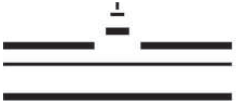
Westfälische Wilhelms-Universität Münster

MÜNSTER GRADUATE SCHOOL OF EVOLUTION

Münster Graduate School of Evolution

5th annual Symposium

Münster, 20 - 21 October 2015



WESTFÄLISCHE WILHELMS-UNIVERSITÄT MÜNSTER

MÜNSTER GRADUATE SCHOOL OF EVOLUTION

5th Annual MGSE Symposium

MÜNSTER GRADUATE SCHOOL OF EVOLUTION

ABSTRACT BOOK 2015

Edited by Joachim Kurtz, Francesco Catania, and Vanessa Kloke

Institute for Evolution and Biodiversity

University of Münster

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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 5th MGSE symposium will provide the doctoral students with the opportunity to present and discuss their ongoing PhD projects. Their posters and presentations will be embedded into contributions from principle investigators of the MGSE and public lectures from internationally outstanding guest speakers. The overall theme of the symposium will be “Evolutionary Medicine”, a growing and exciting field in which the theory of evolution is applied to understand medically relevant processes.

Münster’s city palace and its northern cavalier house will serve as venues for the symposium, providing an historic ambience for lively discussions and fruitful exchange in the heart of Münster.

Prof. Dr. Joachim Kurtz
Speaker of the MGSE

Dr. Vanessa Kloke
MGSE Coordinator

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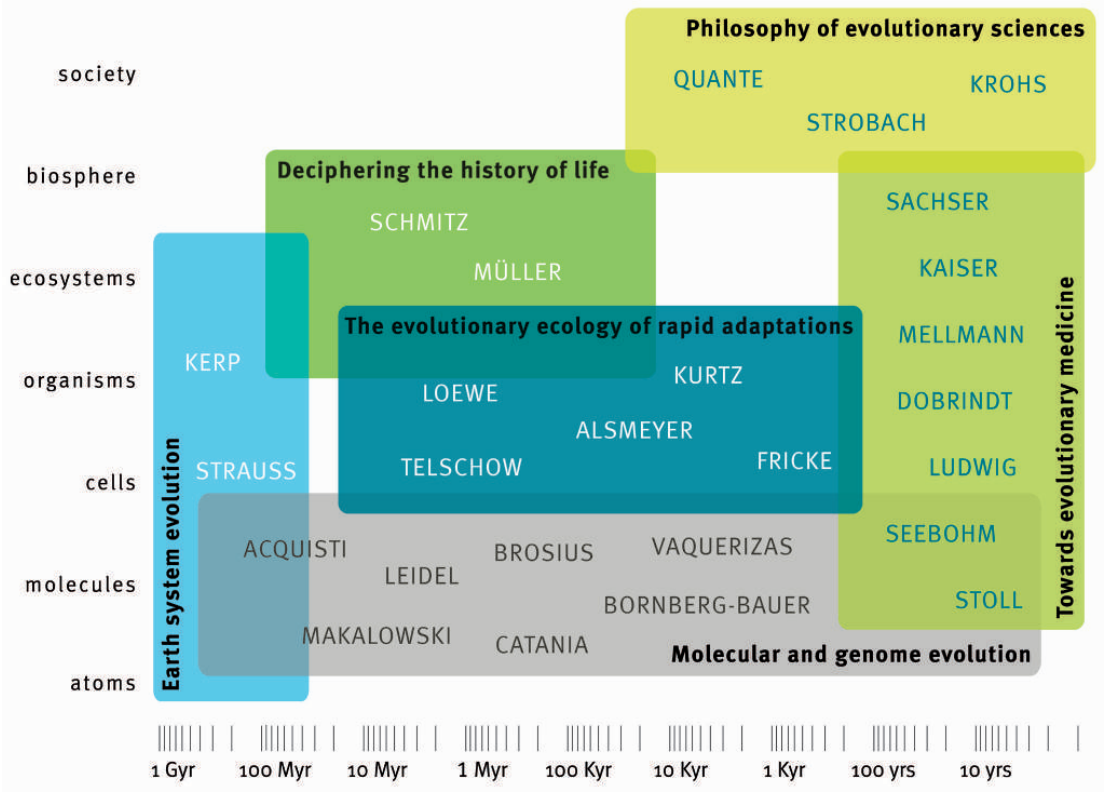
Philosophy of evolutionary sciences
QUANTE
KROHS
STROBACH
society
biosphere
ecosystems
organisms
cells
molecules
atoms
Deciphering the history of life
SCHMITZ
MÜLLER
SACHSER
KAISER
MELLMANN
DOBRINDT
LUDWIG
Towards evolutionary medicine
The evolutionary ecology of rapid adaptations
KERP
KURTZ
LOEWE
ALSMEYER
TELSCHOW
FRICKE
STRAUSS
Earth system evolution
ACQUISTI
LEIDEL
BROSIUS
VAQUERIZAS
BORNBERG-BAUER
MAKALOWSKI
CATANIA
SEEBOHM
STOLL
Molecular and genome evolution
1 Gyr
100 Myr
10 Myr
1 Myr
100 Kyr
10 Kyr
1 Kyr
100 yrs
10 yrs

MÜNSTER GRADUATE SCHOOL OF EVOLUTION

MGSE Principle Investigators

Name, Title	Research Topic	MGSE Research Area
Acquisti, Jun. Prof. Claudia	Evolutionary functional genomics	Molecular and genome evolution
Alsmeyer, Prof. Gerold	Mathematical statistics	The evolutionary 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
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
Leidel, Dr. Sebastian	RNA biology	Molecular and genome evolution
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 philosophy	Philosophy of evolution and education research
Sachser, Prof. Norbert	Behavioural biology	Towards evolutionary medicine
Schmitz, PD Jürgen	Experimental pathology	Deciphering the history of life

Name, Title	Research Topic	MGSE Research Area
Seebohm, Prof. Guiscard	Myocellular electrophysiology	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
Telschow, Jun. Prof. Arndt	Genome evolution	The evolutionary ecology of rapid adaptations
Vaquerizas, Dr. Juanma	Regulatory genomics	Molecular and genome evolution

MÜNSTER GRADUATE SCHOOL OF EVOLUTION

MGSE Graduate Students

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Stefanie Henze
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Kevin Knoblich
Tabea Kischka
Megan Kutzer
Lars Langhanki
Aaron Lecanda
Gildas Lepennetier
Neele Meyer
François Pellet
Hanna Ruhmann
Susanne Sangenstedt
Matthias Schreiner
Lena Strauß
Manuel Talarico
Tobias Tiedtke
Kristina Wensing

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Johannes Kerp
Tabea Kischka
Ulrich Krohs
Joachim Kurtz (Speaker)
Norbert Sachser
Susanne Sangenstedt
Monika Stoll (Deputy Speaker)

Ex officio members

Francesco Catania, Leader of the ETT
Cornelia Denz, Vice-Rector for International Affairs and Young Researchers
Vanessa Kloke, MGSE Coordinator

MGSE Ombudsperson

Hans-Dieter Görtz

Equal Opportunity Commissioner

Claudia Acquisti
Sylvia Kaiser (Deputy)

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Matthias Schreiner Gildas Lepennetier Florian Grziwotz
Patricia Kearney Kevin Knoblich Niklas Kästner Tobias Tiedtke Vanessa Kloke (MGSE Coordinator)
Francesco Catania (Leader of the ETT) Aaron Lecanda Hanna Ruhmann Neele Meyer Megan Kutzer Susanne Sangenstedt Rasha Aboelsoud

"Schloss" (Schlossplatz 2)

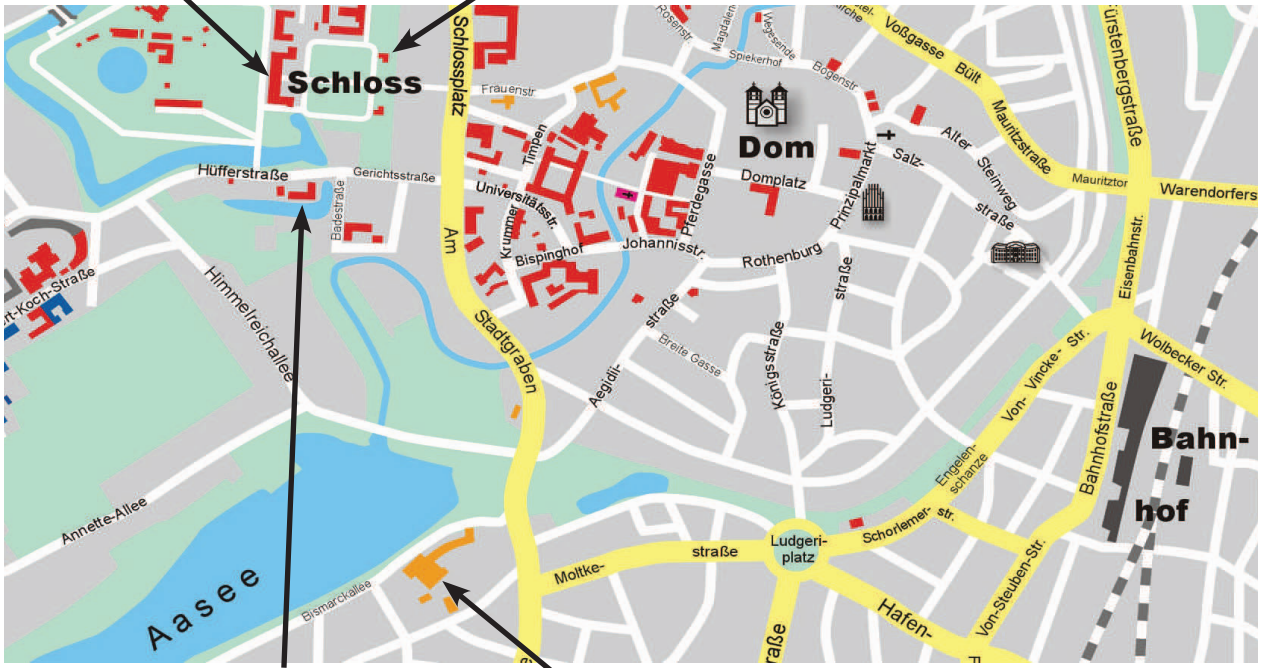
Münster's city palace was constructed from 1767 to 1787 as a three-winged complex by Johann Conrad Schlaun as a baroque residence for the Prince-Bishop. After the end of the Prince-Bishopric of Münster, the city palace served as residence for high ranking officials of the Prussian province of Westphalia.
During the Second World War the city palace suffered severe damage but the exterior aspect was reconstructed true to the original. Today, the palace is the seat of the University's administration and builds the centre of the academic city of Münster. The lecture hall S1 on the ground floor in the south wing will be the venue for the three keynote lectures of the MGSE Symposium. Posters will be presented in the foyer.

"Kavaliershäuschen" (Schlossplatz 6)

The baroque satellite building of Münster's city palace 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 1950th 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 Fundraising, the WWU Graduate Centre, and the Münster Graduate School of Evolution.

Schloss
Lecture Hall S1, Foyer
Schlossplatz 2

Kavaliershäuschen
Münster Graduate School of Evolution
Schlossplatz 6



Institute for Evolution and Biodiversity
Lecture Hall HHü, Hüfferstr. 1

Mensa am Aasee
Bismarckallee 11-11b

13.15 - 13.45: Introduction
Lecture hall S1, Schloss

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 S1, Schloss

Chair: Arndt Telschow

13.45: Edward Hagen
Washington State University Vancouver, US
Recreational substance use: does drug toxicity explain more than drug reward?

14.45: Ted Morrow
University of Sussex, UK
The evolution of sex differences in disease

15.45 - 16.15: Coffee break
Kavaliershäuschen, first floor

16.00: William Martin
Heinrich Heine University Düsseldorf, DE
Microbial genome evolution: a perspective from all genes (*Talk in the IEB Seminar Series „Frontiers in Ecology & Evolution", Lecture hall HHü, Hüfferstr. 1)*

17.15 - 18.15: Session 1, Talks by PhD students
Kavaliershäuschen, ground floor

Chair: Susanne Sangenstedt

17.15: Hanna Ruhmann
Evolution and Sexual Conflict, IEB
Are males in old age still competitive? Age dependent sexual conflict in *Drosophila melanogaster*

17.30: Megan Kutzer
Animal Evolutionary Ecology, IEB
Host tolerance, the path of least resistance? Immune strategies and life history responses in *Drosophila melanogaster*

17.45: Nora Stolte
Animal Evolutionary Ecology, IEB
The role of DNA methyltransferase 1 (Dnmt1) in the red flour beetle *Tribolium castaneum*

18.00: Liliya Doronina
Institute of Experimental Pathology, ZMBE
Untangled relationships of carnivores (Laurasiatheria, Carnivora): a retro-phylogenomic approach

18.30 - 19.45: Poster Session
Foyer, Schloss

20.00 - open end: Dinner buffet
Kavaliershäuschen, ground floor

10.15 - 11.15: Keynote lecture
Lecture hall S1, Schloss

10.15: Frank Rühli
University of Zürich, CH
Evolutionary Medicine: when the past teaches the living doctors

11.15 - 12.00: Coffee break
Kavaliershäuschen, first floor

12.00 - 13.00: Session 2, Talks by PhD students
Kavaliershäuschen, ground floor

Chair: Aaron Lecanda

12.00: François Pellet
Department of Philosophy
Disease as an essence-modifier

12.15: Tobias Tiedtke
Department of Behavioural Biology
Typical teenager: Cortisol stress responsiveness is highly stable over the life time except during adolescence

12.30: Tabea Kischka
Institute of Bioinformatics
Analysing data from the MinION™ nanopore sequencer for tropical disease diagnostics

12.45: Lena Strauß
Institute of Hygiene
Whole Genome Analysis of USA300-like Methicillin-resistant *Staphylococcus aureus* from sub-Saharan Africa

13.00 - 14.15: Lunch break
Canteen at the Aasee

14.15 - 15.45: Session 3, Talks by MGSE Principle Investigators
Kavaliershäuschen, ground floor

Chair: Francesco Catania

14.15 Stephan Ludwig
Institute of Molecular Virology, ZMBE
Novel insights in the evolution of influenza viruses

14.45 Monika Stoll
Institute of Human Genetics
The genetic basis of thromboembolism: lessons from genome wide association studies and next generation sequencing

15.15 Norbert Sachser
Department of Behavioural Biology
The contribution of Behavioural Biology to Evolutionary Medicine

15.45 - 16.15: Coffee break
Kavaliershäuschen, first floor

16.15 - 17.15: General Assembly of all MGSE members
Kavaliershäuschen, ground floor

Recreational substance use: does drug toxicity explain more than drug reward?

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Psychoactive drugs are widely used, it is thought, because they inadvertently activate reward-related neural circuitry. If so, drugs should be equally appealing to children and to adults of both sexes. Many drugs are plant defensive chemicals, however. Hence, children, and to a lesser extent adult women, should have evolved to avoid consuming them to protect their, or their fetuses', developing nervous systems, respectively. Analyses of national and cross-national data find virtually no substance use among children; a switch-like transition to substance use in adolescence; and a nearly universal male bias in substance use. They also find that a higher total fertility rate predicts lower female prevalence of tobacco use, even after controlling for indices of women's social, economic, and educational status. These results suggest that fetal protection helps explain female smoking decisions. The onset of substance use in adolescence might be explained by the diminishing developmental costs of toxin exposure vs. the increasing benefits of toxin exposure in ancestral environments, such as self-medication of macroparasites.

KEYNOTE LECTURE

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KEYNOTE LECTURE

Ted Morrow

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University of Sussex

It is now becoming widely recognized that there are important sex differences in disease. These include rates of disease incidence, symptoms and age of onset. These differences between the sexes can be seen as a subset of the more general phenomenon of sexual dimorphism of quantitative phenotypes. From a genetic point of view, this is paradoxical, since the vast majority of genetic material is shared between the sexes. How can males and females differ in so many ways and yet have a common genetic code? Traditionally, the modifying action of hormones has been offered as a solution to this paradox, but experiments disentangling the effects of hormones and sex-chromosomes have shown that this cannot be the sole explanation. I will outline current ideas about the evolutionary origins of sex differences in phenotypes, with a particular focus on how sex differences in disease can arise, and also describe the approach our laboratory is taking to identify genes with sex-specific effects in the fruit-fly model organism. I will argue that taking an evolutionary view on sex differences in disease provides an opportunity for greater understanding of mechanisms of disease and as such provides a clear motivation for clinicians to explore how therapies may be tailored to the individual in a sex-dependent way.

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Evolutionary Medicine: when the past teaches the living doctors

MÜNSTER GRADUATE SCHOOL OF EVOLUTION

Evolutionary Medicine is a novel transdisciplinary research and teaching field, exemplary addressing health-oriented research issues such as microevolutionary and secular changes of human structure and pathologies. Introducing principles of human evolution and its forces into the knowledge of future practitioners of health-related professions is a crucial part of this upcoming scientific discipline. In this presentation, the wider impact of evolutionary medicine - particularly for medicine -will be shown as well as the very latest research results on morphological and genetic evolutionary changes by us. At the University of Zurich the Institute of Evolutionary Medicine as part of the Medical Faculty has been established in 2014. This unique research and teaching setting will be briefly highlighted too. Finally, the general impact of a broader understanding of human variability as investigated in such research will be addressed.

KEYNOTE LECTURE

Frank Rühli

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Novel insights in the evolution of influenza viruses

MÜNSTER GRADUATE SCHOOL OF EVOLUTION

Influenza is the paradigm of a viral disease in which continued evolution of the virus is of paramount importance for annual epidemics and occasional pandemics in humans. These human negative-stranded RNA viruses are derived from a large viral reservoir in aquatic birds that provide a gene pool with all the genetic diversity required for the emergence of pandemic influenza viruses. All pandemics of the last century were caused by reassortant viruses with a mixed genome of avian and human virus origin. The only exception so far is the Spanish flu pandemic of 1918/19 that was so far believed to go back to a direct transmission of a bird virus to humans. However, we obtained recent evidence that the Spanish flu virus might also have been a reassortant virus, carrying at least a human-like PB1 gene. As a zoonotic pathogen influenza viruses have to adapt to new hosts after crossing the species barrier. In an attempt to identify crucial mutations that occur during adaptation of the pandemic influenza virus of 2009 to a new species we found that only three mutations converted an apathogenic virus isolate to a highly pathogenic strain in mice. Recently influenza-like viruses have been identified in bats, a species which was not known before to be susceptible to influenza virus infection. The current knowledge on how these viruses have to placed in the evolutionary tree of influenza viruses will be discussed.

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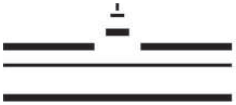

The genetic basis of thromboembolism: lessons from genome wide association studies and next generation sequencing

Monika Stoll

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In the past decade, genome wide association studies (GWAS) emerged as method of choice to dissect the genetic architecture of complex diseases. Particularly, GWAS have greatly contributed to our understanding of the underlying molecular mechanisms and identified previously unknown susceptibility factors and pathways contributing to disease. In my presentation, I will present and discuss data, which we generated in the past 7 years comprising two GWAS on thromboembolic disease, pediatric stroke and venous thrombosis, and the subsequent quest to uncover rare coding variants contributing to the observed association through targeted next generation sequencing (NGS) approaches. In particularly, issues relating to the handling of large data sets coming from such high throughput approaches will be discussed e.g. problems relating to multiple testing correction, linkage disequilibrium in the genome or traces of selection pressure acting upon the genome affecting both, the identification of the true underlying genetic variants as well as the interpretation of the results.

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The contribution of Behavioural Biology to Evolutionary Medicine

In the field of Behavioural Biology several concepts were developed during the last decades with particular relevance for Evolutionary Medicine. Using examples from our own comparative research three of these concepts will be addressed: environmental enrichment, social support, and the adaptive shaping of behavioural phenotypes by social experience. Specifically it will be shown that (1) applying environmental enrichment to mouse models of Alzheimer's disease delays behavioural and neuronal symptoms related to the disease. (2) Social support by social bonding partners buffers hormonal stress responses in a most effective way. (3) Behavioural profiles that were shaped by social experiences during early phases of life are related to good welfare and health in adulthood when they match the environment. In contrast, a mismatch increases vulnerability to disease.

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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, sexual conflict occurs. It is known that female age leads to reduced fecundity. Evidence is accumulating that also male age influences reproductive success. We are studying how ageing might affect the expression of a sexual antagonistic trait in males and how this might alter sexual conflict dynamics. We investigated the reproductive success of ageing males in *Drosophila melanogaster* with a focus on the accessory gland proteins sex peptide and ovulin, as particularly sex peptide is involved in mediating sexual conflict between the sexes. Using the ELISA method we quantified how much of these proteins males of different ages transfer to females and detected significant differences. We also found that the ability to gain a first mating with a virgin female, to prevent females from remating and the competitive power of a male changes significantly over his lifetime. Hence age significantly affects male reproductive success, however this decrease is not constant across male age and already shows a first dip in intermediate aged males.

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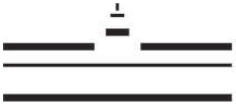

Host tolerance, the path of least resistance? Immune strategies and life history responses in Drosophila melanogaster

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Mounting and maintaining an effective immune response in the face of a persistent infection is costly. Its outcome may ultimately depend upon two host immune strategies: resistance and tolerance. Resistance limits pathogen load but often comes at a fitness cost, while tolerance reduces the fitness impact of an infection. A major challenge in eco-immunology is to understand how a tolerant host can maintain its fitness when infected, as well as how extrinsic, environmental factors, such as diet, affect the host immune response. It is clear that there is a relationship between dietary restriction and fitness, but it is less obvious how an organism responds when faced with an immune challenge when resources are scarce. Here we aimed to test fitness, resistance and tolerance in response to dietary restriction by limiting protein availability and to characterize bacterial infection pathology in individual flies within one population. Because infectious diseases are not always lethal, we tested resistance and tolerance using two non-lethal bacteria: *Escherichia coli* and *Lactococcus lactis*. A low protein diet translated into lower fitness but did not affect bacterial resistance. We found evidence for diet-induced variation in host tolerance to *E. coli*, but not to *L. lactis*, which was dependent upon time after infection. Furthermore, despite the lack of fitness costs, both bacteria species persisted for at least seven days post infection. Our study uncovered considerable individual variation in both resistance and tolerance, indicating that population level means may fail to reveal the full extent of variation in immune traits.

The role of DNA methyltransferase 1 (Dnmt1) in the red flour beetle Tribolium castaneum

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Epigenetic regulation enables rapid phenotypic adaptation to environmental changes. Cytosine methylation of DNA is an important epigenetic mechanism, which is generated by an evolutionarily conserved family of enzymes, so called DNA methyltransferases (DNMTs). The ancestral DNMT toolkit consists of three enzymes DNMT1, 2 and 3. However, the evolution of cytosine methylation systems has generated great variation in the sets of Dnmt genes. While Drosophila lacks a functional DNA methylation system, honeybees possess all three DNMTs, and DNA methylation is crucial for caste determination. In animals, DNMT1 is known to be responsible for maintaining methylation patterns by methylating hemimethylated DNA after replication.

The status of a functional DNA methylation system in the red flour beetle *Tribolium castaneum*, which possesses Dnmt1 and Dnmt2 but lacks Dnmt3, has been under discussion for several years. In the present study, we show that DNMT1 is essential for early embryonic development, although we were not able to detect functional levels of DNA methylation via whole genome bisulfite sequencing. Parental RNAi knockdown of Dnmt1 in the mothers caused a developmental arrest in the offspring embryos within the first four hours after oviposition. This, to our knowledge, first evidence of a functional role of DNMT1 during embryogenesis in *T. castaneum*, calls for further studies investigating additional functions of this enzyme and its role beyond DNA methylation.

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Untangled relationships of carnivores (Laurasiatheria, Carnivora): a retrophylogenomic approach

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Evolutionary relationships of some rapidly radiating mammalian groups persistently resist attempts of phylogenetic resolution in the case speciation events occurred faster than marker fixation. Highly complex, homoplasy-free retroposon insertions, however, provide a reliable source to distinguish fixed and polymorphic markers and were successfully applied to resolve complex phylogenies in different vertebrate groups.
Carnivores experienced several problematic speciation incidences, one of which occurred 42 million years ago during the divergence of Arctoidea into the three groups – Ursoidea, Pinnipedia, and Musteloidea. We applied a combination of high-throughput retrophylogenomic screenings and wet lab approaches to detect genome-wide diagnostic retroposons that we then used to identify inconsistent phylogenetic patterns. Using both full-length SINE and truncated LINE elements we found 192 markers supporting a Pinnipedia plus Musteloidea clade, 60 markers for Ursoidea plus Pinnipedia, and 74 markers indicating Ursoidea plus Musteloidea. The somehow conflicting pattern, nevertheless, significantly supports the Pinnipedia – Musteloidea sister group and indicates an ancient time of incomplete lineage sorting. These results demonstrate the unique power of transposed elements in understanding and solving such problematic phylogenetic zones.

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Disease as an essence-modifier

In the philosophy of medicine, we currently distinguish between two main approaches to defining 'disease'. The first approach, called 'naturalism about disease', tries to ground disease in biological malfunction; the second approach, called 'normativism about disease', defines disease as a physiological or psychological state that organisms want to avoid.
After having presented these two approaches, I shall sketch a new definition of disease as being a modifier of the essence of the disease bearer. According to my definition, for an entity to be diseased is for it to have its essence being modified. I finally show how my definition of disease is related to the two approaches.

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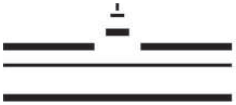

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Typical teenager: Cortisol stress responsiveness is highly stable over the life time except during adolescence

Tobias Tiedtke
Sylvia Kaiser
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Institute of Neuro- and Behavioural Biology
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Cortisol stress responsiveness is an essential feature of biobehavioural profiles as it is critically involved in the control of behaviour and provides the organism with energy to cope with challenge. A series of experiments in guinea pigs (*Cavia aperea* f. *porcellus*) was conducted to examine whether cortisol stress responsiveness represents a temporally stable trait during various life stages. When male guinea pigs housed in large mixed-sex colonies were repeatedly exposed singly to a novel enclosure, the acute cortisol stress response was remarkably stable during postweaning and early adolescent phases. That is, cortisol response values were individually consistent over retesting intervals from 20 to 30 days and 30 to 55 days of age, respectively. This stability was confirmed for adult animals (approximately 7 to 17 months) over even longer retesting intervals of about 2 months. In contrast, no significant consistency of cortisol responses was found from early to late adolescence (55 to 120 days), which covers the phase of sexual maturation where colony-housed males show a socially mediated suppression of HPA reactivity. On the other hand, pair-housed males, which do not show suppressed HPA responsiveness during adolescence, exhibited highly stable individual differences in cortisol responses over exactly the same period.
Taken together, individual cortisol stress responsiveness is a highly stable trait during most life stages. Interestingly, the social environment has remarkable influence on this stability during phases of increased developmental plasticity, as it is the case for adolescence.

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Analysing data from the MinION™ nanopore sequencer for tropical disease diagnostics

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Sequencing single DNA molecules with nanopores is now becoming competitive with other DNA sequencing methods. This is thanks to the MinION™ by Oxford Nanopore Technologies, a low-cost, cheap and simple-to-use sequencing device. However, there still is a shortage in tools to analyse the produced reads.
Here, we describe NanoPipe, a web-based automatic pipeline that can quickly and effortlessly analyse data produced by the MinION™. It was build to detect and genotype pathogens of tropical diseases with dengue virus serotyping and malaria parasite genotyping as study cases. NanoPipe makes these analyses accessible for medical practitioners and researchers with lesser IT experience. Reads can be provided by the user in fastq or in the raw, HDF-based fast5 format that is produced by the sequencer. As the result of the analysis, NanoPipe provides clear information on potential polymorphisms (malaria case) or serotype diagnosis (dengue virus case). The results are supplemented with a number of useful pages, such as consensus sequences, alignment of consensus sequences against the target sequences, read length distribution, or logo plots showing distribution of nucleotides from all reads at each position of the consensus sequence.
We use LAST aligner with optimised parameters as a main engine for the analyses and a set of custom python and R scripts for data processing. While the NanoPipe is an efficient tool with non-IT-savvy user in mind, the whole pipeline is also available for free download for those who would like to run it locally.

Whole genome analysis of USA300-like Methicillin-resistant Staphylococcus aureus from sub-Saharan Africa

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The USA300 clone is a hypervirulent methicillin-resistant *Staphylococcus aureus* (MRSA) lineage, which is dominant in North America since about ten years, but rarely isolated elsewhere. Recently, some MRSA with USA300-like molecular characteristics were also reported from sub-Saharan Africa, but due to differing spa types, they were not regarded as true USA300. Our objective was to clarify the phylogenetic relationship of (i) 52 ST8 MRSA and MSSA (methicillin susceptible *S. aureus*) from different countries of sub-Saharan Africa, (ii) the first identified community-associated ST8 MRSA from Australia (n=6) and two NCBI reference genomes for USA300 and its assumed predecessor USA500. All isolates were whole genome sequenced and analyzed with regard to their species- and lineage-specific core genome and USA300-specific molecular characteristics. Five major clades could be distinguished, including one cluster of isolates closely related to the USA300 reference genome (n=16). The spa types of these African isolates were single locus variants of the typical USA300 spa type. In conclusion, the data suggests that these USA300-related MRSA isolates detected in West and Central Africa are “true“ USA300 clones.

Does HSP90 act as a buffer for phenotypic variation?

MÜNSTER GRADUATE SCHOOL OF EVOLUTION

The concept of 'developmental stability' or the robustness of the phenotype against genetic and environmental perturbations is called 'canalization'. By buffering the expression of traits, canalization has evolved under natural selection to stabilize phenotypes and decrease their variability. Recently, it was found that Heat shock protein HSP90, encoded by the hsp83 gene, plays a special role in the relationship between genotype and phenotype by buffering the phenotypic variation through either accumulating 'cryptic genetic variation' or preventing transposon-induced mutations by suppressing their activity. Here, we reduced the expression of hsp83 gene by RNAi-mediated knock-down in the red flour beetle *Tribolium castaneum* and studied the effects on fitness and phenotypic variation of offspring. So far our results showed that the reduction of hsp83 expression shortened the life span of both male and female beetles. The treated females were significantly less fecund than controls and their fecundity was completely inhibited when hsp83 expression was strongly reduced, when we also observed an ovarian phenotype. By contrast, male fertility was only partially inhibited, even with strong hsp83 reduction, and male gonads didn't change morphologically. Moreover, a low proportion of larvae produced from hsp83-dsRNA treated parents revealed either reduced or missing eyes as abnormal phenotypes, which where never found in controls, and suggest a potential release of cryptic genetic variation. Moreover, we studied the expression of transposable elements as one of the potentially underlying mechanisms, but found only weak effects of hsp83 knock-down, with a trend for down-regulation in the gonads of both sexes of *T. castaneum*.

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Circadian rhythms effect Paramecium tetraurelia growth and sexuality

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In the last century, a huge amount of studies highlights the presence of strong relationships between metabolic state and environmental circadian light fluctuations. The circadian programming pathways involved in the regulation of the internal metabolism shown high levels of gene conservation in flies, mammals and fish. In human, internal clock's factors are essential for achieve the energetic balance and provide adaptation plasticity not only in case of environmental changes, but also in presence of diseases like thyroid malign cancers and others pathogenic conditions.
Ciliates, like *Paramecium tetraurelia* and *Tetrahymena termophila*, are unicellular eukaryotic models highly important for the modern evolutionary molecular biology. In these alveolata species only few informations are available about the circadian rhythmics. Moreover, it was poorly investigated the effect of light changes on genomes and proteins evolution.
In this work, different light/dark conditions were tested on physiologically synchronized cell lines of *P. tetraurelia* in order to identify the possible presence of relationships between metabolic state and light fluctuations. Our preliminary results demonstrate not only the presence of a strong light-related effect, but also a trans-generational conserved growth behaviour. This observations suggest us that light/dark fluctuations matter when we study ciliates evolution, and perhaps future experiments should be performed in order to explain the molecular reasons behind the observed phenotype.

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Benefits of a "vulnerability gene"? A study in serotonin transporter knockout mice

MÜNSTER GRADUATE SCHOOL OF EVOLUTION

Over the past years, certain "vulnerability genes" have been identified that play a key role in the development of mood and anxiety disorders. In particular, a low-expressing variant of the human serotonin transporter (5-HTT) gene has been described that renders individuals more susceptible to adverse experience and hence to the development of psychiatric diseases. However, some authors have recently argued that lower 5-HTT expression not only increases vulnerability to adverse experiences, but also enhances susceptibility to beneficial experiences, thus promoting phenotypic plasticity. The aim of the present study was to assess the effects of 5-HTT expression on susceptibility to beneficial experience in a hypothesis-driven experimental approach. Using a well-established rodent model for the human polymorphism, male heterozygous 5-HTT knockout (HET) and 5-HTT wildtype (WT) mice were either provided with the beneficial experience of cohabitation with a female (mating experience) or kept as naïve controls in single-housing conditions. Following the experimental treatment, they were tested for their anxiety-like behaviour and exploratory locomotion in three widely used behavioural tests.

Interestingly, while cohabitation reduced anxiety-like behaviour and increased exploratory locomotion in the open field test in HET mice, it did not affect WT mice, pointing to a genotype-dependent susceptibility to the beneficial experience. Thus, our results might support the view of the low expressing version of the 5-HTT gene as a "plasticity" rather than a "vulnerability" variant.

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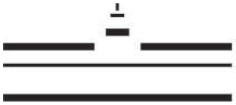

Network analysis of chromatin contacts during the P. falciparum infection cycle

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Plasmodium falciparum is a eukaryotic pathogen causing the most malignant for of malaria in humans. Its ability to express different virulence genes to avoid detection by the host makes it especially dangerous. Recent analyses of the genomic organization of *P. falciparum* revealed a highly dynamic nuclear architecture, and strong association between DNA-DNA contacts and gene expression (Lemieux et al. 2013, Ay et al. 2014). Most notably, virulence genes appear to form spatial clusters with distinct, domain-like structures. Despite these general architectural findings, it is currently unknown how the establishment and loss of specific DNA-DNA contacts between genomic elements during the *P. falciparum* infection cycle contributes to different virulence phenomena. I study the genomic organization of *P. falciparum* from a complex network perspective. Specifically, I construct differential networks of contact changes between infection stages, permitting the time-resolved analysis of individual genomic contacts. This framework allows me to investigate how network properties and contact changes between specific genomic elements are linked to important gene regulatory mechanisms, including virulence gene selection, activation, and silencing. A first major observation is the dramatic change in the amount of specific DNA-DNA contacts among virulence genes during the course of the infection cycle, prompting a more detailed analysis of the association between virulence and the 3D organization of the *P. falciparum* genome.

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Analysis of uORFs in stem cells and derived neurons

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Upstream Open Reading Frames (uORFs) are regions located in the transcript leader sequence of mature mRNAs upstream of the main ORF. The uORFs are generally shorter than 20aa and implicated in the translational regulation of the downstream ORF. They are known to be present in different organisms like yeast, human and mouse which indicates a possible evolutionary conservation.
The regulatory roles that uORFs play are variable and greatly influenced by different factors and characteristics of the whole 5' UTR or their surrounding context. The use of variable transcription start sites (TSS) during development gives rise to different 5' UTRs from the same gene. Hence, different uORFs can be present, playing distinct regulatory roles under different conditions or during different developmental stages. Furthermore, specific RNA binding factors may modify the regulatory potential of uORFs. However, we know very little about these mechanisms due to the previous lack of proper techniques for studying them. The advent of ribosome profiling, allows for a quantitative analysis of translation. This technique, which consists of the next generation sequencing of ribosome protected RNA fragments, has been used as an effective way to detect uORFs. The efficiency of detection can be further enhanced through the use of Harringtonine, a drug that stalls ribosomes during the initiation step of translation.
We performed ribosome profiling in human Embryonic Stem Cells (hESC), Neuronal Precursors (NPC) and neurons of the central nervous system (CNS) to address the differential transcript expression of uORFs during this stages.

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U1-dependent definition is a model of splice site recognition that unifies exon and intron definition. This model specifies how the interplay between splicing factors and cleavage/polyadenylation factors, which compete for access to overlapping or neighbouring binding sites along nascent mRNAs, may potentially contribute to gene expression and gene architecture in eukaryotes.
Here, we use the model organism *Drosophila melanogaster* to test and verify a number of this model's predictions.

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Social experience during adolescence affects anxiety-like but not aggressive behaviour of male mice

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 humans and are regarded as pathologies from a biomedical viewpoint. Extensive research has shown that anxiety and aggressiveness can be shaped by experiences during early life phases. However, the period of adolescence has mainly been neglected so far. In a recent study, we could show that escapable adverse social experiences during adolescence led to decreased anxiety-like behaviour and an increase in exploratory and aggressive behaviour in male mice. The increase in aggressiveness however, could also have resulted from the single housing the animals experienced before performing the test, a factor known to influence agonistic behaviour. To validate these results, we repeated the study with modifications concerning the aggressive behaviour. During adolescence, male mice either experienced escapable social adversity or beneficial conditions and afterwards were either tested for anxiety-like and exploratory behaviour in three standardised tests or for aggressive behaviour in the resident intruder test. Interestingly, aggressive behaviour did not differ between animals that experienced the two different social environments. Similar to the previous study, mice that experienced unfavourable conditions during adolescence showed decreased anxiety-like behaviour and increased exploratory locomotion compared to animals that experienced beneficial conditions. It thus seems that social experience during adolescence does not influence aggressiveness directly but rather the way animals cope with their environments.

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Adaptive strategies of female wild cavies under limited conditions

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Behavioural profiles are shaped during ontogeny - the time from the moment the egg is fertilized until the death of an individual. To increase their fitness, subjects have to adjust themselves to their abiotic as well as their biotic environment. The latter does not only consist of inter- but also intraspecies interactions which is defined as social environment. The social environment can support welfare and health, but can also result in severe stress, eventually leading to diseases and even death. Thus, the social environment represents an influential stressor, which can even be crucial for the development of the offspring as well. For example in wild cavies, instability of the social environment during pregnancy and lactation affects the development of offspring: Daughters of mothers living in unstable social environments exhibit a profound behavioural masculinization in contrast to daughters of mothers which had lived in stable social environments.
We investigated whether daughters of mothers living in unstable social environments have advantages over daughters of mothers living in stable social environments in situations where resources are scarce. The idea of this experiment is that in situations, in which resources are limited, competitive abilities are important and masculine traits facilitate the attainment of dominant social positions which in turn help to secure resources more efficiently. Under such conditions masculinized females might fare better than non-masculinized. We analysed cortisol reactivity, body weight and dominance establishment and will discuss whether the different behavioural phenotypes are caused by maternal effects and may represent adaptations to environmental conditions.

Genome-wide Analysis and Comparison of Enterohaemorrhagic E. coli for Improved Strain Typing

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Enterohaemorrhagic *Escherichia coli (EHEC)* are a major human pathogen which can cause non-bloody and bloody diarrhoea. In a subset of cases EHEC infections can lead to haemolytic uremic syndrome (HUS). Additionally EHEC strains possess the ability to cause major outbreaks as in Japan 1996 with over 6000 patients or in Germany 2011 with over 800 HUS patients. Additional problems arise due to the ability of *E. coli* to acquire pathogenicity islands via conjugation from other EHEC or even other evolutionary distant enteropathogenic *E. coli*. Therefore creating novel strains, like the O104:H4 strain responsible for the 2011 outbreak in Germany.

Rapid identification of rare and novel EHEC variants is severely impaired in many diagnostic labs, due to the focus on 5 serotypes which are responsible for the majority of disease cases and the concentration on the detection of Shiga-toxin stx and the intimin-encoding eae genes. A reliable risk assessment of all EHEC isolates requires the determination of marker combinations which allow unambiguous discrimination of EHEC variants. To achieve this goal a profound understanding of the genome plasticity and variation of EHEC strains is needed. In a first step 56 EHEC and 22 commensal and environmental *E. coli* genome sequences were subjected to whole genome-based phylogenetic analyses including MLST, rMLST, MLST+.

First results show that high resolution analysis like MLST+ are needed to resolve the genome plasticity of EHEC strains. Future work will focus on virulence gene content and detection of novel discriminatory genome regions.

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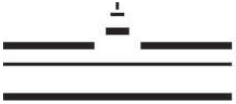

Westfälische Wilhelms-Universität Münster

Behavioural changes of G. aculeatus by infection with the cestode Schistocephalus solidus - Handicap or Specific Manipulation?

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The cestode *Schistocephalus solidus* affects morphological and physiological characteristics as well as behavioural traits of its obligatory intermediate host, the three-spined stickleback (*Gasterosteus aculeatus*). Infected stickleback have swollen abdomens and (occasionally) brighter skin colours, differ in their tendency to shoal, swim closer to the water surface and exhibit less escape behaviour under the risk of predation. Although it is evident, that the latter changes of stickleback behaviours improve the transmission of the parasite to its final host, a fish eating bird, there is no consensus yet, if these alterations are physical handicaps caused by the parasite burden or specific manipulations by the parasite. If the behavioural abnormalities of *S. solidus* infected sticklebacks were indeed physical handicaps, the changes in activity behaviours of *S. solidus* infected sticklebacks would presumably differ from that of uninfected sticklebacks even in contexts, which are unlikely to affect parasite transmission to the final host. Therefore, we monitored the activity of *S. solidus* infected and not infected sticklebacks in an exploration of a new environment setting and a locomotion while foraging test. The sticklebacks' response to an artificial bird strike served as a positive control. As expected, infected sticklebacks returned much faster to foraging after the artificial bird strike and spent more time close to the water surface than not infected sticklebacks. However, locomotion during foraging and activity during exploration of a new environment did not differ significantly between infected and not infected sticklebacks. These results imply that the influence of *S. solidus* on the three-spined stickleback is a specific manipulation of predator avoidance behaviour rather than a general handicap.

Divergence of Drosophila melanogaster populations in female sensitivity to sex peptide

Sexual conflict is hypothesised to be an important driver of divergence in reproductive traits between conspecific populations. Female *Drosophila melanogaster* pay a fitness cost due to multiple mating that is mainly caused by receipt of the sex peptide. This short peptide is produced in the male accessory gland and transferred to the female at mating. Previous research has shown that females can evolve resistance against male harm however the extent to which *D. melanogaster* populations might diverge in their sensitivity to sex peptide has not been studied before. Here we fill this gap in our knowledge by testing for divergence in female resistance to sex peptide by phenotypically comparing cost of mating effects in different *D. melanogaster* populations. We exposed females of three different wild type populations continuously to standardised males unable to produce sex peptide or control males throughout their whole life. We measured survival, lifetime reproductive success, and mating frequency and used those variables to calculate and compare a fitness index across the different populations. We found significant male x female interactions for lifetime reproductive success, survival, and fitness; indicating divergence between different female wildtypes in their response to the receipt of sex peptide. This divergence may reflect differences in patterns of sexually antagonistic coevolution, underlying genetic variance and/or mating dynamics.

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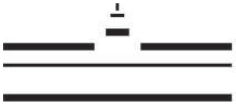
New comparison and annotation methods of the phylogenetic tree editor TreeGraph 2



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TreeGraph 2 is a user friendly tree editor with the main focus on processing, visualizing and comparing phylogenetic trees carrying numerous annotations. Here, new features added since its initial publication in 2010 are presented.

The ability to import and visualize probabilities for ancestral character states (e.g. by pie charts attached to internal nodes) has been extended. A special reader allows importing according data from the software package BayesTraits, while importing from similar software is indirectly possible using the new and more powerful annotation table import function.

In addition to the published feature that compares conflicting support values from alternative trees, a new visual comparison method allows the user to directly investigate topological and support differences by highlighting according nodes or regions with conflicting topologies and support in multiple opened trees.

Calculating node and branch annotations from each other using custom expressions has been extended by several functions which e.g. allow whole columns or rows as input. Additional new features include the closest possible sorting of terminal nodes according to a specified order, automatic collapsing of internal nodes depending on annotations (e.g. support) or rerooting trees by a given outgroup which may be in topological conflict with the tree.

This poster also shows the application of TreeGraph in a recent project investigating the influence of different automated and manual multiple sequence alignments of non-coding sequences containing certain microstructural mutations on phylogenetic inference.

Software and poster download and documentation: http://treegraph.bioinfweb.info/

Presenters in alphabetical order

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