlling gene regulatory networks. On the surface the process seems rather straightforward, with transcription factors (TFs) either enabling or suppressing transcription. Also, TF binding sites (TFBSs) are rather short, technically allowing for numerous accidental matches without biological significance. Even the threshold for biological significance of binding interactions is debated. While some consider weak interactions to be spurious, studies indicating biological significance of weak interactions exist. Generally, weak interactions gain functional significance through either combinatorial binding or the accumulation of numerous interactions at the same site. The interactions between TFs and the genes they regulate place an evolutionary constraint. Each mutation in either component has the potential to disturb the interaction. So how does this system deal with mutations in binding sites? Are there further mechanisms in place to conserve the regulatory interactions? Here, we address the complexity of interactions regulating transcription. The analyzed data was obtained from the uniprobe database and covers a variety of species and TF binding domains. Due to the nature of our dataset we focus on the specificity of binding interactions that are functionally significant on their own. Furthermore, we compare the observed binding interactions with predictions based on epistasis calculations on binding motifs. Our results elucidate the nature of promiscuous binding interactions and the role of epistasis in the determination of binding specificities.

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DNA replication errors is when a nucleotide is not accurately copied to the reference molecule during the replication process. These genotypic errors, or mutations, occur at a very low rate and are considered to be deleterious. Transcriptional and translational error (phenotypic) rates are manifold higher than genotypic error rates. Many researchers describe phenotypic mutations as ‘functional’ or ‘programmed’ on account of their high frequency. Instead, phenotypic mutations are depicted as something else than errors, and perhaps not even errors at all. We argue that the notion of ‘functional’ or ‘programmed’ mutations should be questioned on the grounds that it improperly obscures how we understand (in)fidelity to the genetic code. ‘Errors’ can be conceived as ‘deviations from norm’, but that what counts as the relevant ‘norm’ will vary in different contexts. We advocate that researchers should not refrain from speaking of ‘errors’ regarding mutations, but rather carefully define the relevant norm and context. Importantly, the issues of frequency and functionality should also be kept distinct, and frequency should not be automatically interpreted as evidence for functionality or fitness enhancement. These distinctions can only be appreciated by adopting a more contextualized notion of error. We argue that the appropriate null hypothesis is that any event of infidelity to the genetic code - regardless of fitness impact - is an error.

PLASTICITY AND EVOLUTION: TOWARDS A NEW THEORY

What is evolution (or plasticity)? While evolutionary biologists have rightly associated the notion of evolution (or of phenotypic plasticity) with the one of change, contemporary philosophers of biology have largely failed to relate until now the discussions about the notion of evolution (or plasticity) to the metaphysical discussions about the notion of change.

My purpose is precisely to offer an original answer to the issue of what evolution (or plasticity) is, on basis of a certain view on change.

In a nutshell, my answer is that an evolutionary process (or plasticity) just is, actually, substantial change i.e. the mere generation (or destruction) of a biological process: talk about e.g. human evolution just is talk about how a human being (as a specific biological process) is (being) generated (or destroyed).

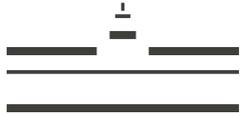
Within the philosophical literature on the notion of change, a preliminary distinction between accidental change and substantial change is usually drawn; how to understand this distinction is highly controversial.

Along a certain line, I argue that, with accidental change, in our case, a biological process does not itself change, but only its accidental properties (e.g. for a human being to wear clothes), while, with substantial change, a biological process is (being) generated or destroyed (e.g. for a caterpillar to get destroyed); substantial change can be said to imply that, while a certain biological process is (being) generated or destroyed, another one is (being), simultaneously but reversely, destroyed or generated (e.g. the destruction of a caterpillar, and the generation of a butterfly).

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Studies on plant phenotypic plasticity commonly focus on a single environmental factor. Under natural conditions, however, multiple environmental factors often vary simultaneously. I studied the consequences for lifetime fitness caused by single treatments or treatment combinations by investigating patterns of phenotypic plasticity within and between generations. The parental plants (3 genotypes of *Arabidopsis thaliana*) received zero, one or two stress treatments at an early life-stage. The treatments included wounding, shading, chilling, and their pairwise combinations. In the second generation, offspring of treated plants received either the parental or no treatment. Offspring of non-treated plants were reared under all treatment conditions. Treatment combinations triggered stronger within-generation plasticity than single treatments, often delaying reproduction. Because delayed reproduction was offset by delayed senescence, the treatments resulted in a fitness gain. However, in natural environments when time is limiting, this delay represents a potential fitness cost. The response to parental treatments was qualitatively different. The treatments wounding and shading triggered parental effects that increased fitness only in plants that themselves received the treatment. Untreated offspring of wounded or shaded parents performed like control plants. Also, these parental effects were not accompanied by potential fitness costs of delayed reproduction. Chilling triggered genotype-specific parental effects that increased or reduced fitness. These results suggest that the response of annual plants to treatment combinations triggers predominantly within-generation plastic responses that include potential fitness costs, which cannot be inferred from studies that manipulate environmental factors individually. Therefore, single treatment studies likely underestimate the costs of plasticity in natural environments.

RAPID EVOLUTION IN NOVEL ENVIRONMENT: A MULTISPECIES APPROACH

In the face of global change, the need for restoration following ecosystem degradation is increasing. Growing number of restoration projects require large amounts of seeds. As wild harvest cannot cover the demand, wild plants are propagated on fields as crops. Specialized companies collect seeds of native species in multiple wild populations with proven natural origin, mix them to ensure high genetic diversity and establish monocultures for seed production. Parts of the seeds harvested from these farms are then sold, while another part is used for establishing the next generation for seed production. During the on-farm propagation, the plants face a novel environment with new selection pressures, and it is possible they adapt to the cultivation. In an experiment with 22 species, we grew seeds from several consecutive generations in cultivation in a common garden and tested for genetic differentiation in traits. Even though we are still in the data analysis, we can see that many of the species changed during the time in monoculture. The novel environment of the propagation site lead to increased biomass, higher rates of germination and a more synchronised phenology. In one species, the proportion of genotypes that do not shed their seeds increased across generations in cultivation, a typical pattern observed within domestication syndrome in crops. In summary, fitness relevant plant traits change during cultivation in seed propagation sites due to unintended selection.

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Individuals differ. This seemingly trivial statement has nevertheless led to paradigm shifts, as three different fields of organismal biology have seen a marked change in key concepts over the last years. In animal behaviour, there are profound differences between individuals in their behaviour, giving rise to the concept of animal personalities. In ecology, an increasing focus is likewise on the considerable variation in the ecological niche realised by species, populations, and even individuals, giving rise to the concept of niche specialisation or individual niche variation. In evolutionary biology, the complexity with which genotypes interact with the environment produces unique phenotypes. Recent theoretical and empirical work shows that the fitness landscape is rather complex with multiple peaks and which local or global fitness peak is attainable depends on genotypes, the specific environment and their interaction. Over the past 15 years, the need for more integrated conceptual frameworks transcending classic disciplines has been voiced ever more strongly. While in each of these fields, the concept of individualisation has contributed to major scientific knowledge increase, we currently lack sufficient cross-fertilisation. Beyond fields of research which, even in their name, combine two fields such as behavioural ecology and evolutionary ecology, a unification process is well under way. I propose a new level of conceptual unification: the individualised niche. By merging the niche concept with the fitness concept and consistent differences in behaviour between individuals, new explanatory power for both ecological and evolutionary processes emerges. I propose to combine behaviour, ecology and evolution in an etho-eco-evo approach to develop a novel synthesis of individualisation via individualised niches.

The concept of ecological niches has been extremely successful in the field of ecology and with the growing interest in inter-individual variation with populations, it is desirable to adopt the concept for the study of individualization. Niches have been treated in many conceptual papers with a number of different formal definitions, the most popular one being Hutchinson's ecological niche as the n-dimensional environmental hypervolume that allows a non-negative population growth rate. I here argue that none of the formal variants is very suitable for studying individualized niches. However, the concept of the niche has already been tweaked to make it suitable for a number of different contexts and although most variants make reference to the n-dimensional environmental hypervolume, they are not always applying it according to the original definition. I think it is time to acknowledge these discrepancies and propose a modified concept of the niche that unites the fields of ecology and evolution and allows a study of individualization from niche perspective.

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Choosing a suitable habitat for breeding is a prerequisite for reproductive success and hence, strongly determines an individual's fitness. This is especially true for long-lived, territorial animals such as raptors, that once settled, show strong site-fidelity and often use the same nest throughout the entire reproductive life-span. For several raptor species, it has been shown that micro- and macrohabitat characteristics of the nest site can have strong fitness consequences and consequently, selection should favour mechanisms which allow individuals to claim territories matching their phenotype. Given the longevity of parents, it is nearly impossible for recruiting offspring in birds of prey to obtain the nest and the territory they were raised in, proposing that habitat imprinting as a form of ecological inheritance could lead offspring to choose nesting sites that are similar to the parental territory. Evidence for this is hard to obtain and this process is rarely investigated in the wild. Here, we make use of a long-term study on a population of individually marked common buzzards inhabiting a heterogenous landscape in Germany. We compiled a dataset comprising more than one hundred individuals that were marked with wingtags as nestlings, allowing us to follow when and where they recruited within as well as outside the study area. We hypothesise that offspring select nest sites similar to their parents, irrespective of dispersal distance. Furthermore, we predict that individuals raised in top territories are more likely to start reproducing at a younger age than conspecifics that were raised under less favourable conditions.

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HOW NOVEL IS NEW? REVISITING THE NOVEL OBJECT PARADIGM

Consistent individual differences in behavioural phenotypes have been the subject of intense research for the last few decades. Such individual differences are variously called animal personalities or temperament, since the goal is to study general responses to environmental challenges, such as individual differences in risk-taking, exploration and novelty-seeking. Temperament traits are typically measured through standardized testing paradigms and one frequently used paradigm is the novel object test. In novel object tests, animals are exposed to new objects and their reaction is quantified in terms of approach latency, distance, arousal or activity. However, demonstrating individual consistency requires multiple testing sessions. Researchers therefore face the dilemma of using the same or different ‘novel’ objects in repeated trials. Repeated exposure of an individual to the same stimulus can result in habituation, while exposure to different objects can result in different responses – both processes may result in an underestimation of individual consistency. In the absence of detailed knowledge about animal memory and cognition, it is also difficult to judge when a time interval between trials is long enough, so that individuals respond to the same object as if it was entirely novel. We performed a quantitative assessment of published data on novel-object trials to evaluate the properties of this testing paradigm. We will present a formal meta-analysis that assess the importance of genuine novelty and time gap in novel-object trials.

Elina Takola¹

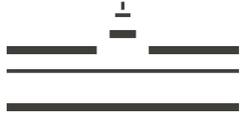
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Niche construction theory (NCT) has been hailed as a conceptual tool for uniting and transforming ecology and evolutionary theory. Yet NCT has proved a controversial proposition. Much of the debate has focused on the ‘construction’ side of niche construction, the idea that organisms have widespread and systematic impact on their environments that may be ecologically and evolutionary significant. Less attention has been accorded to the ‘niche’ side of niche construction: what is it, exactly, that organisms are constructing? In this talk I compare and contrast standard Hutchinsonian niche definitions with the NCT definition of a niche as the sum of selection pressures faced by a population. I explore the way each concept can be used to define niche construction, and what this implies for the potential for NCT and the niche concept more specifically to successfully integrate evolutionary biology and ecology.

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SIZE MATTERS: RISK-TAKING ACTIVITY OF FIRE SALAMANDER LARVAE (*SALAMANDRA SALAMANDRA*) IS AFFECTED BY SIZE RATHER THAN BY ORIGIN

Animal behaviour is driven by several factors and selective pressures. Thereby, different environments promote phenotypic variation within species as well as local adaptation to specific niches. In particular, the early environment has long-term consequences on niche conformance, which may benefit organisms in predictable habitats, but can be maladaptive in unpredictable environments. Amphibians like the fire salamander, which have a biphasic life cycle, provide the opportunity to study those long-term effects under natural conditions. In the Kottenforst, a forest near Bonn, female salamanders show different larval deposition behaviours in concordance with their genotype. Females deposit their larvae either into ponds or streams and therefore choose the early environment for their offspring. Using a reciprocal transplant experiment, larvae of both habitat types were transferred into the matching (original) or mismatching (contrasting) habitat. We investigated the development and the risk-taking behaviour (time spent under a cover) of each larvae. So far, there were no significant developmental or behavioural differences between larvae of both habitat types. However, larval size seems to be an important indicator of risk-taking behaviour, as larger larvae were more risky. Future research on niche conformance in the fire salamander population in Bonn should include additional phenotypic traits and life stages reaching from the larval stage to adulthood.

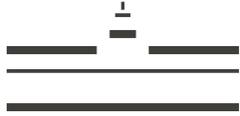
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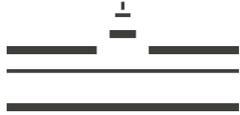
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Phenotypic plasticity describes the ability of individuals to change phenotypic traits in response to the environment. After focusing on pre- and postnatal development as sensitive phases, adolescence has recently been identified as another time window for adjustment of the phenotype in mammals and birds. In previous studies, male guinea pigs kept at low and high individual numbers during adolescence were found to develop two different neuroendocrine profiles. These profiles further build the basis for two completely different adaptive behavioural strategies. The aim of the present study was to investigate, whether these neuroendocrine profiles can be reshaped after transfer to another social environment even beyond adolescence. To test this, male guinea pigs were either kept in heterosexual pairs (P) or in large mixed-sex colonies (C). When fully adult at 240 days of age, neuroendocrine profiles were assessed including testosterone levels and cortisol responsiveness to novelty. Thereafter, males of both conditions were individually placed into heterosexual pairs with an unfamiliar female. One month later, hormonal measures were taken again. The major findings were that before transfer, P-males were shaped for low testosterone levels and high cortisol responsiveness, whereas C-males showed the opposite pattern of high testosterone levels and low cortisol responsiveness. After transfer to a P-situation in adulthood, neuroendocrine profiles of C-males were reshaped towards a P-like profile with low testosterone levels and high cortisol responsiveness, whereas P-males maintained their original profile. The present study clearly shows that neuroendocrine profiles can still be reshaped beyond adolescence, most likely in an adaptive way.

POSTERS (PRESENTERS IN ALPHABETICAL ORDER)



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Orphan genes are a specific type of novel genes without homologs in other species or taxa. Those genes can either emerge from non-coding sequences, called *de novo* genes, or via gene duplication and divergence. New genes can also occur by interbreeding events, resulting in introgression. To detect putative *de novo* genes, genome or transcriptome data can be screened for open reading frames (ORFs) which are not present in outgroup data. Novel ORFs can be located in intergenic regions, introns, or coding sequences (CDS). Genomic data indicates that Neanderthals and Denisovans, ancient relatives of the modern human, interbred with modern humans, hence certain genes have been introgressed into the modern human population. Novel genes have been suggested to play a role in the evolution of lineage-specific traits, e.g. for evolving radulas in molluscs or cnidocytes in *Hydra* as a novelty in their innate defense system. However, little is known about novel ORFs and their possible origin via introgression from Neanderthal or Denisovan to humans. I used human transcribed ORFs with various conservation level, identified in a previous study, and mapped them to the most likely introgressed genomic regions from Neanderthals in modern humans, finding 2.7 % overlap. Further investigations showed that putative introgressed ORFs are more likely to be located in introns or CDS rather than intergenic DNA. This differs from the genomic locations of novel ORFs as a whole. Therefore, I am currently exploring potential explanations for why this may be the case.

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ECOLOGICAL FUNCTIONS OF NATURAL RUBBER BIOSYNTHESIS IN RUSSIAN DANDELION

Natural rubber, a cis-1,4-polyisoprene with more than 10,000 isoprene units, is one of the economically most important plant polymers. Although its phylogenetically widespread distribution and likely convergent evolution suggests important adaptive functions for plants, the ecological roles of these compounds remain unknown. We investigated the effects of natural rubber on herbivore resistance and root microbial colonization during the interaction of the high-rubber producer *Taraxacum kok-saghyz* with its soil-dwelling enemy, the common cockchafer (*Melolontha melolontha*). In a choice experiment, addition of ecologically relevant 1,4-cis-polyisoprene concentrations to diet deterred *M. melolontha* feeding. In a non-choice setup *M. melolontha* larvae gained less weight on artificial diet supplemented with 1,4-cis-polyisoprene compared to diet with solvent control. Moreover, transgenic *T. kok-saghyz* plants deficient in natural rubber biosynthesis suffered stronger reduction in above ground biomass accumulation under *M. melolontha* attack compared to control plants. These experiments provide the first line of evidence that natural rubber protects plants from herbivore attack. Whether natural rubber additionally restricts the colonization of microorganisms under root herbivory will be addressed in future microbiome analyses.

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One of the most important environmental stressors for many organisms is temperature. Especially ectotherms are strongly influenced by this factor, as their body temperature and biological processes are directly affected by it. At a population level, temperature also determines their abundance and distribution. Hence, this is a matter of special interest to understand species ecology and is currently gaining importance due to climate change.

One factor limiting some species distribution is sterility at high temperatures. This phenomenon is documented for *Drosophila*, but potential evolutionary constraints are not well studied. However, flies can recover fertility when transferred to milder temperatures, indicating that germ cells are not destroyed. I want to understand: first, how high temperatures affect fertility in different *Drosophila* species and how this affects fitness. Second, I want to determine if flies can evolve to expand their fertility range and employ experimental evolution to test whether males can adapt to elevated temperatures and remain fertile when exposed to critical temperatures. For this purpose, the male reproductive tract and sperm quality and functionality will be studied. Previous studies have demonstrated that accessory glands and its proteins transferred to females at mating have an important role for male reproductive success. Hence, I analyzed the thermal sensitivity patterns and male accessory gland size for a temperate Portuguese *D. melanogaster* strain. These observations support that both accessory gland size and temperature are important factors involved in determining male fertility. Finally, I want to understand the molecular mechanisms of temperature-induced sterility by combining experimental evolution and sequencing.

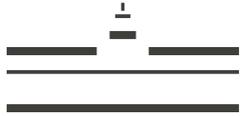
During invasion, populations experience large environmental changes and often have reduced genetic variation as a consequence of founder effects. In spite of this limited genetic variation, these species can rapidly colonize and adapt to new habitats. This raises the question of how successful invaders cope with this supposedly detrimental low genetic variation during invasion. Species adaptation might be facilitated by induced structural and functional variations in the genome (in addition to standing genetic variation). This may occur via structural units such as transposable elements. In addition, social Hymenoptera have the highest rates of recombination in all animals studied so far which may facilitate the generation of genetic variants. Here we propose to study the role of increased recombination rates and genomic rearrangements in rapid adaptation to novel habitats using the invasive ant *Cardiocondyla obscurior*. First, we will construct high-resolution recombination maps in this species. Second, we will analyse single nucleotide polymorphism and structural variations (indels, CNVs) between different *C. obscurior* populations. We will analyse the function of candidate loci resulting from genomic rearrangements, using gene function assays (RNAi), to test their role in rapid adaptation in this species. This project will improve our understanding of the relationship between recombination rate and genetic variation and also contribute to our understanding of how invasive species deal with environmental constraints during invasion despite their low genetic variation.

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In most laboratories, mice are fed ad libitum, despite well-known health impairments. In contrast, a reduction of bodyweight by feeding less food once per day (24h schedule) is known to enhance life span and reduce disease susceptibility. Yet, the repeated removal of food for up to one day is classified as ‘mildly severe’ by the European Directive 2010/63/EU. Thus, this study aimed at evaluating different feeding routines. Three alternatives, including a 24h group, an AUTO group, i.e. automated supply of small food pellets throughout the day, and a 4h removal group, i.e. daily removal of food for 4h, were compared to ad libitum feeding. Effects on bodyweight and welfare were studied. While the 4h removal did not cause lower bodyweights, and hence is unlikely to prevent negative effects of overfeeding, the 24h and the AUTO group led to the expected effects. In the AUTO group, however, high levels of corticosterone metabolite concentrations and stereotypies were observed, implying an adverse impact on welfare. By contrast, no distinct negative effects of a 24h schedule were found.

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THE EFFECT OF NUCLEAR-CYTOPLASMIC INCOMPATIBILITIES ON METABOLIC RATES/ ENERGY PRODUCTION IN *NASONIA*

Well-functioning mitochondria are essential for the survival of all eukaryotes including humans. To make a functioning mitochondrion, both nuclear and mitochondrial genes have to interact harmoniously. In general, mitochondrial genomes evolve faster, posing a potential problem due to nuclear-cytoplasmic incompatibilities. In humans, mitochondrial mutations are causing the most frequent human genetic diseases. Additionally, nuclear-cytoplasmic incompatibilities contribute to early post-zygotic isolation between incipient species. We plan to study the physiological results of hybrid incompatibilities in parasitoid wasp genus, *Nasonia*. Ultimately, we want to understand the genetic architecture of the nuclear-cytoplasmic incompatibilities in F_2 male hybrids. The mitochondrial incompatibility will be tested in hybrid crosses of *N. vitripennis* and *N. giraulti* by comparing the difference in RCR (Respiratory control ratio) of the isolated mitochondria in parental, F_1 females (diploid: two complete sets of both parental genomes) and recombinant F_2 hybrid males (haploid-recombinant genome of both parental genomes) and F_3 clonal sibships (diploid females). We will use QTL analyses to find genetic region and genes that are responsible for this incompatibility. This should help us to generally identify and understand the gene regulatory networks that keep the interaction between nuclear and mitochondrial encoded genes functioning and how which evolutionary processes lead to nuclear-cytoplasmic incompatibilities.

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Bacterial pathogens have the potential to evolve rapidly. Due to their enormous genomic plasticity, fast microevolutionary processes pose a great challenge to their host organisms in a coevolutionary scenario. Hosts often evolve more slowly, but with their flexible immune systems, they have the potential to phenotypically adapt to pathogens. It has been shown in the red flour beetle that a previous ‘priming’ of the immune system leads to higher resistance that can be specific for the strain of pathogen encountered during priming. Therefore, the red flour beetle (*Tribolium castaneum*) and the bacterium *Bacillus thuringiensis* make an experimental model system to study host-parasite interactions. Using an experimental evolution approach, this study is trying to answer how will the specific immune response of the beetle drive the micro-evolution of a pathogen. Host immune memory might lead to more rapid pathogen adaptation, because of the associated stronger selection pressure. Since *B. thuringiensis* is a spore forming insect pathogen that can infect insects via the oral route, serial passage experiments with oral exposure to orally primed and non-primed beetles are conducted. Bacterial evolutionary processes are studied by tracking changes of both the bacterial phenotype (e.g., virulence) and the genotype (e.g., resequencing of bacterial populations and representative clones).

THE IMPACT OF INDIVIDUAL IMMUNE EXPERIENCE ON NICHE CONSTRUCTION IN RED FLOUR BEETLES, *TRIBOLIUM CASTANEUM*

Adult red flour beetles, *Tribolium castaneum* produce external secretions containing high levels of antimicrobial quinones (benzoquinone and hydroquinone), which have been shown to inhibit the growth of bacteria, yeast and fungi commonly found in flour and the beetle's natural environments. As group living animals that share the same niches, potentially, the secretions from adult beetles could in turn influence the levels of pathogenic threat that their conspecifics or offspring are exposed to and thus modify the selective environment of both the niche constructors and recipients. In response to the sparse experimental tests of the ecology and evolutionary consequences of niche construction, we here start using the worldwide pest of stored grains, *T. castaneum* along with their natural parasite *Bacillus thuringiensis tenebrionis* (Btt) as a host-parasite model system for niche construction.

Interestingly, *T. castaneum* demonstrated immune priming (i.e. increased immune response against previously encountered microbes) within and across generations. As the magnitude of animals' niche construction likely varies with individual experience, i.e. exposure to environmental stressors, we hypothesise that individual immunological experiences in *T. castaneum* might lead to the construction of individualised niches.

In our studies, individual beetles were either left naive, sham-exposed by injection of PBS or primed via injection of heat-killed vegetative Btt. We compared the chemical composition and quinone levels in secretions of adult beetles undergoing different treatments. We will present our preliminary work on the influence of individual immune experience on niche construction and our plan to test the evolutionary consequences of individual niche construction via experimental evolution.

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In many organisms, across the animal kingdom the Fecundity/Longevity (F/L) trade-off results in a negative association between higher investment into reproduction and an organism's survival. This according to the 'Disposable Soma Theory' is a result of an organism's limited resources being used for the purposes of reproduction as opposed to somatic maintenance and repair. The major molecular pathways underlying the F/L trade-off, predominantly Target of Rapamycin (TOR), and insulin/IGF-1 signalling (IIS), appear to be conserved across species. There are however interesting exceptions to this F/L rule in eusocial insects. Wherein reproductive individuals of those species both reproduce at a high rate, and live longer than their non-reproductive siblings. It would seem eusocial insects have used parts of these conserved molecular pathways, TOR, and IIS in novel functions to help reverse the trade-off. The aim of my PhD then is to work with collaborators using eusocial insects to identify candidate genes within the TOR/IIS pathways, as well as potential candidates outside of these pathways. The objective of this being to characterise these genes within a non-social model; *Drosophila melanogaster*. The second aim of the project will be to highlight the interactions in the pathways, and find potential central pleiotropic hubs, which will be made possible by the *Drosophila's* position as a well characterised molecular model. The major question of my PhD being whether social insects have managed to reverse the F/L trade-off by evolving novel changes in these conserved pathways.

THE ROLE OF EVOLUTIONARY CAPACITANCE FOR EVolvABILITY IN THE RED FLOUR BEETLE, *TRIBOLIUM CASTANEUM*

Evolutionary capacitance is the storage and release of cryptic genetic variation, which may help to sustain fitness under stressful environmental conditions. It modifies the genotype-phenotype-environmental relationship and has the potential to enhance adaptability. HSP90, an important mediator of the evolutionary capacitance is found to be downregulated in naïve red flour beetles (*Tribolium castaneum*) upon cohabitation with wounded conspecifics. Also, Hsp90 reduction by RNAi and chemical inhibition with 17-DMAG produced offspring with new morphological phenotypes. Thus, using the model system *Tribolium castaneum*, this project tries to explore the effect of individual immunological experiences on evolutionary capacitance and also to use long term experimental evolution for understanding the role of this process for evolvability. This study would help us to have a novel understanding of the process of rapid adaptation.

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For social animals, the environment is highly influenced by interactions among conspecifics. Stable group-living allows for communication via consistent behavioral cues among group members, and this often results in the generation and maintenance of individualized social niches. Early phases in life have been identified as sensitive periods for individuals to modify their phenotype to match their environment. Adolescence has also recently been proposed as a sensitive period for the development of the behavioral phenotype. However, only little is known to what extent individuals, especially females, can adjust their behavior to their social environment in adolescence and adulthood. In adolescence, individuals can directly assess the social environment via interactions with conspecifics and modify their behavior accordingly rather than obtaining information from their mother, and there is a high fitness incentive for behavioral adjustment with the onset of the reproductive phase. Therefore, the social environment likely contributes to individualization of the behavioral phenotype during adolescence. Using guinea pigs as a model system, we will examine if females adjust their behavior to the social environment in adolescence and adulthood. Specifically, we will investigate how dominance rank attained in adolescence influences the development of the behavioral phenotype and the underlying neuroendocrine mechanisms. Furthermore, the dominance rank will be manipulated in adulthood to determine whether reshaping of the behavioral phenotype and underlying neuroendocrine mechanisms is possible. This project will contribute substantially to the question of whether individuals conform adaptively to their social environment during adolescence and adulthood.

RIGHTY OR LEFTY: LATERALIZED BEHAVIOR IN MICE?

Lateralized behavior is not unique to humans. In the last decades, numerous studies detected lateral biases in various vertebrate and invertebrate species. Food-reaching tasks are the most widely used method for assessing behavioral asymmetries in forelimb use in rodents. However, lateralization of spontaneous behaviors has been largely neglected. This study investigates the consistency of the direction and strength of a set of spontaneous lateralized behaviors in two strains of mice. Paw and/or body-side preferences of male and female CD-1 and C57BL/6 mice are observed during a traditionally used food-reaching task and during spontaneous grid-climbing, barrier-climbing and self-grooming. Additionally, to test for temporal consistency, mice are re-observed five weeks later. We assume that mice show consistent lateral biases across the four behavioral observations. Presumed that mice show paw and/or body-side preferences, we hypothesize the direction and strength of lateral biases to be consistent over time. First pilot results reveal paw and/or body-side preferences in all behavioral observations. Furthermore, lateral biases are consistent over time in at least two of the above mentioned behaviors.

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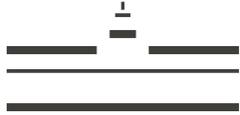
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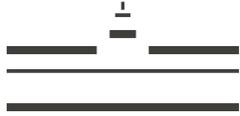
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