Westfälische
Wilhelms-Universität
Münster

MÜNSTER
GRADUATE
SCHOOL OF
EVOLUTION

4th annual Symposium

Münster Graduate School of Evolution

30 June & 01 July 2014 - Münster, Germany

4th Annual MGSE Symposium

MÜNSTER GRADUATE SCHOOL OF EVOLUTION

ABSTRACT BOOK 2014

Edited by Joachim Kurtz and Rebecca Schreiber

Institute for Evolution and Biodiversity

University of Münster

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Münster Graduate School of Evolution (MGSE)

Modern evolutionary thinking can provide a unifying conceptual framework and is thus particularly suited as a topic for an interdisciplinary graduate school. The *Münster Graduate School of Evolution* (MGSE) is based on biology, medicine, geosciences, philosophy, and mathematics. MGSE students benefit from one another because similar general principles act across disciplines, thus allowing common theoretical approaches and experimental testing at different levels.

The 4th MGSE symposium will provide the MGSE doctoral students with the opportunity to present and discuss their ongoing PhD projects. Their presentations and posters will be embedded into contributions from scientists of the MGSE research groups and invited speakers.

The “Kavaliershäuschen”, the lecture hall of the IEB, and the “Geomuseum” bulding site will serve as venues for the talks, the poster session, and the social dinner. We are looking forward to lively discussions and fruitful exchange in these atmospheric buildings in the heart of Münster.

Prof. Dr. Joachim Kurtz
Speaker of the MGSE

Dr. Rebecca Schreiber
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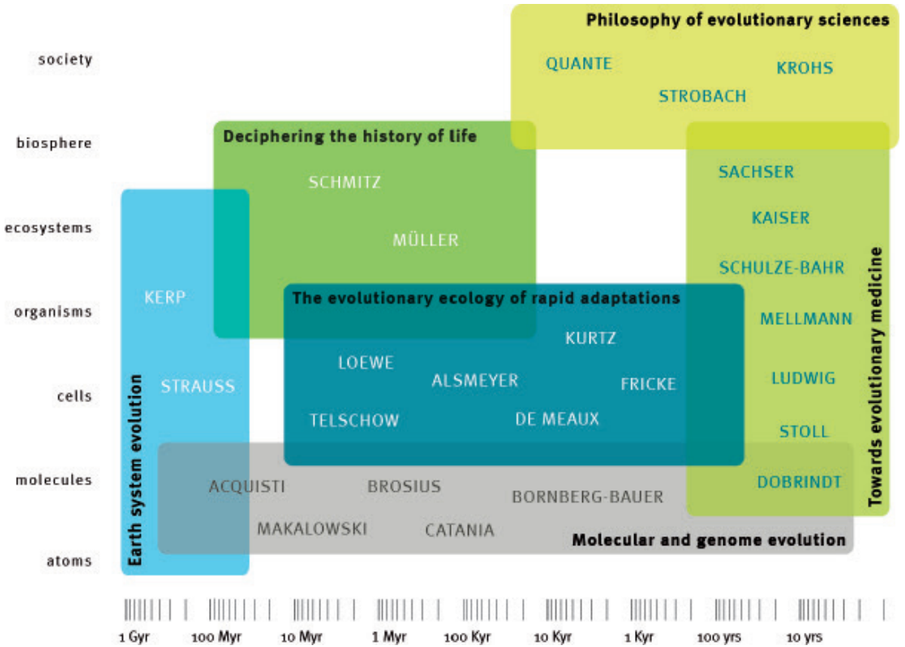
Name, Title	Research Topic	MGSE Research Area
Acquisti, Jun. Prof. Claudia	Evolutionary Functional Genomics	Molecular and genome evolution
Alsmeyer, Prof. Gerold	Mathematical Statistics	The ecology of rapid adaptations
Bornberg-Bauer, Prof. Erich	Evolutionary Bioinformatics	Molecular and genome evolution
Brosius, Prof. Jürgen	Experimental Pathology	Molecular and genome evolution
Catania, Dr. Francesco	Evolutionary Cell Biology	Molecular and genome evolution
De Meaux, Prof. Juliette	Plant Molecular Evolution	The evolutionary ecology of rapid adaptations
Dobrindt, Prof. Ulrich	Microbial Genome Plasticity	Towards evolutionary medicine
Fricke, Dr. Claudia	Evolution and Sexual Conflict	The evolutionary ecology of rapid adaptations
Kaiser, Prof. Sylvia	Behavioural Biology	Towards evolutionary medicine
Kerp, Prof. Johannes	Paleobotany	Earth system evolution
Krohs, Prof. Ulrich	Philosophy of Science and of Nature	Philosophy of evolutionary sciences
Kurtz, Prof. Joachim	Animal Evolutionary Ecology	The evolutionary ecology of rapid adaptations
Löwe, Prof. Matthias	Mathematical Statistics	The evolutionary ecology of rapid adaptations
Ludwig, Prof. Stephan	Molecular Virology	Towards evolutionary medicine
Makalowski, Prof. Wojciech	Bioinformatics	Molecular and genome evolution
Mellmann, PD Alexander	Hospital and Environmental Hygiene	Towards evolutionary medicine
Müller, Prof. Kai	Evolution of Biodiversity of PLants	Deciphering the history of life
Quante, Prof. Michael	Philosophy of Ethics and Practical Phil.	Philosophy of evolution and education research
Sachser, Prof. Norbert	Behavioural Biology	Towards evolutionary medicine
Schmitz, PD Jürgen	Experimental Pathology	Deciphering the history of life
Schulze-Bahr, Prof. Eric	Cardiology and Angiology	Towards evolutionary medicine
Stoll, Prof. Monika	Genetic Epidemiology	Towards evolutionary medicine
Strauss, Prof. Harald	Historical and Regional Geology	Earth system evolution
Strobach, Prof. Niko	Philosophy of Logic and Language	Philosophy of evolution and education research



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Mona Riemenschneider
Hanna Ruhmann
Susanne Sangenstedt
Manuel Talarico
Tobias Tiedtke

MGSE ETT-Fellow
Jürgen Gadau

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Ulrich Krohs
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Cornelia Denz, Vice-Rector for International Affairs and Young Researchers
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MGSE - Members 2014

MGSE Graduate Students, March 2014
Back row: Mona Riemenschneider, Stefanie Henze, Megan Kutzer, Liliya Doronina, Frederik Franke
Middle row: Manuel Talarico, Neele Meyer, Patricia Kearney, Angela Noll, Diana Ferro, Tobias Tiedtke, Florian Grziwotz
Front row: Francesco Catania (Leader of the ETT), Gildas Lepennetier, Hanna Ruhmann, Rasha Aboelsoud, Joachim Kurtz (MGSE Speaker), Kevin Knoblich, Rebecca Schreiber (MGSE Coordinator)

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Lecture hall IEB (Hüfferstraße 1)

The Institute of Evolution and Biodiversity (IEB) is situated near the castle at the Hüfferstraße 1. The lecture hall of the IEB will be the venue for the three keynote lectures of the MGSE Symposium.

„Kavaliershäuschen“ (Schlossplatz 6)

The baroque satellite building of the castle was originally used as a guardhouse and received its name from the mounted guards (“chévaliers”). Later, the “Kavaliershäuschen” was inhabited by the caretaker of the castle. After its demolition during the Second World War it was reconstructed as home for employees of the district government, so that by the 1950s four families could live inside the house. In 1960 the building became property of the University of Münster and was used by the seminar for musicology. After a fundamental renovation, the “Kavaliershäuschen” became the seat of the University Marketing and Fund-raising, the Graduate Centre, and the Münster Graduate School of Evolution.

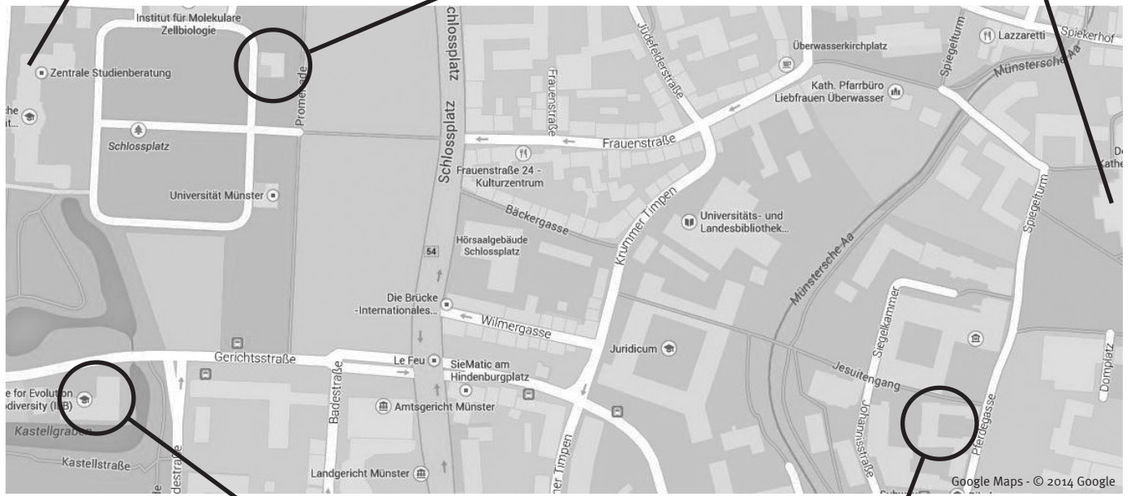
„Geomuseum“ (Pferdegasse 3)

The University of Münster plans to convert the Baroque Landsberg Kurie building near the cathedral to a new Geo-museum. The reconstruction will be finished by the end of 2015. At present, the so-called “Building Site Department” is a popular venue for events due to its unique atmosphere. Also the poster session and social dinner of the MGSE Symposium will take place in this gutted baroque building.

University of Münster
(Main Building, Castle)
Schlossplatz 1

Kavaliershäuschen
Münster Graduate School of Evolution
Schlossplatz 6

St. Paulus Cathedral
Domplatz 28



Lecture hall IEB
Institute for Evolution and Biodiversity
Hüfferstraße 1

Geomuseum
Pferdegasse 3

13.15-13.45: Introduction
Lecture hall IEB, Hüfferstraße 1

13.15: Welcome address by the speaker of the MGSE, Joachim Kurtz

13.30: Address from the Rector's Office by Stephan Ludwig

13.45-15.45: Keynote lectures
Lecture hall IEB, Hüfferstraße 1

13.45: Franjo Weissing (University of Groningen, NL)
„Consequences of individual differences for social evolution"

14.45: Michael Lässig (University of Cologne)
„Predicting the evolution of influenza"

15.45-16.30: Coffee break in the "Kavaliershäuschen"
"Kavaliershäuschen", first floor

16.30 - 17.30: Session 1, Talks by PhD- and MSc-students
"Kavaliershäuschen", ground floor

16.30: Gildas Lepennetier (Evolutionary Cell Biology, IEB)

16.50: Stefanie Henze (Evolutionary Functional Genomics, IEB)

17.10: Fritjof Lammers (Evolutionary Functional Genomics, IEB)

17.45-19.00 : Poster Session in the "Geomuseum"
Geomuseum, Pferdegasse 3

19.00-open end: Dinner buffet in the "Geomuseum"
Geomuseum, Pferdegasse 3

10.00-11.00: Session 2, Talks by PhD-students
"Kavaliershäuschen", ground floor

10.00: Florian Grziwotz (Genome Evolution, IEB)

10.20: Manuel Talarico (Animal Evolutionary Ecology, IEB)

10.40: Shirin Glander (Plant Molecular Evolution, IEB)

11.00-11.30: Coffee break in the "Kavaliershäuschen"
"Kavaliershäuschen", first floor

11.30-13.00: Session 3, Invited talks
"Kavaliershäuschen", ground floor

11.30: Sebastian Leidel (MPI for Molecular Biomedicine)

12.00: Juanma Vaquerizas (MPI for Molecular Biomedicine)

12.30: Guiscard Seebohm (University Hospital Münster)

13.00-14.15: Lunch break in the "Kavaliershäuschen"
"Kavaliershäuschen", first floor

14.15-15.15: General Assembly of all MGSE members
"Kavaliershäuschen", ground floor

15.15-15:45: Coffee break in the "Kavaliershäuschen"
"Kavaliershäuschen", first floor

16.00-17.00: Keynote lecture
Lecture hall IEB, Hüfferstraße 1

16.00: Jürgen Gadau (Arizona State University, USA)
„From Genotype to Phenotype and Back - Network analysis of aggressive behavior and the evolution of sociality"

Keynote lectures (speakers in chronological order)

In the past, individual differences in behaviour have typically been considered as ‘noise’ that can be neglected in evolutionary analyses. This view has radically changed in the last decade. Empirical studies in more than 400 species, ranging from primates to snails, suggest that variation in animal behaviour is not random but strongly patterned. Individuals consistently differ in whole suites of correlated behaviours and these differences are often heritable. The evolutionary causes and consequences of such ‘behavioural syndromes’ or ‘animal personalities’ are not well understood, but the contours of an evolutionary theory of individual variation are starting to emerge. In my talk, I will briefly review some evolutionary explanations for the coexistence of behavioural types and for stable and consistent behavioural variation across contexts. The main part of the talk will be on the implications of behavioural variation on various aspects of social evolution. By means of empirical examples and theoretical arguments, I will make three points. First, individual variation is important, since the degree and patterning of variation may strongly affect the direction of evolution. Second, behavioural consistency is important, since it selects for social sensitivity, which in turn may strongly determine the outcome of social evolution. Third, correlations across contexts are important, since they necessitate an overarching view of behaviour; such a new perspective will often lead to a completely new interpretation of the function of the behaviours under scrutiny.

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KEYNOTE LECTURE

Franjo Weissing

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The human flu virus undergoes rapid evolution, which is driven by interactions with its host immune system. In this talk, I discuss a fitness model that successfully predicts the evolution of influenza one year into the future. Thus, evolutionary analysis transcends its traditional role of reconstructing past history. This has important consequences for public health: evolutionary predictions can inform the selection of influenza vaccine strains. These results establish a link between population genetics and epidemiology of fast-evolving pathogens. In a broader context, we will discuss the fundamental question of how predictable evolution can be.

KEYNOTE LECTURE

Michael Lässig

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From Genotype to Phenotype and Back - Network analysis of aggressive behavior and the evolution of sociality

One of the biggest challenges in biology is how to predict a phenotype from the genotype. A little bit less challenging is the mapping of genotypes onto phenotypes and the analysis of the genetic architecture of complex phenotypes. I will start with some examples of "simple" phenotypes and gradually move on to more complex and arguably interesting phenotypes. In particular, I will discuss how a change in the aggressive behavior of an individual has significant effects for the social organization and fitness of the whole colony. In the end I will discuss how genotypes in interacting individuals will influence the expression of each others genes and phenotypes producing adaptive phenotypic plasticity.

KEYNOTE LECTURE

Jürgen Gadau

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When speed matters - tRNA modification defects are linked to perturbed protein homeostasis.

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Chemical tRNA modifications are found in all domains of life and thought to modulate all aspects of tRNA biology. Their absence leads to increased sensitivity to stress in many organisms and is linked to human diseases. However, the molecular mechanisms that lead to these phenotypes remain unclear. We used ribosome profiling to quantitatively analyze translation in wild-type yeast and strains deficient in U34 modification and found that U34 hypomodification leads to codon-specific translational slowdown in vivo. This effect was conserved in Caenorhabditis elegans underscoring the importance of U34 modifications for decoding efficiency in higher eukaryotes. Surprisingly, we found that protein quality control pathways are significantly upregulated in yeast strains with aberrantly modified U34. Furthermore, these strains accumulate protein aggregates, establishing that U34 hypomodification perturbs protein homeostasis. Overexpression of specific tRNAs, is known to suppress the phenotypes of yeast strains with hypomodified U34. Importantly, overexpression of these tRNAs also decreased the translational slowdown of their cognate codons and alleviated proteotoxic stress. Using quantitative mass spectrometry we found that the protein content of aggregates from strains lacking either U34 modification or cotranslational chaperones largely overlaps, suggeting that aggregates are not specifically formed by proteins that are enriched for certain codons. Taken together, our findings provide the first in vivo evidence, that codon-specific translational slowdown, negatively affects protein folding. This establishes the critical importance of tRNA anticodon modifications for protein homeostasis. Finally, our findings suggest that the phenotypic expression of tRNA anticodon modification defects mainly stems from a systemic toxicity of misfolded proteins.

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Dosage compensation in fruit flies - a tale of parallel evolution?

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Dosage compensation is a process that balances the expression of sex-linked genes in species that have evolved unequal numbers of sex chromosomes. In the fruit fly, this involves a hyperactivation of the single male X chromosome to equalise for the combined transcriptional activity of both female X chromosomes. The two-fold increase in expression is regulated by the MSL complex and involves extensive chromatin modifications and chromosomal organisation. In this talk, I will present some of our latest results in the characterisation of this process and I will review some of evolutionary implications associated with dosage control. First, I will focus on a genomic analysis of the MSL complex and will show how it regulates the recruitment of RNA polymerase II to dosage compensated genes. Then I will focus on how specific components of the MLS complex have evolved parallel functionalities to regulate the expression of housekeeping genes. Finally, I will introduce how dosage compensation is regulated in other species and the level of functional conservation for several regulators of this process.

Common infections with coxsackieviruses of type B (CVB) induce severe forms of myocarditis that are often accompanied by ventricular arrhythmias and sudden death. It is likely that these common infections represent an evolutionary relevant factor. However, the mechanisms underlying the development of virus-induced, life-threatening arrhythmias, remain largely elusive. Here, we show time-dependent CVB3-induced modulation of the cardiac ion channels Kv7.1/KCNE1 in vitro. Channel protein localizations within cells and plasma membrane abundance are altered in infected mouse cardiac cells. In silico analyses of infected human myocytes suggest increased risk of arrhythmogenesis. These modifications are attenuated by the common Asian polymorphism Kv7.1-P448R, a genetic determinant preventing coxsackievirus-induced effects in vitro and therefore polymorphic Kv7.1-P448R may represent an evolutionary driver. Summarising, a combination of genetics, cell biology and in silico modeling proves suitable to test pathogen-host interactions as evolutionary drivers.

Guiscard Seebohm

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Molecular interactions rather than adaptive selection may shape gene architecture in Drosophila melanogaster

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Eukaryotic genes contain exons and intervening spliceosomal introns. Unlike exons, introns do not instruct protein synthesis and are transcribed only to be subsequently spliced from messenger RNAs. How did the exon-intron architecture originate? And, to what extent does natural selection shape gene structure? These questions are still unanswered.

We tested the hypothesis that the interplay between mRNA-associated processing factors is primarily responsible for shaping exon-intron structure in eukaryotic genes. According to the recently proposed U1-dependent definition (see Catania and Lynch, Bioessays 2013), the cooperative and antagonistic interactions between mRNA-associated processing factors can generate structural constraints and trade-offs, whose level of preservation is contingent on the intensity of natural selection. A computational study of the Drosophila melanogaster's genes reveals that (experimentally-verified) interactions between factors involved in capping, splicing, and cleavage and polyadenylation do indeed appear to leave sequence signatures that are consistent with the aforementioned model.

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Westfälische Wilhelms-Universität Münster

Combining metabolomics and transcriptomics to track the dynamics of nitrogen allocation in Escherichia coli

Nutrients are taken up by bacterial cells and used for the de novo synthesis of amino acids and other monomers. Since the different amino acids vary in their elemental stoichiometry, several studies have addressed the role for selection for efficient nutrient allocation in shaping amino acid composition. However, nothing is known on the cellular processes that enable selection to shape amino acid composition for parsimonious nutrient allocation. One possibility is that the environmental availability of nutrients drives the efficiency of translation via biased concentration of free amino acids.
To test this hypothesis we have designed a short-term Carbon and Nitrogen starvation experiment in Escherichia coli cultures. Combining Transcriptomics and Metabolomics we examined the distribution of these nutrients in the cellular pool of free amino acids and their incorporation in the proteins expressed in response to starvation. We could see that the abundance of the different free cellular amino acids varies, depending on their elemental composition, between Carbon and Nitrogen starved cultures. Furthermore, we see a reduction of Nitrogen-rich amino acids in proteins highly upregulated in response to Nitrogen starvation. These data support the idea that transcriptional efficiency plays a role in shaping the evolution of the stress response.
To extend our understanding of the dynamics of nitrogen allocation in response to nitrogen availability we established a continuous culture in which E. coli evolved for ›1500 generations under Nitrogen limiting conditions. Preliminary analyses on this population will be presented.

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When Biology needs Geology: a lesson from patterns of codon usage bias in the Bison Pool Hot Spring

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Recent advances in genomics have suggested that adaptation to the availability of key nutrients in the environment may be one of the factors that drive genome evolution. In this framework, the content of nitrogen in genes and proteins has been established as a marker to link genome evolution with environmental and metabolic traits. Rarely these stoichiogenomic analyses have been conducted in natural environments. In this study, we present an analysis of a geothermal spring and quantify the impact of biogeochemical factors on genome evolution.
Bison Pool, a flowing alkaline hot spring in the Lower Geyser Basin of Yellowstone National Park, represents an ideal ecosystem to investigate the relation of nitrogen availability and evolutionary change in natural microbial communities. In a 20 meters long outflow, boiling source water with low organic and mineral nitrogen content creates an opposing temperature and nitrogen gradient.
We found that nitrogen allocation in bacterial proteins follows the environmental availability of nitrogen and (i) clearly identified arginine as the driver of this phenomenon, leaving the impact of other proteinogenic amino acids negligible, (ii) provide evidence that, due to high nitrogen costs, arginine is substituted by lysine in hot sites and (iii) present an hypothesis how temperature-induced selection on ApG-dinucleotides provides the basis for thermo-adapative amino acid substitutions.
These results directly link environmental nitrogen availability to adaptive strategies of genome evolution, and reinforce the relevance of the material costs of evolutionary change in natural ecosystems.

Wolbachia can destabilize the population dynamics of Aedes albopictus mosquitoes

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Mosquitoes are important vectors for disease transmission in humans and livestock, causing worldwide problems for public health and agriculture. Recent efforts in pest control focus on biological control strategies that incapacitate the pathogen inside the vector by altering the vector's microbiome. A prominent example is the release of intracellular bacteria Wolbachia into natural mosquito populations with the aim to eliminate dengue fever. However, whether such artificial infections can be a successful strategy to control vector-borne diseases and minimize the risks associated with releasing potential disease vectors is still under debate. Here, we demonstrate that Wolbachia can destabilize mosquito population dynamics by contrasting Wolbachia-infected versus uninfected cage populations of the Asian tiger mosquito (Aedes albopictus). We found that the population variability (measured as coefficient of variation of population size) of the infected cages is higher than that of the uninfected cages. The elevated population variability is explained by the increasing nonlinear dynamics, as quantified by nonlinear time series analyses (S-Map analysis, state space reconstruction). In conclusion, the results suggest two potential risks for using Wolbachia in biological control programs. First, boom-and-bust of the mosquito population size is more likely to occur in Wolbachia-infected than in uninfected populations. Second, Wolbachia-infected mosquito populations are more difficult to manage because the higher degree of non-linearity makes their population dynamics less predictable. These findings have important management implications for the use of artificial bacterial infections as control of mosquitoes and vector-borne diseases.

Exploration of the association of animal personality and basal immune parameters in the stickleback (Gasterosteus aculeatus)

MÜNSTER GRADUATE SCHOOL OF EVOLUTION

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For many years, the three spined stickleback (Gasterosteus aculeatus) has been used as a model organism in numerous fields, such as animal behaviour and immunology. A growing body of work from all over the animal kingdom is reporting individual variation in the form of correlated behaviours. These behaviours are referred to as behavioural syndromes or animal personality if they are consistently found across time or context. In short, an individual in a population represents one behavioural type that is one possible combination of correlated behaviours found inside the population (for example, one individual tends to be bolder and more aggressive relative to the others). However, the possible fitness benefits of such correlations are still highly debated.
We combine the animal personality approach with a characterization of the basal immune functions. We hypothesize that various behavioural types might be exposed to infection pressure by parasites in a different manner. Bold, more explorative individuals might encounter higher infection risk, than shy, less explorative individuals. Consequently, a bold individual should have a higher immune activity than a shy individual. In a first set of experiments, laboratory bread sticklebacks from a German population near Münster were characterised in their aggressive and risk-taking behaviours at two time points. At the end of the observation period, leucocytes from the head kidneys of the sticklebacks were isolated and functional immune parameters, the respiratory burst activity and the granulocyte to lymphocyte ratio, were determined. Here, I will present the first set of results from my PhD project.

How are flowering time and immune defense related in Arabidopsis thaliana?

Westfälische Wilhelms-Universität Münster

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In order to survive, plants rely heavily on having an effective immune system to combat pathogens. Just like animals and humans, depending on their genetic composition, a plant can have a stronger (effective) or weaker defense machinery. Another trait of major importance for plants is flowering time. In Arabidopsis thaliana, the longer the plant grows before flowering, the more seeds are being produced. Generally, late flowering plants have higher fitness if they survive. As the plant waits until producing seeds, the risk of an infection increases. Thus, we expect late flowering plants to benefit more from investing into strong immune defense.
In nature we find large inter- and intra-specific variation regarding flowering time and defense. And indeed, it has often been observed that early flowering plants tend to be more susceptible to diseases than late flowering plants.
However, the genetic and evolutionary basis of this correlation is not understood. We have grown a collection of Recombinant Inbred Lines (RILs) from two accessions showing strong differences in flowering time and defense (Bur-0 and Col-0). With these plants, a QTL (Quantitative Trait Loci) analysis of flowering time will be associated with gene expression profiles of early and late flowering lines. If both traits have common underlying genes, we expect to find a correlation of the expression patterns of defense related genes with flowering time.

Phylogenetic relationships within Carnivora (Mammalia) based on retroposon insertions

MÜNSTER GRADUATE SCHOOL OF EVOLUTION

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The phylogeny of the order Carnivora has been studied in various ways, including morphologically, mt-DNA analyses, nuclear-DNA analyses, and combinations of such information in a supertree application. However the relationships of families within this group are still controversal.
We examined the evolutionary relationships within Carnivora using retroposed elements (Short INterspersed (SINEs) and Long INterspersed Elements (LINEs)) as phylogenetic markers. Retroposed elements represent neutral, nearly homoplasy-free phylogenetically informative characters, so the presence of a retroelement at an ortologous genomic locus in a group of species indicates a common ancestry. We found significant support for the monophyly of the order Carnivora (15 preliminary markers), of the clade Caniformia (Cynoidea+Arctoidea: 9 markers), of the clade Arctoidea (Ursoidea+Pinnipedia+Musteloidea: 20 markers), and of the clade Musteloidea (10 markers).
Based on retroposon insertions in Carnivora we also detected two problematic speciations. First, the relationships among Ursoidea, Pinnipedia, and Musteloidea remain unclear and, second, there are different variants of possible phylogenetic trees within Musteloidea. To resolve most of these problems, advanced multi-genome comparisons are in progress to find substantially more phylogenetically informative retroposon insertions.

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Natural selection shapes the evolution of DNA splicing signals in Paramecium

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DNA splicing plays a central role during the development of several organisms. In ciliated protozoa, it contributes to the formation of a functional somatic macronucleus (MAC), which is regenerated from the micronuclear genome (MIC; germline) after events of sexual reproduction. This developmental process involves the removal of micronuclear DNA regions known as internal eliminated sequences or IESs.
Previously, we found that hundreds of IESs are inaccurately spliced from the developing MAC of three closely related Paramecium species. A fraction of these IESs appear to have integrated into the MAC of each of these species. In addition, our in-silico study identified a set of IES-flanking sites that may have a role in the process of IES recognition/excision (Catania et al., 2013).
Here, we examine the role that these putative cis-regulatory sequences have in DNA splicing process in the species P. tetraurelia. We characterize the association between the quality of the putative signals - measured in terms of degree of sequence conservation - and the extent to which IESs are inaccurately excised. Furthermore, we identify patterns of these signals' association with characteristics such as IES size, IES genomic position, and the level of expression of the host gene. Our results provide original insights into the molecular mechanisms of IES excision. They provide further support to the regulatory role of the surveyed set of IES-flanking sites and suggest that natural selection affects the level of accuracy of DNA splicing in Paramecium.

In vitro leukocyte response of three-spined sticklebacks (Gasterosteus aculeatus) to helminth parasite antigens

Helminth parasites of teleost fish have evolved strategies to evade and manipulate immune responses of their hosts. Here, we used an in vitro system to investigate the response of Gasterosteus aculeatus leukocytes to antigens from helminth fish parasite species and parasite populations. Leucocytes responded with decreasing in vitro immune activity from generalist parasites (with a broad host spectrum) to specialists and among specialists from parasite species that do not infect G. aculeatus to those that do. Furthermore, in vitro immune activity of stickleback leukocytes, as well as antigenicity of parasite proteins, increased with the parasite prevalence in populations.

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The effects of microbiota on development and resistance in Tribolium castaneum

The relevance of microbial communities inhabiting different animal species is increasingly being studied in a broad spectrum, ranging from sponges to primates. Although the red flour beetle Tribolium castaneum represents a well-established experimental model organism for studying questions in ecology, evolution and development, the relevance of its microbial communities is still unknown. Using a newly established protocol for microbe eradication and raising germ-free beetles, we found that individual, sterile T. castaneum larvae show a slower growth rate in comparison to the ones harboring commensal bacteria. Moreover, we demonstrate that upon an oral infection with the natural entomopathogen Bacillus thuringiensis tenebrionis, larval survival was decreased in comparison to control animals. Therefore, this study represents a contribution to the accumulating evidence showing the importance of the microbiota in insects.

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Vision Impossible? Using synchrotron x-ray tomographic microscopy to visualise tissue and organ development in the earliest land plants

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For the past century the early Devonian (~407 million years) Rhynie chert from Aberdeenshire, Scotland has been a treasure-trove of information regarding the biology, ecology and evolution of the earliest land plants. The Rhynie chert plants, preserved at the cellular level, are traditionally studied using petrographic thin sections and a light microscope. There are many drawbacks to studying thin sections, such as loss of material during the sectioning process, flat two-dimensional imaging, and poor resolution of the plant tissues. Here we demonstrate a new method of chert analysis using synchrotron x-ray tomographic microscopy (SRXTM). Specimens of chert were bombarded with high energy x-rays which resulted in virtual slices of scanned specimens that could be stored as .tiff files. Using Avizo Standard imaging software, high-detail, 3D models of major tissues and organs of the extinct chert plant Rhynia gwynne vaughanii could be produced. The results show unprecedented levels of detail of structures such as the shoot apical meristem, stomatal complexes and vascular tissues. This new method of chert study is highly complementary to the traditional petrographic techniques and provides an extra tool in helping uncover the details of early land plant evolution, development and morphology.

Evolutionary significance of specific immunity and genetic specificity in Tribolium castaneum

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Host-parasite coevolution is defined as reciprocal genetic change in both antagonists due to selection imposed on each other. This process critically relies on genetic specificity and is often thought to be dominated by the parasite rather than the host. The phenomenon of phenotypic plasticity in immunity, also called “specific immunity”, could potentially alter the dynamics of this coevolutionary arms race: The selection pressure induced on the host by the faster evolving parasite would be relaxed within one host generation. The potential impact of specific immunity on host-parasite coevolution might be even stronger, if specific immunity would be an evolvable trait in itself.
We study host-parasite coevolution between the red flour beetle Tribolium castaneum and its natural parasite Bacillus thuringiensis (B.t.) in two separate selection line projects. For the first project the antagonists are allowed to coevolve over several generations to monitor changes in virulence of the parasite and/or resistance of the host. The second project aims at understanding the evolutionary significance of specific immunity of T. castaneum. For this, the beetles are primed and challenged with non-coevolving bacterial parasites, including B.t., over several generations. Evolved material from both projects will be analysed for transcriptomic and genomic changes to identify candidate genes responsible for the observed adaptations.

Assessing the effects of mating and infection status on host resistance and fecundity tolerance in Drosophila melanogaster

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In principle, hosts can employ two strategies to limit parasite load. Resistance, a host's ability to limit pathogen load, has been well studied. While tolerance, a host's ability to limit the damage caused by a parasite, a phenomenon well documented in the plant literature, is less well understood in animals. Previous work on resistance and tolerance in animals focuses primarily on host survival or health rather than on fitness measures or life history traits like fecundity. Egg production for insects like Drosophila melanogaster is especially costly, so it is reasonable to predict a tradeoff in egg production in response to bacterial infection depending on the defense strategy employed by the host. Alternatively, a host may employ a terminal investment strategy when infected, manifested by an increase in fecundity to compensate for shorter lifespan. Here we aimed to assay resistance and tolerance in D. melanogaster at the individual level to establish baseline methods for future studies of immune specificity. Using fecundity as our fitness measure, we examined the effect of mating status and immune challenge with a low dose of Lactococcus lactis and Escherichia coli on these host strategies in D. melanogaster females. We found that mating status but not infection status significantly affected the number of eggs laid over the experimental period, but observed a non significant trend for an effect of infection status on egg number. Future studies will examine resource limitation and infection load to better ascertain the mechanisms surrounding host defense strategies in D. melanogaster.

Social experience during adolescence and serotonin-transporter genotype affect anxiety-like and aggressive behavior

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Across mammalian species, behavioural traits like anxiety and aggressiveness are means to optimally cope with environmental challenges. However, in their exaggerated form they pose psychiatric problems to human societies and are regarded as pathologies from a biomedical viewpoint. Extensive research has shown that anxiety and aggressiveness can be shaped by genotype and experiences during early life phases. However, the period of adolescence has mainly been neglected so far. To elucidate how levels of these behaviours are shaped by genotype and experience during adolescence, experiments were conducted with serotonin-transporter (5-HTT) knockout mice. During adolescence, males of all three genotypes (wildtype, heterozygous and homozygous 5-HTT knockout mice) either experienced a mildly adverse social situation or they found themselves in an excellent social environment. For this purpose both groups were housed in custom-made cage systems. Mice experiencing a mildly adverse environment were repeatedly introduced to the territory of an established couple; but had the possibility to escape to a safe cage. Mice encountering beneficial social conditions had free access to a mating partner. Afterwards, anxiety-like behaviour was assessed in three standardised tests; aggressive behaviour was determined in a resident-intruder paradigm. The main results were: (1) Surprisingly, unfavourable conditions during adolescence led to decreased anxiety-like behaviour and increased exploratory locomotion. (2) Aggressive behaviour was more pronounced in animals that experienced social adversity. (3) Concerning genotype, homozygous knockout mice were more anxious and less aggressive. In conclusion, genotype and environment during adolescence can profoundly shape anxiety and aggressiveness.

GPAC – A Genome Presence/Absence Compiler for large-scale comparative multi-species analyses

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During the last decades the amounts of genomic data available from large numbers of species has grown considerably. To use such information for genome-wide and comparative studies, the University of California Santa Cruz (UCSC) Genome Bioinformatics Department provides so-called multiple-way alignments. Currently, the UCSC Genome Browser provides the possibility to only visualize and analyze orthologous information within a range of species stored in the multi-way alignment locus by locus. For scientific questions considering only a few loci, this tool represents an easy and fast way for analysis. However, in the present high-throughput genomic era, this approach is only of limited use and needs to be updated to a multi-locus application. In order to meet this request, we created a tool enabling the user to analyze multi-species presence/absence patterns of thousands of genomic loci simultaneously. The Genome Presence/Absence Compiler (GPAC) calculates the respective presence or absence statuses for all requested loci using the information stored in the multi-way alignments and summarizes all results in a flexible, color-coded table linked to the corresponding UCSC Genome Browser alignments. Accordingly, it is possible to analyze up to 1,000 loci of maximally 100 species in parallel. We demonstrate the usefulness of GPAC for genome-wide presence/absence analyses of various different transposable elements (7SL-derived retroposons, DNA-transposons, and endogenous retroviruses), nuclear mitochondrial DNAs, micro RNAs, exons, and introns in primates as well as exon/intron gain and loss in insects.

A protein network of common susceptibility genes provides a link between inflammation and cardiovascular disease

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Genome-wide association studies (GWAS) have identified hundreds of susceptibility loci for chronic and inflammatory disease phenotypes in humans. There is increasing evidence that chronic inflammation is a crucial driver in the pathogenesis of cardiovascular diseases (CVD), which may be genetically determined. To understand the genetic architecture underlying chronic inflammation and CVD we performed a systematic analysis of (1) common risk alleles coming from published GWAS, (2) of protein-protein interaction (PPI) networks informed by (3) gene expression data with a defined molecular target involved in the inflammatory processes promoting CVD, myeloid-related protein (MRP) 8. (4) Through analysis of integrated haplotype scores (iHS) and Fst values in HapMap phase 2 data, we investigated whether recent selection pressure acting upon inflammatory genes affected CVD susceptibility loci. Our findings provide significant evidence for a PPI network ($P = 0.033$), which connects inflammatory and cardiovascular susceptibility genes, and establish a genetic framework of inflammatory CVD. 41.59% of PPI genes are associated with immune functions. 28.3% of integrated genes can be linked to both, an inflammatory and cardiovascular disease phenotype. Interestingly, CDKN2B, and CELSR2/PSRC1/MYBPHL/SORT1, unequivocally replicated CVD loci, are integrated within this network as are several SNPs located in transcription factor recognition sequences, i.e. NFKB1, STAT3, which are key factors in inflammation. Finally, we observed a significant enrichment of inflammatory variants within CVD loci that are targets of selection ($P=2.001e-11$ in CEU population), suggesting that recent selective sweeps may have affected the genomic architecture underlying CVD.

Are males in old age still competitive? Age-dependent sexual conflict in Drosophila melanogaster

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In most species males and females have divergent reproductive strategies. When traits are favoured by one sex but cause fitness costs in the other sex, sexual conflict can occur. We are interested in studying ageing in sexual antagonistic traits and how this might alter the expression of sexual conflict. It is known that female age plays an important role in fecundity, but evidence is accumulating that also male age influences fertility. We conducted a study to investigate the reproductive success of ageing males in Drosophila melanogaster. We focus on age dependent effects of the sex peptide (Acp70A), a protein that is transferred along with sperm at mating to the female. Sex peptide is known to be beneficial for males as it increases egg laying rate and reduces female receptivity. At the same time it is harmful to females, because it is known to shorten female lifespan and thus mediates sexual conflict between the sexes. Thus documenting age-specific changes in male sex peptide expression allows us to study the demographic dynamics of sexual conflict across ageing individuals.

AlignmentComparator – A GUI application to efficiently visualize & annotate differences between alternative multiple sequence alignments

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With a growing number of alternative algorithms for automated multiple sequence alignment (MSA) and different strategies for manual alignment corrections it becomes more and more relevant to visualize the differences between alternative MSAs of the same data set. This allows the researcher to decide which alternative alignments to take into account as the bases of e.g. a phylogenetic study or numerous other tasks in biological research. Furthermore, manual alignment corrections can be visualized or a bioinformatician can determine the effect of changes made to a MSA algorithm, which both is very relevant in our current research focusing on the improvement of MSA for phylogenetic purposes.
Here we present AlignmentComparator, a platform independent open-source GUI application that reveals the differences and shifts in alternative MSAs by calculating and displaying a super alignment (similar to a profile-profile-alignment) that distinguishes between gaps previously contained in a single MSA and super gaps that originated from the comparison. This super alignment allows to directly identify matching regions in the alternative alignments, which otherwise would be very time-consuming with a conventional alignment editor, especially with an increasing column count and therefore a potentially increasing column shift. All differences can be commented and annotated with the AlignmentComparator GUI and saved to a XML file.

Software and poster download: http://bioinfweb.info/AlignmentComparator

Shaping of biobehavioural profiles during adolescence: An adaptation to the prevailing environment?

The social environment male guinea pigs experience during adolescence profoundly influences the development of their biobehavioural phenotypes. These socially shaped profiles are considered to represent adaptations to the respective environment the animals live in, with males stemming from high-density situations adopting a queuing strategy (QU) and males stemming from low-density situations adopting a resource defence strategy (RD).
In order to test whether these different biobehavioural profiles indeed have an adaptive function, match-mismatch experiments are conducted in which endocrine status, social behaviour and reproductive success are assessed. In a first experiment, groups consisting of one QU, one RD and two females each were kept together for up to five weeks simulating a low-density contest situation. RD were hypothesised to perform better within this condition as it matches their prevailing environment.
First results show that RD exhibit significantly higher cortisol and testosterone responses compared to QU, indicating RD to extensively mobilise energy reserves and to dominate the competitive situation. Beyond that, development of body weights is significantly more affected in RD than in QU during the initial hours of confrontation, which is likely due to the high energy expenditure in RD. However, this difference disappears afterwards, thus arguing against long-term negative effects. Taken together, these findings indicate an advantage of RD over QU at least in terms of the underlying neuroendocrine mechanisms. This supports the assumption of an adaptive function of the shaping of biobehavioural profiles during adolescence, although insight from behavioural data and reproductive success is needed to further validate this.

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