

1st Münster Evolution Meeting

4 – 6 October 2018

www.uni-muenster.de/Evolution/MEM/main.shtml

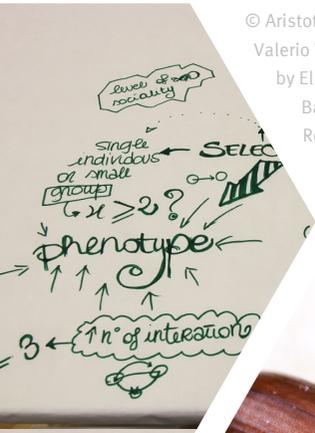
 #MEM2018WWU

The Münster Evolution Meeting is kindly supported by



Program & Information

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Abstracts



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WELCOME TO THE 1ST MÜNSTER EVOLUTION MEETING,

We are excited to host the 1st Münster Evolution Meeting encompassing many facets of evolutionary research. When we started with the idea, we were wondering if 'yet another' evolutionary meeting would be needed at all. Yet we hoped to arrange for a meeting which would attract researchers who traditionally would visit different meetings and would rarely meet in person, at least not in Germany. Apparently, the interest in a smaller, more local (and cheaper) evolutionary meeting seemed to be high. This became also clear since everyone of the 20 evolutionary biologists in Germany I asked to participate and give an invited talk said yes. Number 21 had to decline due to a previous commitment, which is when I stopped to ask. On the downside, the luxury of having so many excellent speakers entailed some scheduling problems because we had scheduled only 3 days and no parallel sessions. While this demonstrated the need for such a meeting we had to reduce the number of talks we could offer because we wanted to avoid parallel session – for above mentioned reasons. Accordingly, we apologize to everyone who's request for a talk we could not accommodate because many interesting and excellent research had to be moved to the poster session. However, we think poster sessions allow a much more in depth discussion of subjects. Accordingly, we offer free drinks and food and encourage everybody to consider the poster session as a big party (in the 'SCHLOSS'!!! – where else do you get that?) with the added benefit to learn about new evolutionary research and get to meet and maybe even know other evolutionary biologists.



I think we achieved our first goal of bringing together a critical mass of Evolutionary Biologists across the German speaking research community, but the success of this meeting depends on all participants. I wish us all a great and lively meeting. A meeting where old and new ideas are shared, discussed and challenged. In short, a scientific meeting that brings evolutionary biologists together and advances evolutionary biology as a field in general.

I want to thank all speakers and poster presenters who will come to Münster to share their insights and present their research. To keep the conference costs low, we relied on the active and volunteer help of students, staff and other scientists who did a fantastic job. As well as the willingness of the invited speakers to pay for their travel and accommodation (BIG THANKS). Additionally, the meeting is supported by the Evolution Think Tank of the Münster Graduate School of Evolution, funded by Santander Universities.

For the organization team,

Jürgen Gadau

INSTITUTE FOR EVOLUTION AND BIODIVERSITY (IEB)

In recent years, evolutionary research has become one of the focus areas of the research profile of the University of Münster. Since its founding in 2005, the Institute for Evolution and Biodiversity (IEB) within the Faculty of Biology covers a diverse research spectrum in evolution. It has attracted a number of new professors and junior groups from within and outside of Germany. The IEB currently integrates six professorships and three junior research groups working in the fields of molecular evolution and bioinformatics (Bornberg-Bauer), evolutionary cell biology (Catania), evolution and sexual conflict (Fricke), molecular evolution and sociobiology (Gadau), animal evolutionary ecology (Kurtz), limnology (Meyer), evolution and biodiversity of plants (Müller), plant evolutionary genomics (Wicke), and plant adaptation-in-action (Xu). Their research covers all levels of the biological hierarchy and addresses the core question how biodiversity and biocomplexity arise through evolutionary processes. The highly integrated and interdisciplinary structure of the IEB combines the study of micro- and macroevolutionary processes with ecological approaches in which present-day patterns of biodiversity are analysed.

The IEB hosts the Spokesman of the DFG Research Training Group 2220 EvoPAD as well as the Deputy Spokesman of the DFG Collaborative Research Centre Transregio 212 NC³.

The IEB offers project-based teaching in German and English in close cooperation with international partners. Master students can participate in a Special Study Program 'Evolution & Biocomplexity' which is funded by the Volkswagen Foundation. Closely affiliated to the IEB is the Botanical Garden, which plays a significant role in teaching plant evolution to students and the general public.



Institute for Evolution and Biodiversity, Hüfferstraße 1, 48149 Münster, Germany.

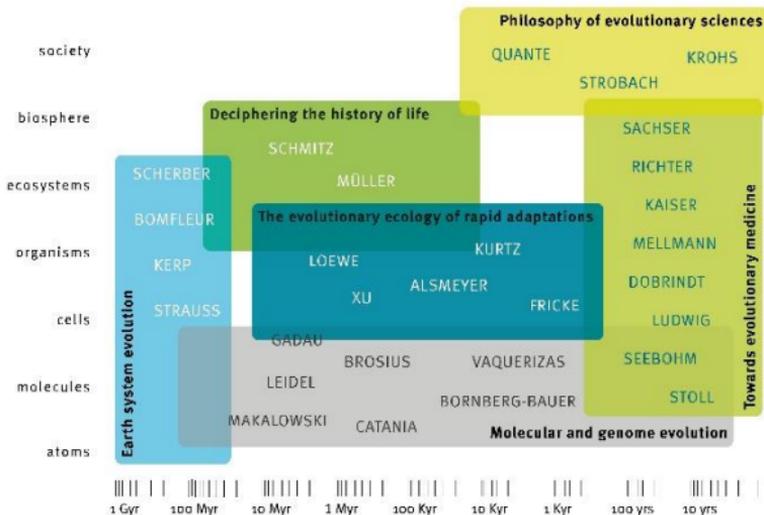
E-mail: evolecol@uni-muenster.de

MÜNSTER GRADUATE SCHOOL OF EVOLUTION (MGSE)

The Münster Graduate School of Evolution (MGSE) is an interdisciplinary graduate school at the University of Münster, bridging the faculties of Biology, Medicine, Geosciences, Mathematics, and Philosophy. Currently, 29 research group leaders from the different faculties and the Max Planck Institute for Biomedicine in Münster contribute to the MGSE.

The MGSE provides a structured study programme for doctoral students in the general field of evolution. The doctoral students of the MGSE address a broad range of questions, from the evolution of earth to the evolution of evolutionary theory. MGSE students benefit from one another because similar general principles act across disciplines, thus allowing common theoretical approaches and experimental testing at different levels. The programme, as well as a modern mentoring system ensure interdisciplinary networking, while the work in the projects is performed at the highest interdisciplinary level.

A key element of the MGSE is the Evolution Think Tank (ETT), which is funded by Santander Universities. Within this framework, the MGSE regularly invites leading scientists from around the globe, holds workshops and organizes further networking events, aiming at an advancement of evolutionary theory and its application across fields.



Research areas and groups of the Münster Graduate School of Evolution, which is located next to the Institute for Evolution and Biodiversity at Hüfferstraße 1a.

E-mail: mgse@uni-muenster.de

GENERAL INFORMATION

Congress Venue

The Münster Evolution Meeting 2018 will take place in the *Schloss* – the main university building. See the map on page 8 for further information.

Registration and Information

The registration desk is located in the foyer of the *Schloss* opposite to the main entrance. Opening hours are Thursday 12.00 – 20.00, Friday 8.30 – 19.00 and Saturday 8.30 – 16.00. If you have any questions, feel free to ask there.

Talks

All talks will be held in the auditorium of the *Schloss*. Oral presentations will either be 15 minutes long including two to three minutes for questions/discussion or 30 min long including five to ten minutes for questions/discussion.

Speaker Preview Room

The Speaker Preview Room is located in lecture hall S8 on the first floor of the *Schloss*. Speakers are requested to bring their PowerPoint or PDF presentations on USB sticks to the speaker preview room at least one hour before their session starts or one day in advance if the session starts early in the morning. Personnel are available there half an hour before the first and after the last talk of a day as well as during coffee and lunch breaks.

The presentation computers will be running Windows 10 and are equipped with PowerPoint 2016 and Adobe PDF reader. If there are videos embedded in the presentation, make sure they are uploaded correctly. Please do not consider projecting your presentation from your own laptop, as this will inevitably cause delays.

Posters

Poster boards are set up in the foyer of the *Schloss*. The posters should be prepared in portrait format in ISO A0 size (119 cm x 84 cm). Attachment pins will be available on the poster boards. Posters can be on display during the entire conference, but there will be two poster sessions, one on Thursday at 18.45 (even numbers) and one on Friday at 18.00 (odd numbers). For poster numbers and further information on the program, see the poster abstracts provided in this book.

Message Board

A message board is set up in the foyer of the *Schloss*. If you have a message for a colleague, feel free to fix it there.

Catering

Coffee, tea and snacks are available in the foyer all day. There are various opportunities to have lunch in the vicinity of the *Schloss* including two university refectories as shown on page 8. During the poster sessions, self-serving finger-food buffets with vegetarian and vegan options and alcoholic beverages are offered.

Cloakroom

The cloakroom is located in the basement of the *Schloss*. Opening hours are Thursday 11.30 – 21.30, Friday 8.00 – 20.30 and Saturday 8.00 – 17.00.

Washrooms

Washrooms are located in the basement of the *Schloss*.

WiFi

Visitors of the University of Münster can register for the university's network via **eduroam**, which enables a visitor from one participating institution to gain network access at another. A prerequisite is that the home institution takes part in the eduroam project.

WiFi (SSID): Eduroam

UserID: username@domain (e.g. if your username is darwin123 and your home institution is the University of Cambridge, you would enter darwin123@cam.ac.uk)

Password: Use the password you use to access services at your home institution.

Guests from other institutions which are not a member of the eduroam project can log in to the open WiFi **GuestOnCampus**, which has a daily data limit of 1 GB per device.

Public Transport

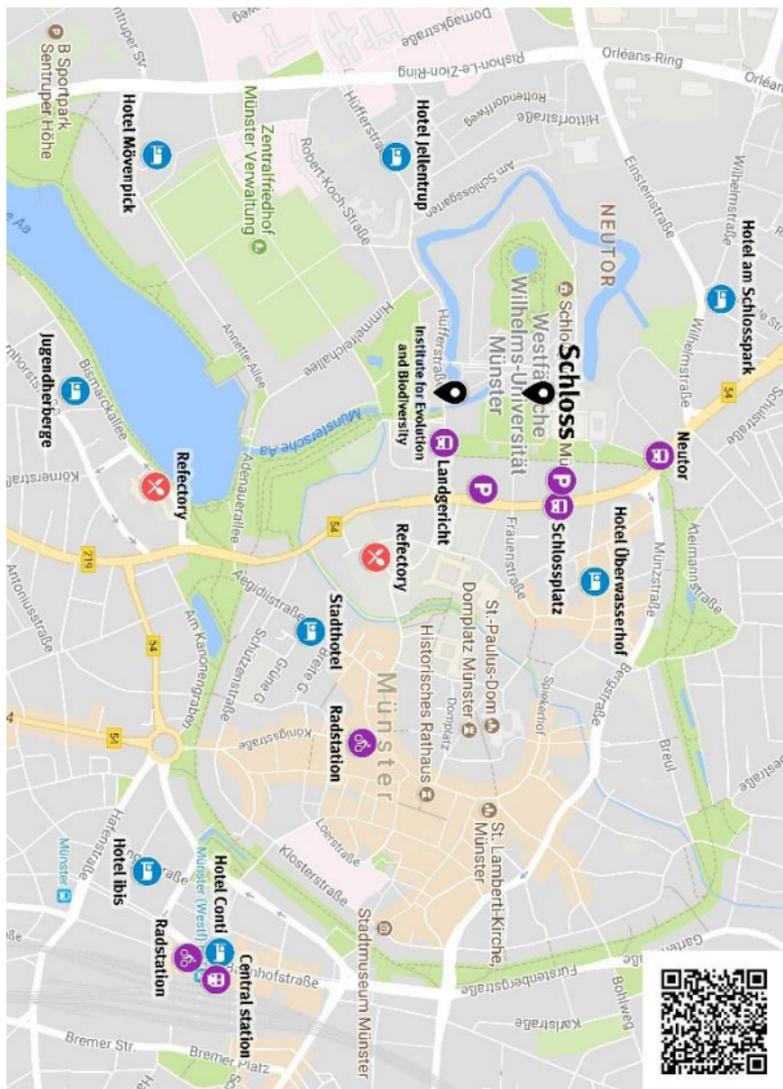
You can park your car free of charge at P+R facilities and take the bus (subject to fare) to the conference venue. Buses leave the P+R facilities at the Weseler Straße Mobilstation stop, at Preußenstadion (Hammer Straße) and at Albersloher Weg for the old town at very short intervals. An overview of paid parking opportunities is available at <https://www.stadt-muenster.de/tiefbauamt/parkleitsystem>. PP Schlossplatz Nord and PP Schlossplatz Süd are closest to the conference venue.

Participants of the 2018 MEM will receive a ticket for free bus and rail use in the city of Münster called the 'Willkommen! Ticket'. The ticket is valid during all 3 days of MEM. You will receive your ticket upon arrival at the conference venue. The closest bus stops to the conference venue are **Landgericht**, **Schlossplatz**, and **Neutor**. Bus schedules can be found at <https://www.stadtwerke-muenster.de/privatkunden/busverkehr/> or using the 'Fahrplan MS' mobile app.

Another nice and practical way to get around in Münster is by bike. Münster has a well-developed web of bike paths, and the very flat landscape makes the bike a nice alternative to public transportation. Bikes can be rented at the 'Radstationen' which you can find directly in front of the main station and in the city centre. See www.radstation.de for more information.

Evaluation

To make better plans for the future, you will be handed an anonymous questionnaire that asks about whether this meeting should be repeated, and if so, how often and in what format? We are loosely planning to hold a similar meeting every 2 years (in the off years of the ESEB meetings) and move the meeting to spring. So, if a majority of participants thinks that this is a good idea, the 2nd Münster Evolution Meeting would be in spring 2020.



Map of Münster. Please scan the QR code for an interactive version.

PROGRAM

THURSDAY 4 th OCTOBER 2018		
12.00 – 13.00		Registration & Coffee
13.00 – 13.15		Opening remarks by MEM chair Jürgen Gadau
<i>Chair</i>	<i>Jürgen Gadau</i>	
13.15 – 13.45	Diethard Tautz	Mutual genomic introgression and immune gene evolution in house mice
13.45 – 14.00	Stephan Drukewitz	A dipteran's sucker punch – Evolution of venom in robber flies
14.00 – 14.15	Anne Kupczok	Rates of mutation and recombination in <i>Siphoviridae</i> phage genome evolution
14.15 – 14.30	Shuqing Xu	Low genetic variation is associated with low mutation rate in the giant duckweed
14.30 – 15.00		Coffee break
<i>Chair</i>	<i>Shuqing Xu</i>	
15.00 – 15.30	Erich Bornberg-Bauer	Emergence of <i>de novo</i> protein coding genes from 'dark genomic matter' - fact or fiction?
15.30 – 15.45	Katrin Hammerschmidt	Polarization of ancestor relations reveals the order of traits in the evolution of cyanobacterial multicellularity
15.45 – 16.00	Francesco Catania	The environment: a catalyst for genome re-patterning?
16.00 – 16.15	Michael Hiller	Less is more: The role of gene losses for adaptive evolution in mammals
16.15 – 16.30	Neel Prabh	Deep taxon sampling reveals the evolutionary dynamics of novel gene families in the <i>Pristionchus</i> genome
16.30 – 16.45	Chen Xie	Recently evolved <i>de novo</i> genes function in distinct biological pathways in mice
16.45 – 17.15		Coffee break
17.15 – 17.30		Welcome address by Vice-Rector Monika Stoll

<i>Chair</i>	<i>Jürgen Gadau</i>	
17.30 – 18.45	Peter Hammerstein	The evolution of theory in evolutionary biology
18.45 – 21.00		1 st Poster session (even numbers) & Reception with finger food buffet

Day one is hosted by the Evolution Think Tank of the
Münster Graduate School of Evolution, funded by



FRIDAY 5th OCTOBER 2018

<i>Chair</i>	<i>Susann Wicke</i>	
09.00 – 09.30	Julia Fischer	Guinea baboons: a test case for studying the link between social systems, communication and cognition
09.30 – 09.45	Sandra Steiger	The evolution of family life: why should we care about caring insects
09.45 – 10.00	Claudia Fricke	Sexual maturation in <i>Drosophila melanogaster</i> males – what is going on in young males?
10.00 – 10.15	Klaudia Witte	Mate choice in the public: does distance matter?
10.15 – 10.45		Coffee break

<i>Chair</i>	<i>Joachim Kurtz</i>	
10.45 – 11.15	Ralf Sommer	The mechanisms of developmental plasticity: from switch genes and epigenetics to canalization
11.15 – 11.30	Joshua Payne	A comparative analysis of empirical genotype-phenotype maps
11.30 – 11.45	Gregor Bucher	The cellular and genetic mechanisms of central complex diversification
11.45 – 12.00	Nico Posnien	Context dependent regulatory divergence in closely related <i>Drosophila</i> species

12.00 – 12.15	Gregor Rolshausen	Evolutionary rates for evolutionary space. Perspectives on trait evolution
12.15 – 13.30		Lunch break (self-catering)
<i>Chair</i>	<i>Francesco Catania</i>	
13.30 – 14.00	Hinrich Schulenburg	Evolutionary ecology meets the antibiotic crisis: Can we control pathogen adaptation?
14.00 – 14.15	Christian Kost	Synergistic coevolution speeds up molecular evolution
14.15 – 14.30	Leonardo Oña	The role of ecological factors on the evolution of microbial individuality
14.30 – 14.45	Joachim Kurtz	Host-parasite coevolution and evolution of immunological specificity
14.45 – 15.00	Carolin Wendling	Different ways to resistance – coevolution of bacteria and temperate phages along the parasite-mutualism continuum
<i>Chair</i>	<i>Erich Bornberg-Bauer</i>	
15.00 – 15.30		Coffee break
15.30 – 16.00	Judith Korb	Why can termite queens live so long?
16.00 – 16.15	Susanne Foitzik	Immune challenge alters expression of more genes in fertile ant workers and causes a drastic reduction in gut microbiome diversity
16.15 – 16.30	Lukas Schrader	Genome evolution and speciation of inquiline social parasites in leaf-cutting ants
16.30 – 16.45	Jos Kramer	The other facets of family life and their role in the evolution of animal sociality
16.45 – 17.15	Wolfgang Stephan	Population genetics of rapid evolutionary adaptation
17.15 – 17.30	Stefan Laurent	An experimental test of the genomic consequences of local adaptation in deer mice
17.30 – 18.00		Evolution in Germany
18.00 – 20.00		2 nd Poster session (odd numbers) with beer and snacks

Saturday 6th OCTOBER 2018

<i>Chair</i>	<i>Claudia Fricke</i>	
09.00 – 09.30	Susanne Renner	Will aDNA from herbarium collections and a pharaonic tomb reveal who domesticated the watermelon?
09.30 – 09.45	Susann Wicke	Nutritional specialization and host-related diversification in parasitic plants
09.45 – 10.00	Stefan Abrahamczyk	Floral key innovations triggered the evolution of the Malagasy Impatiens (Balsaminaceae) clade
10.00 – 10.15	Harald Letsch	Evolution of the minute seed weevils (Ceutorhynchinae, Curculionidae, Coleoptera) – the impact of Earth's climate changes and host-plant associations
10.15 – 10.45	Coffee break	
<i>Chair</i>	<i>Ulrich Krohs</i>	
10.45 – 11.15	Axel Meyer	<i>Agouti-related peptide 2</i> drives convergent evolution of stripe patterns across cichlid fish radiations
11.15 – 11.30	Thomas Schmitt	Studying the evolution of cuticular hydrocarbons in insects: a model for a complex trait
11.30 – 11.45	Oliver Niehuis	Evolutionary history of the Hymenoptera
11.45 – 12.00	Liliya Doronina	Retrotransposon-based phylogeny in the era of genomics
12.00 – 12.15	Johannes Steidle	Speciation in the Hohenheim park? Ecological separation in a population of the jewel wasp <i>Nasonia vitripennis</i> (Hymenoptera: Pteromalidae)
12.15 – 13.30	Lunch break (self-catering)	
<i>Chair</i>	<i>Jürgen Gadau</i>	
13.30 – 14.00	Katja Nowick	Evolution of transcription factor networks in primate brains
14.00 – 14.15	Ulrich Krohs	Explaining evolution: Models go first
14.15 – 14.30	Panagiotis Provataris	Comparative analyses suggest reduced DNA methylation levels in Holometabola

14.30 – 14.45	Robert Peuß	Approaching ‘Old Friends’ with a new model: How pathogen diversity shaped the adaptation of <i>Astyanax mexicanus</i> to the cave
14.45 – 15.00	Camilo Barbosa	Antibiotic combination efficacy (ACE) networks in <i>Pseudomonas aeruginosa</i>
15.00 – 15.30		Coffee break
15.30 – 15.45	Maryam Keshavarz	Existence of a major control locus for basic behavioural traits
15.45 – 16.00	Jürgen Gadau	The evolution of social niches in ants
16.00 – 16.15		Farewell and closing of the conference

TALK ABSTRACTS – THURSDAY (CHRONOLOGICAL ORDER)

Mutual genomic introgression and immune gene evolution in house mice

Diethard Tautz

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Max-Planck Institute for Evolutionary Biology, Plön

The house mouse (*Mus musculus*) has a long-standing history as a model system in genetics and biomedical research. Currently, three major lineages of *Mus musculus*, classified as subspecies, are distinguished: the western house mouse *Mus musculus domesticus*, the eastern house mouse *Mus musculus musculus* and the southeast-Asian house mouse *Mus musculus castaneus*. All three lineages have their origin in Southern Asia and diverged roughly 0.5 million years ago, but still share haplotypes and exchange genomic material. Hybrid zones have been detected at areas of secondary contact between the subspecies and these serve for tracing genes involved in hybrid incompatibility as well as quantitative trait mapping. During the past 10,000 years house mice have developed commensalism with humans, which allowed them to a spread across the world. This has led to the invasion of new climate zones with ensuing local adaptations to new parasites. Hence, mice have also emerged as an excellent model system for studying a range of evolutionary questions. In my talk I will focus on the patterns of genomic introgression, which are particularly relevant for immune genes. This includes new insights into how the allelic diversity of MHC genes is generated and maintained.

A dipteran's sucker punch – Evolution of venom in robber flies

Stephan H. Drukewitz

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Molecular Evolution & Animal Systematics, University of Leipzig

Venoms are evolutionary key adaptations, but the understanding of toxin evolution is dominated by the analyses of a few lineages like Snakes, Spiders, Scorpions and Cone Snails. In the recent years, more and more long-time neglected groups were added to a diverse list of species using a venom for predation, defence or inner species competition.

Predatory robber flies (Diptera, Asilidae) have been suspected to be venomous due to their ability to overpower well-defended prey. With over 7000 species, a comparable small genome size (200 - 600 mb) and some highly specialized groups (California-beekiller) the Asilidae are an interesting model group added to the picture of venom evolution.

This study provides a detailed characterization of the venom system of robber flies through the application of comparative transcriptomics, proteomics and functional morphology. Our results reveal asilid venoms to be dominated by peptides and non-enzymatic proteins. Contrary to what might be expected for a liquid-feeding predator, the venoms of robber flies appear to be rich in novel peptides, rather than enzymes with a putative pre-digestive role. One group of identified peptides closely resemble cysteine inhibitor knot peptides (ICK), of which neurotoxic variants occur in cone snails, assassin bugs, scorpions and spiders. Toxicity assays of these ICK-like peptides against honeybees revealed a role as a neurotoxin involved in the immobilization of prey.

The novelty of the robber fly toxins suggests that the venom system evolved independently from hematophagous dipterans and other venomous insects.

Venomics studies which included genome data showed that the processes of toxin evolution might be more variable and complex than implicit by the analyses of only prominent groups.

Rates of mutation and recombination in *Siphoviridae* phage genome evolution over three decades

Anne Kupczok

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Institute of Microbiology, University of Kiel

The evolution of asexual organisms is driven not only by the inheritance of genetic modification but also by the acquisition of foreign DNA. The contribution of vertical and horizontal processes to genome evolution depends on their rates per year and is quantified by the ratio of recombination to mutation. Here we delineate the contribution of mutation and recombination to dsDNA phage genome evolution. Analyzing 34 isolates of the 936 group of Siphoviridae phages that were sampled using a constant *Lactococcus lactis* strain from a single dairy over 29 years, we estimate a constant substitution rate of 1.9×10^{-4} substitutions per site per year due to mutation. This substitution rate is within the range of estimates for eukaryotic viruses. The reconstruction of recombination events reveals a constant rate of five recombination events per year and 4.5×10^{-3} nucleotide alterations due to recombination per site per year. The recombination rate thus exceeds the substitution rate to a great extent, resulting in a relative effect of recombination to mutation (r/m) of ~ 24 that is homogenous over time. Especially in the early transcriptional region, we detect frequent gene loss and regain due to recombination with other phages of the 936 group, demonstrating the role of the 936 group pangenome as reservoir of genetic variation. The observed substitution rate homogeneity conforms to the neutral theory of evolution; hence, we demonstrate that the neutral theory can be applied to phage genome evolution and also to genetic variation brought about by recombination.

Low genetic variation is associated with low mutation rate in the giant duckweed

Shuqing Xu^{1,2}, Jessica Stapley², Saskia Gablenz³, Justin Boyer³, Klaus J. Appenroth⁴, K. Sowjanya Sree⁵, Jonathan Gershenzon³, Alex Widmer⁶ and Meret Huber^{3,7}

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⁴Matthias-Schleiden-Institute, Plant Physiology, University of Jena

⁵Department of Environmental Science, Central University of Kerala, Periyar 671316, India

⁶Institute of Integrative Biology, ETH Zürich

⁷Institute of Plant Biology and Biotechnology, University of Münster

Mutation rate and effective population size (N_e) jointly determine intra-specific genetic diversity, but the role of mutation rate is often ignored. We investigate genetic diversity, spontaneous mutation rate and N_e in the giant duckweed (*Spirodela polyrrhiza*). Despite its large consensus population size, whole-genome sequencing of 68 globally sampled individuals revealed extremely low intra-species genetic diversity. The genome-wide spontaneous mutation rate, assessed under natural conditions, is at least seven times lower than estimates made for other multicellular eukaryotes, whereas N_e is large. These results demonstrate that low genetic diversity can be found in species with large N_e , where selection can reduce the mutation rate to a very low level, and accurate estimates of mutation rate can help to explain unexpected patterns of genetic variation.

Emergence of *de novo* protein coding genes from 'dark genomic matter' - fact or fiction?

Erich Bornberg-Bauer

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Institute for Evolution and Biodiversity, University of Münster

Proteins are the workhorses of the cell and, over billions of years, they have evolved an amazing plethora of extremely diverse and versatile structures with equally diverse functions echoing the evolution of all forms of life. Recent computational developments and availability of thousands of genomes make it possible to reconstruct the course of evolution, often at amazing accuracy. Previously, it was assumed that all proteins result from old ones but recent advances in comparative genomics have repeatedly called some 10% - 30% 'orphan' genes which contain ORFs, are expressed and translated but lack a homolog in closely related outgroups. Since some map to inter-genic regions, they have emerged '*de novo*' from previously non-coding 'dark genomic matter'. While novel proteins in general tend to be disordered, fast evolving, weakly expressed but also rapidly assuming novel and physiologically important functions, *de novo* transcripts already show clear signs of structural maturity. We investigated the dense and data-rich insect phylogeny genomes which features many major innovations such as sociality, viviparity etc. First, we find that recently split lineages undergo accelerated genomic reorganisation, including the rapid gain of several hundred novel genes. Second, novel genes are particularly abundant in social insects. Third, novel genes in ants are scattered uniformly across genome and between established genes. Finally, our results indicate that the genetic mechanisms creating orphan genes - such as gene duplication, frame-shift fixation, creation of overlapping genes, horizontal gene transfer, and exaptation of transposable elements - act at different rates in insects when compared to other animals.

Polarization of ancestor relations reveals the order of traits in the evolution of cyanobacterial multicellularity

Katrin Hammerschmidt

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Institute of Microbiology, University of Kiel

Understanding the events during the evolution from unicellular organisms to multicellularity is a long-standing challenge. The first known transition to multicellularity occurred more than 3 billion years ago in cyanobacteria. This is a monophyletic phylum that nowadays still includes unicellular and filamentous genera, some of which represent the peak of prokaryotic complexity. Previous research on the evolution of multicellularity in this phylum has been hampered by the lack of knowledge on the phylogenetic relations among unicellular and filamentous genera. We present a novel approach that does not depend on previous knowledge of phylogenetic relationships but infers ancestor-descendent relations of ancestral nodes in phylogenetic trees. Combining the method with the assignment of phenotypic traits to ancestral nodes enable the inference of pairwise relative priority, without the need to postulate a species tree. Applying our approach to 199 cyanobacterial genomes yields a temporal sorting of traits. Our results reveal, for example, that the formation of filaments co-occurred with the ability to fix nitrogen before higher complexity evolved. This finding is in line with theory that predicts the trade-off between oxygen-producing photosynthesis and oxygen-sensitive nitrogen fixation to be the main driving force for multicellularity in this phylum.

The environment: a catalyst for genome re-patterning?

Francesco Catania

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Institute for Evolution and Biodiversity, University of Münster

The role of environmental effects in evolutionary processes is incompletely understood. The empirical data presented here support the possibility that the intracellular environment — the interaction between mRNA-associated processes, in particular — imposes significant constraints on the evolution of eukaryotic gene structure. Moreover, observations drawn from a mutation accumulation study suggest that external environmental conditions can actively contribute to the emergence of functional genetic novelties by perturbing intracellular developmental programmes. Together, these findings point to an active and catalytic role for the environment in genome re-patterning.

Less is more: The role of gene losses for adaptive evolution in mammals

Michael Hiller

hiller@mpi-cbg.de

Max Planck Institute of Molecular Cell Biology and Genetics, Dresden

Identifying the DNA changes that underlie phenotypic adaptations is a key challenge in genomics and evolutionary biology. I will present our work on studying the role of gene loss for adaptive evolution in mammals. To detect differences in the gene repertoire between mammals, we developed a genomics pipeline to accurately detect the inactivation (loss) of ancestral protein-coding genes. By applying this approach to obtain catalogs of inactivated genes of 60 placental mammals, we found that gene losses can provide new insights into species' biology and the molecular mechanisms underlying adaptive phenotypes. I will present gene losses that reveal hitherto unknown metabolic characteristics of dietary specialists and the loss of a DNA damage repair system following the convergent evolution of body armor, which shows that gene loss can be a predictive consequence of phenotypic adaptations. Remarkably, we also discovered a number of lineage-specific as well as convergent gene losses that may contribute to morphological, physiological and metabolic adaptations of different mammals to life in water, extreme diving abilities, and dietary specializations. In summary, even though one would intuitively expect that gene loss is often maladaptive, our results provide evidence that loss of gene function is an evolutionary mechanism for phenotypic adaptations that may be more frequent than previously anticipated

Deep taxon sampling reveals the evolutionary dynamics of novel gene families in the *Pristionchus* genome

Neel Prabh, Waltraud Röseler, Hanh Witte, Gabi Eberhardt, Ralf J. Sommer, Christian Rödelsberger

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The widespread identification of genes without detectable homology in related taxa is a hallmark of genome sequencing projects in animals, together with the abundance of gene duplications. Such genes have been called novel, young, taxon-restricted, or orphans, but little is known about the mechanisms accounting for their origin, age and mode of evolution. Phylogenomic studies relying on deep and systematic taxon sampling and employing the comparative method can provide insight into the evolutionary dynamics acting on novel genes. We used a phylogenomic approach for the nematode model

organism *Pristionchus pacificus* and sequenced six additional *Pristionchus* and two outgroup species. This resulted in 10 genomes with a ladder-like phylogeny, sequenced in one laboratory using the same platform and analyzed by the same bioinformatic procedures. Our analysis revealed that 68 - 81% of genes are assignable to orthologous gene families, the majority of which defined nine Age classes with presence/absence patterns that can be explained by single evolutionary events. Contrasting different Age classes, we find that older Age classes are concentrated at chromosome centers whereas novel gene families preferentially arise at the periphery, are lowly expressed, evolve rapidly, and have a high propensity of being lost. Over time, they increase expression and become more constrained. Thus, the unprecedented phylogenetic resolution allowed a comprehensive characterization of the evolutionary dynamics of *Pristionchus* genomes indicating that distribution of Age classes and their associated differences shape chromosomal divergence. This study establishes the *Pristionchus* system for future research on the mechanisms that drive the formation of novel genes.

Recently evolved *de novo* genes function in distinct biological pathways in mice

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For decades, people believed that the evolutionary innovation was from the changes in existing genic and regulatory sequences and the new genes originating through duplications from ancestral genes. In recent years, *de novo* genes, the molecular entities which originated recently in evolutionary history of a given lineage from non-genic ancestral sequences, were found in many species. However, their functions and how they affect global gene networks have not been extensively addressed in previous studies. We used available genome sequences and gene annotations to identify mouse-specific *de novo* genes. Then we chose three of them to study their functions in detail using knockout mouse lines. The open reading frames of all three genes only exist in *Mus musculus* which indicates they originated in the past 1.2 million years. A830005F24Rik is expressed relatively high in postnatal brains. We found 1,399 differentially expressed genes in postnatal 0.5-day heads between knockout and wildtype mice using high-resolution RNA-Seq, and they were statistically significantly enriched in cell communication pathways. The results of a behavioral test, elevated plus maze, indicated a decision-making related phenotype and an anxiety related phenotype. A930004D18Rik is expressed broadly across different developmental stages and tissues. We found 1,592 differentially expressed genes in postnatal 0.5-day heads and 3,854 ones in 12.5-day embryos between knockout and wildtype mice and only 403 genes were overlapping, which suggests it is involved in different transcriptional networks in these two samples. Gm13030 is specifically expressed in adult oviducts. We found 21 differentially expressed genes in a specific estrous cycle stage between knockout and wildtype mice. The top three genes are mouse-specific recent duplicates previously found having functions in oviducts.

The evolution of theory in evolutionary biology

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Early last century, Darwin's picture of evolution was met with biological criticism because it appeared inconsistent with Mendelian genetics. Thanks to the mathematical efforts made by Fisher, Haldane and Wright, however, the emerging neo-Darwinian framework of population genetics bridged this gap and gave rise to the 'modern synthesis'. The synthesis was soon challenged again. Controversial and sometimes vicious debates arose between the proponents of either genetic or phenotypic modeling approaches in evolutionary biology. Phenotype-centered fields, such as behavioral ecology, kin selection theory, and evolutionary game theory, served as the intellectual 'battleground' for this debate. The critics of these fields were essentially claiming that genetic constraints would all too often act as impediments to phenotypic adaptation. While this point of view can to some extent be substantiated for population genetics models of short-term evolution, it is also fair to say that many constraints to phenotypic adaptation are likely eliminated through genetic rearrangements in long-term evolution. From this perspective, phenotypic models deserve their own place in the mathematical theory of evolutionary dynamics. Furthermore, crucial constraints to phenotypic adaptation seem far more deeply rooted in an organism's structural organization than in the nitty gritty of genetics. Developmental biologists have particularly emphasized this point, which plays a major role in the conceptions of an 'extended evolutionary synthesis (EES)'. The talk addresses several aspects of this synthesis and discusses recent models in which the organism is depicted as an evolved information processor. These models explore how genetic, epigenetic and sensory inputs (cues) are integrated during development, and why endosymbionts have their own word to say. This requires an unorthodox perspective on how organisms 'read' their genes. Using this perspective, it can be shown that the informational value of different cues depends crucially on the time scale of environmental variation, and that there is scope for a 'Lamarckian dimension' in biology. Furthermore, the extent to which a particular cue is used may alter the informational value of this cue. The developmental process then partially determines the selective regime under which it evolves.

TALK ABSTRACTS - FRIDAY (CHRONOLOGICAL ORDER)

Guinea baboons: a test case for studying the link between social systems, communication and cognition

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Primate social systems are remarkably diverse, and thus not only play a central role in understanding social evolution, including the selective pressures that operate on primate cognition and communication. Although baboons have been featured prominently in this research context, historically, little has been known about the westernmost member of the genus, the Guinea baboon (*Papio papio*). I will summarize the findings from the first years of observation at the field site CRP Simenti in the Niokolo Koba National Park in Senegal. Guinea baboons reveal a nested multi-level social organization, with reproductive units comprising one 'primary' male, one to several females, young, and occasionally 'secondary' males at the base of the society. Three to five units form 'parties', which team up with other parties to form a 'gang'. Although different gangs have largely overlapping home ranges, agonistic interactions between different parties or gangs are rare. Some, but not all strongly socially bonded males are highly related, and population-genetic and behavioral evidence indicate female-biased dispersal. Females play an important role in intersexual bond formation and maintenance, and female tenure length varies between a few weeks and several years. While the social organization resembles that of hamadryas baboons (*P. hamadryas*), the social structure differs considerably, specifically in terms of low male aggressiveness and female freedom. Despite substantial differences in social organization and social structure, the acoustic structure of Guinea baboon vocalizations does not differ substantially from that of other baboon taxa. I will present initial findings from our studies that tap into the social knowledge of this species, and discuss some of the challenges and limitations of studying cognition in the wild.

The evolution of family life: why should we care about caring insects

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Scientists have long been fascinated by the fact that parents of some animals go to great lengths to increase survival and growth of their offspring, usually at a cost to their own survival and reproduction. They invest time and energy to feed their young, to carry them around, or to protect them from parasites, desiccation and other environmental hazards. In the last decades, the vast majority of studies have investigated parental care and family life in birds and mammals. However, in these systems care is always obligate and a highly derived character, which implies that these studies can only deliver limited information about the early and dynamic evolution of family life. Using burying beetles as model system, I will show that 'social' insect systems can provide novel and important insights into our general understanding of family living and its evolution, including topics such as communication, conflict resolution, social immunity and parent-offspring coevolution.

Sexual maturation in *Drosophila melanogaster* males – what is going on in young males?

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Even short-lived insects often display a period after adult-eclosion in which they mature to reach sexual capacity. Here we document the progression of male sexual maturation in the fruit fly *Drosophila melanogaster* with a special emphasis on the maturation of the accessory gland. The accessory gland is the production site of male seminal fluid proteins, the non-sperm component of the ejaculate. The >100 different proteins and peptides are crucial for male reproductive success and we found them to significantly contribute to males attaining sexual maturity. We integrated data on male behavioural and physiological maturation and the effect on male reproductive success for males shortly after eclosion up to several days of age to better understand the process of sexual maturation. We found the accessory gland to increase in size and overall protein content with male age. Similarly, male ability to successfully court a female and gain a mating improved. Over the first five days after eclosion, males increased their competitive abilities and gained higher fertilization success when competing against a rival ejaculate. These insights will be combined with comparisons from males evolved under polygamy versus monandry to understand how mating system affects sexual maturation. For each of six replicated selection populations (3 per regime) we measured changes in accessory gland size as well as gene expression patterns in the male reproductive tract after they had evolved >160 generations under the two contrasting selection regimes. We found no differences in accessory gland growth trajectories due to differences in pre- and post- mating sexual selection. Instead, we found differences in seminal fluid gene expression dynamics, with seminal fluid gene expression being initially lower in monogamous males compared to polygamous ones. While this pattern reverses later on and monogamous males catch-up we interpret this time-sensitive pattern to indicate that the evolutionary history reshaped the process of male sexual maturation and less the overall SFP production. A fast sexual maturation might give males a fitness advantage in becoming competitive earlier on.

Mate choice in the public: does distance matter?

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Animals use public information during mate choice to evaluate conspecifics as potential mates. Individuals gain public information by observing conspecifics during their sexual interaction and often copy the mate choice of others they just witnessed. In experiments on mate choice-copying the interacting individuals were always in close proximity to each other. In nature, however, individuals may also sexually interact with each other at distance. Thus, we tested whether sailfin molly females would still copy the mate choice of conspecifics when a male and a female interact at a distance of 40 cm. We found that sailfin molly females still copied the choice of other females even when the interacting individuals were apart. The use of public information is not free of risk. The copier might be recognized by an interacting pair which can react to the 'audience'. In most cases, an observed male spent less time and interact less with a previous preferred female when another male is nearby, which is called the 'audience-effect'. It might be, therefore, beneficial for the audience to observe an interacting pair from distance to receive reliable information about mate choice decisions of others. Here we tested, whether Atlantic molly males exhibited an

audience effect, when the audience male was watching in a distance of 80 cm. Atlantic molly males still showed an audience effect even though the audience male was far away. In both experiment we found, that distance did not matter when using public information. Our results showed that the public information network still is more complex and works at long distances which has important impact on mate choice decisions and thus, on the evolution of mate preferences.

The mechanisms of developmental plasticity: from switch genes and epigenetics to canalization

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Developmental plasticity is increasingly recognized as primary mechanism for the emergence of novelty. However, molecular mechanisms underlying this phenomenon remain elusive. The nematode *Pristionchus pacificus* exhibits developmental plasticity for its mouth-form and feeding strategies. Individuals develop one of two alternative mouth-forms, a predatory eury stomatous (Eu, wide-mouthed) or a bacteriovorous stenostomatous (St, narrow-mouthed) form. Using genetic screens, we have identified developmental switch genes that regulated plasticity. *eud-1* mutants are all-St, whereas mutants in the downstream nuclear-hormone-receptor *nhr-40* are all-Eu. More recent work indicates that *eud-1* is part of a multi-gene locus with some supergene characteristics. Furthermore, *eud-1* expression is under epigenetic control involving the histone acetyltransferase *lcy-12* and an antisense RNA at the *eud-1* locus itself that up-regulates *eud-1* expression. Here we present our most recent molecular findings on i) the genetics and epigenetics of plasticity, ii) environmental perception and iii) first insight into associated trans-generational effects and canalization.

A comparative analysis of empirical genotype-phenotype maps

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Much of gene regulation is carried out by proteins that bind DNA or RNA molecules at specific sequences. One class of such proteins is transcription factors, which bind short DNA sequences to regulate transcription. Another class is RNA binding proteins, which bind short RNA sequences to regulate RNA maturation, transport, and stability. Here, we study the robustness and evolvability of these regulatory mechanisms. To this end, we use experimental binding data from 172 human and fruit fly transcription factors and RNA binding proteins as well as human polymorphism data to study the evolution of binding sites *in vivo*. We find little difference between the robustness of regulatory protein–RNA interactions and transcription factor–DNA interactions to DNA mutations. In contrast, we find that RNA-mediated regulation is less evolvable than transcriptional regulation, because mutations are less likely to create interactions of an RNA molecule with a new RNA binding protein than they are to create interactions of a gene regulatory region with a new transcription factor. Our observations are consistent with the high level of conservation observed for interactions between RNA binding proteins and their target molecules as well as the evolutionary plasticity of regulatory regions bound by transcription factors. They may help explain why transcriptional regulation is implicated in many more evolutionary adaptations and innovations than RNA-mediated gene regulation.

The cellular and genetic mechanisms of central complex diversification

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The insect brain is built by a conserved set of neuropils. However, relative size, shape and developmental timing of these neuropils differ between insects, reflecting evolutionary adaptations. An intriguing example of a heterochronic developmental shift is provided by the central complex (CX). In most insects, the CX develops entirely during embryogenesis while in *Drosophila* it emerges only postembryonically during late larval stages and metamorphosis. Interestingly, the red flour beetle *Tribolium castaneum* represents an intermediate situation where the CX develops partially during embryogenesis. We want to understand the cellular and the genetic basis of heterochronic development of CX connectivity by combining the power of these two genetic model systems.

We have been identifying genes involved in anterior neuroectoderm patterning by using both a candidate gene approach and unbiased genome wide RNAi screening (iBeetle project). Indeed, we found several genes involved in embryonic CX embryonic development like for instance *Tc-six3*, *Tc-foxQ2* and *Tc-rx*.

In order to compare homologous neural cells throughout development, we have tagged the *rx*-locus in both fly and beetle by using genome editing. Indeed, we find comparable patterns of cell body locations and projections into the CX in enhancer trap lines that mark the expression of *rx* in these two model systems. Careful study of their development reveals the stage of neural development where *Tribolium* and *Drosophila* diverge. Identification of the cellular basis of heterochronic development will subsequently allow to scrutinize the genetic basis of the observed differences.

Context dependent regulatory divergence in closely related *Drosophila* species

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The great morphological diversity that can be observed in different animals is the result of millions of years of evolution of the underlying developmental programs. Developmental gene regulatory networks (GRNs) need to be highly constraint to ensure consistent organ formation throughout varying environmental conditions. However, these networks also must be flexible enough to allow natural variation in organ morphology to occur. Since many developmental genes are highly conserved across distant animal phyla, it has been proposed that gene expression divergence plays an important role in phenotypic diversification.

Here, we study tissue and stage specific regulatory divergence in developing wings and heads between the three closely related *Drosophila* species *D. melanogaster*, *D. simulans* and *D. mauritiana*. We analyzed genome wide expression differences between species and compare these to allele specific expression in F1 hybrids. This way we can infer, whether inter-species expression differences are due to changes in the *cis*-regulatory region of a gene or due to changes in upstream factors that regulate their expression (variation in *trans*). Our results indicate that most differences are due to changes in *trans*. A detailed analysis of gene expression in the context of developmental GRN connectivity revealed that a few central and highly connected genes vary in expression, what explains the extent of *trans*-regulatory differences observed. Additionally, we show that developing wing and head tissue show differences in the regulatory divergence. In summary, our data strongly suggests that gene regulation evolves tissue and stage specifically.

Evolutionary rates for evolutionary space. Perspectives on trait evolution

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Characterizing evolutionary radiations benefits from describing the temporal patterns of trait disparification. Comparative methods attempt this by evaluating the statistical fit of trait distributions to a phylogenetic hypothesis under assumed evolutionary models. However, it can be challenging to differentiate between models, with discriminatory power depending on the modes of evolution underlying trait distributions. We suggest rates of 'trait space saturation', standardized for limits to evolutionary change, as an additional tool to distinguish between modes of trait evolution. We evaluate this approach using simulations, and show that trait space saturation can identify the true model of trait evolution in cases where traditional comparative methods can fail. We illustrate our approach using diverse empirical studies that represent contrasting scenarios of evolutionary radiation.

Evolutionary ecology meets the antibiotic crisis: can we control pathogen adaptation?

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Evolutionary processes are responsible for the current antibiotic crisis. Surprisingly, they are usually ignored during design of novel therapy, which mainly focuses on finding new drugs. In general, bacteria show an enormous potential to adapt. Therefore, it is critical to consider bacterial evolution for the design of sustainable treatment. In my talk, I will present examples of our work on using evolutionary concepts to enhance efficacy of antibiotic therapy. Our work currently focuses on two main treatment protocols: combination therapy and sequential treatments. Our work demonstrates that combination therapy can be optimized by using drugs that interact synergistically (i.e., they enhance each other's effect) and also produce evolutionary trade-offs (e.g., evolved collateral sensitivity). Sequential treatments can similarly increase bacterial clearance and reduce adaptation rates, if changes between antibiotics are fast, thereby producing highly fluctuating selection conditions. Our work highlights the potential power of the currently emerging field of evolutionary medicine. It simultaneously yields fascinating insights into the selective processes and underlying molecular mechanisms that determine rapid adaptation to novel environments.

Synergistic coevolution speeds up molecular evolution

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Ecological interactions are key drivers of genome evolution. Parasitic interactions for example have been shown to increase the rate of molecular evolution through a process of recurrent natural selection for adaptation and counter-adaptation. In contrast, the genomic consequences of a synergistic coevolution remain poorly understood. We addressed this issue by experimentally coevolving two amino acid auxotrophic *Escherichia coli* strains, whose growth depended on a reciprocal exchange of amino acids. Populations of prototrophic wild type cells that evolved under the same conditions served as controls. The

obligate by-product interaction showed initially poor growth in coculture, yet rapidly evolved towards cooperative cross-feeding within less than 150 generations. The growth enhancement of auxotrophic consortia was significantly increased relative to cultures of prototrophic cells, suggesting that synergistic coevolution increased the rate of adaptation. Derived cocultures of auxotrophic genotypes produced significantly more of the exchanged amino acids than their evolutionary ancestors and derived prototrophs, which is consistent with an increased cooperative investment of auxotrophs into their respective partners. Resequencing the genomes of isolated clones identified a significantly increased number of mutations in auxotrophic relative to prototrophic genomes. Finally, comparing mutation rates of derived and ancestral genotypes corroborated that auxotrophic genotypes have indeed evolved increased rates of molecular change, presumably to generate increased numbers of cooperative phenotypes. Taken together, our results suggest that similar to host-parasite interactions, also a synergistic coevolution can increase the rate of molecular evolution

The role of ecological factors on the evolution of microbial individuality

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One of the most fundamental topics in evolutionary biology is the emergence of new organizational structures, where biological units (cells) form groups that evolve into new units of biological organization (multicellular organisms). Previous theories have mainly focused on the conditions under which natural selection can shift from acting on individual cells, to operate at the level of group of cells. However, less attention has been paid on the role that ecological interactions will have on the emergence and maintenance of early cell clusters. Using a mathematical model of the early stages of cell group formation in cooperative cross-feeding bacteria, we find many trade-offs that affect cluster formation and maintenance. In our model, cooperative cross-feeding bacteria are modelled as two types of bacteria, where one is unable to produce a metabolite that is produced by the other type and vice-versa. The environment is given by an external additional source of the metabolites exchanged. Changes in the environment, modelled as fluctuations in the external metabolites, have therefore a crucial role in the population dynamics of clusters formation. Our model suggests that several traits in bacteria play a crucial role in cluster formation and maintenance, such as chemotaxis, production of substances favouring adherence between cells, and level of investment in the interchanged metabolite. Moreover, we observed that the effect on fitness of mutations affecting these traits can substantially differ if cells are part of clusters or live independently. More importantly, we find scenarios where beneficial mutations in cells belonging to different clusters can be successfully combined when clusters are allowed to interchange cells through the dissolution and reformation of clusters. We conclude that these ecological factors can play a crucial role and are important to unravel the evolutionary trajectory of hierarchical transitions.

Host-parasite coevolution and the evolution of immunological specificity

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Immunological specificity is highly relevant for the fields of evolutionary and ecological immunology. First, host-parasite coevolution critically relies on genetic specificity, which will facilitate reciprocal genetic change in interacting hosts and parasites. On the other hand, specificity can also come in a phenotypically plastic form, when induced immune responses show specificity for a certain parasite type (i.e. immune memory or 'specific immune priming' in invertebrates). We here address the question to what extent these different forms of specificity can evolve.

Experimental host-parasite coevolution between the red flour beetle *Tribolium castaneum* and its microparasite *Bacillus thuringiensis* served to test whether coevolution creates genetic specificity. Moreover, selection lines of beetles that were re-exposed to either similar or different bacterial species or strains served to test whether the immune system can evolve towards higher or lower capacity for specific immune priming. After several generations of evolution, the analysis of the transcriptomes of evolved beetles was used to identify genetic changes that are underlying these forms of specificity.

Different ways to resistance – coevolution of bacteria and temperate phages along the parasitism-mutualism continuum

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Bacteriophages are shaping bacterial populations and community structures. Whereas lytic phages are purely parasitic, temperate phages are considered mutualistic and parasitic simultaneously. Based on an evolution experiment between bacteria and two temperate phages that provide the same beneficial genes but differ in their lytic activity, and thus vary along the parasitism-mutualism continuum, we show how such two-sided symbionts coevolve with their bacterial host.

Bacteria rapidly gained resistance against both phages. Whole genome sequencing revealed that in both treatments, phage-resistant lysogens, were dominating during the first generations, but were rapidly outcompeted by phage-resistant mutants. Mutants, who acquired resistance by a complete deletion of the flagellum operon, spread significantly faster in populations that coevolved with highly lytic phages. Furthermore, low lytic phages remained at low densities during the entire experiment, whereas highly lytic phages became extinct after 30 generations. Our data indicate that lysogeny (where an integrated prophage protects the bacterium against superinfection) is a fast mechanism for bacterial populations to gain rapid resistance against temperate phages but will be outcompeted by resistance mutations, if the costs of the integrated prophage outweigh its benefits. We will discuss this population turnover and the phage extinction risk in the light of diverging fitness advantages of each resistance-form depending on environmental conditions, e.g. during infections of a eukaryotic host.

Why can termite queens live so long?

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Social insect queens can have extraordinary lifespans and at the same time, be extremely fecund. Thus, they seem to have overcome the (almost) universal fecundity/longevity trade-off which characterizes and limits the lifetime reproductive success/fitness of other individuals. We are studying mechanisms (proximate) and causes (ultimate) why termite reproductives (queens and kings) can overcome this trade-off and live so long. Our recent data suggest that transposable elements (TEs) play an important role in termite ageing. Reproductives in the fungus growing termite *Macrotermes bellicosus* seem to be protected by a TE-defence mechanism, the piRNA pathway, that normally protects the germline against TE activity. In another experiment, addressing ultimate causes of the change of the fecundity/longevity trade-off, we provide evidence that the workers on take on the queen's costs of reproduction. Here, we increased the reproductive effort for queens. This did neither affect queens' survival nor did we detect changes in gene expression. But workers suffered from increased mortality and also gene expression changed, especially for genes associated with development. Our data provide insights into the convergent evolution of a long lifespan with sociality, in a lineage that evolved eusociality independently from social Hymenoptera.

Immune challenge alters expression of more genes in fertile ant workers and causes a drastic reduction in gut microbiome diversity

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In most organisms, fertility and longevity are traded-off, so that individuals with many offsprings pay a price of dying earlier. Social insects appear to be an exception to this rule, as the most long-lived individual the queen also has by far the most offspring. Also, within each caste, fertility appears to be positively linked to longevity. In the ant *Temnothorax rugatulus*, workers fight over dominance, develop their ovaries and start laying eggs, when the queen dies or is removed. We showed earlier that fertile workers live longer than infertile ones and we study here the proximate basis for this lifespan extension. We immune-challenged fertile and infertile workers by pricking them with an LPS-treated needle and analysed consequential changes in gene expression in the fatbody. While worker fertility had only a minor effect on gene expression, the immune challenge led to changes in the expression of several thousands of genes. As predicted, fertile workers altered their gene expression more strongly indicating a stronger investment in immune-competence. This was also evidenced by an upregulation of many immune genes and we were interested whether this immune system upregulation affected the gut microbiome. Our analyses show a drastic loss in microbiome diversity as a response of the immune challenge. Indeed, microbial diversity was directly correlated to the expression of important insect immune genes, indicating that an upregulation of the insect immune system has a strong impact on the gut microbial community. Our study is the first to reveal changes in gut microbiome diversity with immune challenge in insects and opens up new avenues for research. Open questions include whether the reported microbial changes increase the fitness of individuals attacked by parasitic bacteria or are by-products of the immune gene upregulation. We also plan to study how fast the normal microbiome diversity can be restored.

Genome evolution and speciation of inquiline social parasites in leaf-cutting ants

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The leaf-cutting ant genus *Acromyrmex* contains five known species of inquiline social parasites, each usurping different host species and with distinct geographical distributions in Latin America. All parasites show different degrees of convergent phenotypic modifications common to inquiline social parasites, such as the partial or complete loss of the worker caste and the reduction in body size. Extant *Acromyrmex* social parasites evolved between 1.5 to 4 MYA from their respective hosts and two social parasite species likely acquired reproductive isolation from their hosts in sympatry. Comparing eight reference genome sequences of host and parasite species, we find that gains and losses of genes are hallmarks of inquiline social parasite genome evolution. In particular, we detect convergent reductions of the olfactory receptor gene repertoire. Based on whole genome alignments of available ant genomes, we also identify rapidly evolving loci in the social parasites that are otherwise conserved in non-parasitic ant species. Furthermore, using genome-wide population genomic data for one host-parasite pair, we retrace the demographic and evolutionary history of the speciation event.

In conclusion, we demonstrate that the genome evolution of inquiline social parasites in *Acromyrmex* leaf-cutting ants involves extensive changes affecting traits associated with eusociality in ants and that speciation of social parasites can have complex demographic histories.

The other facets of family life and their role in the evolution of animal sociality

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Family life forms an integral part of the life-history of species across the animal kingdom and plays a crucial role in the evolution of animal sociality. Our current understanding of family life, however, is almost exclusively based on studies that (i) focus on parental care and associated family interactions (such as those arising from sibling rivalry and parent-offspring conflict), and

(ii) investigate these phenomena in the advanced family systems of mammals, birds, and eusocial insects. Here, we argue that these historical biases have fostered the neglect of key processes shaping social life in ancestral family systems, and thus profoundly hamper our understanding of the (early) evolution of family life. Based on a comprehensive survey of the literature, we first illustrate that the strong focus on parental care in advanced social systems has deflected scrutiny of other important social processes such as sibling cooperation, parent-offspring competition and offspring assistance. We then show that accounting for these neglected processes – and their changing role over time – could profoundly alter our understanding of the origin and subsequent evolution of family life. Finally, we outline how this ‘diachronic’ perspective on the evolution of family living provides novel insights into general processes driving the evolution of animal sociality. Overall, we infer that the explicit consideration of thus far neglected facets of family life, together with their study across the whole diversity of family systems, are crucial to advance our understanding of the processes that shape the evolution of social life.

Population genetics of rapid evolutionary adaptation

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We are proposing two population genetic mechanisms that may drive rapid evolutionary adaptation: polygenic selection and viability selection in highly fecund populations with sweepstakes reproduction. First, while it is known that strong positive selection at major polygenic loci may lead to rapid adaptation, we show that the same evolutionary outcome may result in highly polygenic systems with mostly (or only) minor loci (e.g. human height). Second, we demonstrate that viability selection in highly fecund populations with a skewed offspring distribution (such as marine species) may lead to much faster evolution than in low-fecundity populations.

An experimental test of the genomic consequences of local adaptation in deer mice

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Cryptic coat color evolution in the Nebraskan deer mice occurred as a response to the formation of a dune field (Sand Hills) around 12000 years ago. On the Sand Hills, dark-coated wild-type mice are subject to higher predation by visually hunting predators. Light-coated mutants increase their fitness by improving their camouflage, which explains the observed correlation between substrate color and coat color. Recently, we showed that the genetic variation at *Agouti*, a gene known to control coat color, exhibits signatures of past positive selection. During this talk, I will present the results of a manipulative field experiment designed to elucidate the relations between phenotype, genotype, and fitness in semi-natural populations, for the coat-color/*Agouti* system. In this experiment, survival rates and changes in genome-wide allele frequencies (before/after predation) have been measured in controlled populations of dark and light mice in both environments. Results highlight 1) the evidence of positive selection acting on *Agouti* variants during the experiment, 2) the reproducibility of positive selection on *Agouti* across replicates of the experiment, 3) the importance of coding and regulatory variation as the genetic basis of adaptation in this system, and 4) the indirect effect of selection on linked neutral variants. Finally, I will discuss statistical issues related to the estimation of fitness in such field experiments.

TALK ABSTRACTS – SATURDAY (CHRONOLOGICAL ORDER)

Will aDNA from herbarium collections and a pharaonic tomb reveal who domesticated the watermelon?

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A quick online search shows that the origin of the plant we call watermelon is thought to be South Africa, perhaps the Kalahari Desert. Molecular data since 2015 have rejected this idea. The genus *Citrullus* comprises 7 African species (one extending to southern India), most of them never studied in the wild, and one only discovered in 1990. The resulting under-sampling of the geographic and morphological diversity of *Citrullus* has resulted in years of misdirected breeding and genomic efforts. A combination of DNA from nomenclatural types - the oldest from 1773 - with high-quality genomic data from geographically relevant regions, such as Sudan/Darfur and West Africa, is gradually clarifying the evolution of watermelon, narrowing the area of domestication to the Nile region. However, watermelon DNA from a Pharaonic tomb now raises new questions. I cannot give this all away in an abstract.

Nutritional specialization and host-related diversification in parasitic plants

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Parasitism is a successful way of life, one that is ubiquitous to all organismal domains. In plants, the transition from a free-living organism to being a parasite that steals water and nutrients either from another plant or from mycorrhizal networks provides an important ecological-evolutionary advantage in highly competitive and/or resource-scarce environments. However, it is unknown to date how shifts of the nutritional mode affect the diversification of a group as parasitism intensifies. The Broomrape family (Orobanchaceae) represents an ideal model system for studying the spatio-temporal and host-ecological consequences of parasitism in plants. The cosmopolitan Orobanchaceae comprise nonparasitic species as well as hundreds of haustorial parasites that differ in their lifestyle as photosynthetic or nonphotosynthetic species, their degree of host dependency, and host preferences. Here, we test whether an increasing dependency on another plant represents an isolating barrier absent from nonparasites, which eventually changes diversification rates. A compilation of validated ecological and geographic data for the parasites' host and abiotic environments from over 350 species of 77 genera, covering all nutritional specializations, allows us to (i) reconstruct the biogeographical and host-ecological history of Orobanchaceae and (ii) test if host or abiotic environmental preferences, or both, drive their diversification. To this end, we disentangle the host effect from abiotic environmental influences using both Maximum Likelihood approaches and a Bayesian framework. This work thus is the first to elucidate the eco-evolutionary history across the entire Orobanchaceae, thereby providing an important resource to assess the risk of newly emerging pest species from this agronomically most important family of parasitic plants.

Floral key innovations triggered the evolution of the Malagasy Impatiens (Balsaminaceae) clade

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Abiotic factors have been considered as instrumental in Madagascan plant diversifications. The Madagascan Impatiens clade (>260 species) is a striking example of an explosive radiation and evolved from a single ancestor within just a few million years. However, the tremendous floral diversity in the clade implies that biotic factors must also have played a role in this radiation. This seems particularly likely for endemic Madagascan section *Trimorphopetalum* (127 species). It is characterized by a combination of floral traits unique in Impatiens: small, spur-less, cup- or lip-shaped, greenish, reddish-brown or yellowish-brown flowers. However, so far, no conclusive hypothesis on the floral function of this peculiar group has been proposed. We analysed flower display size, nectar volume, pollen and ovule numbers, breeding system and pollination syndromes for 34 Madagascan Impatiens and six outgroup species in a phylogenetic framework. We found that all pollination syndromes occurring in the (universally spurred) African species are also found in the Madagascan species with similar floral morphology. However, species of section *Trimorphopetalum* represent two new, endemic flower types, corresponding to two different subgroups within the fly-pollination syndrome. The evolution of the spur-less species is correlated to a near-complete loss of nectar production and decreases in display size, pollen number and ovule number. However, *Trimorphopetalum* is predominantly outcrossing, apart from the evolution of autogamy in one sub-clade. Our data indicate the evolution of a - possibly deceptive - fly pollination syndromes and the stepwise development of an autogamous breeding system in section *Trimorphopetalum*. This likely was the prerequisite for diversification via pollinator-mediated isolation in the humid undergrowth of dense montane forests of Madagascar with a limited range of pollinator groups. Thus, the peculiar flower type of *Trimorphopetalum* seems to represent a rare example floral key innovation that may have triggered diversification.

Evolution of the minute seed weevils (Ceutorhynchinae, Curculionidae, Coleoptera) - the impact of Earth's climate changes and host-plant associations

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Using a molecular phylogenetic approach, based on 3502 bp DNA sequence information from 204 species worldwide, we infer divergence times and diversification patterns for the weevil subfamily Ceutorhynchinae in the context of host plant associations and Earth's climate changes. With Bayesian methods, we detect four major diversification shifts that correlate with both host shifts and major climate events. Ceutorhynchinae experienced an increase in diversification rate at ~53 Ma, during the Early Eocene Climate Optimum, congruently with a host shift to Lamiaceae. A second major diversification phase occurred at the end of the Eocene (~34 Ma). This contrasts with the overall deterioration in climate equability at the Eocene-Oligocene boundary, but tracks the diversification of important host plant clades in temperate higher latitudes, leading to increased diversification rates in the relevant weevil clades infesting these hosts. A third diversification phase is correlated with the rising temperatures of the Late Oligocene Warming Event (~26.5 Ma). Diversification then declined shortly after the Middle Miocene Climate Transition (~14.9 Ma). The patterns of interactions observed among the radiation of Ceutorhynchinae and

environmental factors indicate that the interplay of biotic and abiotic factors might better explain their evolution than each of these drivers viewed in isolation.

Agouti-related peptide 2 drives convergent evolution of stripe patterns across cichlid fish radiations

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Color patterns of African cichlid fishes provide striking examples of phenotypic convergence. Across the 1,200 East African Rift Lake species, melanic horizontal stripes have evolved numerous times. Here, we detail the discovery that regulatory changes of *agouti-related peptide-2* (*agrp2*) act as molecular switch controlling this evolutionarily labile phenotype. Reduced *agrp2* expression is convergently associated with stripe patterns across independent species flocks. Yet, *cis*-regulatory mutations are not conserved, indicating independent regulatory mechanisms. Genetic mapping confirms the importance of the *agrp2* locus for stripes in both Lake Victoria and Malawi cichlids. This crucial role is further substantiated by CRISPR-Cas9 knockouts of *agrp2* that reconstitutes stripes in a non-striped Lake Victoria cichlid. Thus, we unveil how a single gene affects convergent evolution of a complex color pattern.

Studying the evolution of cuticular hydrocarbons in insects: a model for a complex trait

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The evolution of complex traits is currently not well understood. Cuticular hydrocarbons (CHCs) in insects are a perfect model for a complex trait since the hydrocarbons are product of multiple genes, exhibit a large variety of phenotypes and are ubiquitous in insects. The CHC profiles are often species- and sex-specific and play a crucial role in intra- and interspecific recognition and communication, defence and desiccation resistance. Although CHC composition and function are studied intensively, our knowledge of the evolution of this ubiquitous trait is rather scarce. In order to understand the factors that are shaping these chemical profiles, we studied the mutualistic and antagonistic network of interaction of solitary and social Hymenoptera with their biotic environment. Additionally, we used molecular phylogenies to understand the nature of selection factors responsible for qualitative and quantitative changes in the CHC profile composition. In my talk I will show how specific selection factors impact the composition of complex CHC profiles due to their physicochemical properties and structural complexity.

Evolutionary history of the Hymenoptera

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Hymenoptera (sawflies, wasps, ants, and bees) represent one of four mega-diverse insect orders, comprising more than 150,000 described extant species. The species richness of Hymenoptera is frequently attributed to the evolution of parasitoid and of eusocial lifestyles within this group. I will summarize recent progress in inferring the evolutionary history of Hymenoptera using phylogenomic approaches, in particular transcriptome sequencing and target DNA enrichment. I will then outline the implications of the obtained phylogenetic insights for interpreting results in recent whole genome sequencing projects of the i5K initiative, namely those on the turnip sawfly, *Athalia rosae*, and the parasitoid wood wasp, *Orussus abietinus*.

Retrotransposon-based phylogeny in the era of genomics

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For the last two decades, retrotransposons have been used as powerful phylogenetic markers in vertebrates. Their insertion is virtually homoplasy-free, largely selectively neutral, and the presence of the same retroelement in orthologous loci of several lineages indicates their monophyletic origin. However, growing amounts of genomic data and comprehensive bioinformatic screens also revealed many apparently conflicting retrotransposon insertion patterns in various mammalian groups. These incongruences can be explained by ancestral hybridization and most commonly incomplete lineage sorting (ILS), whereby ancestral polymorphism persists during successive speciation events in rapidly radiating lineages, processes that also affect other molecular marker systems. To correctly interpret this 'noise', genome-wide, multi-directional screens testing all possible evolutionary scenarios are necessary to obtain reliable phylogenetic reconstructions of lineages with complex evolutionary histories.

Here, we show the results of retrotransposon presence/absence analyses from three rapidly radiating lineages: the marsupial order Dasyuromorphia, the carnivoran group Arctoidea, and the laurasiatherian group Scrotifera. We performed genome-wide, multi-directional bioinformatic screens to compile thousands of diagnostic retroelements from genomes of representative species, and experimentally amplified the loci in species with unsequenced genomes. We were able to reconstruct bifurcating phylogenetic trees revealing strong support for the outermost positions of thylacine in Dasyuromorphia (thylacine (numbat, Tasmanian devil); KKSC test, $P < 0.005$) and bear in Arctoidea (bear (seal, ferret), KKSC test, $P < 3.3 \times 10^{-21}$). However, scrotiferan inter-family relationships could only be reconstructed as a more complex phylogenetic network. Finally, although they had significantly different effects, ILS-derived markers were evident in all three groups.

Speciation in the Hohenheim park? Ecological separation in a population of the jewel wasp *Nasonia vitripennis* (Hymenoptera: Pteromalidae)

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There is agreement that speciation can occur due to geographic isolation in allopatry, but also in the same geographic area in sympatry, e.g. due to ecological separation. However, sympatric speciation has been demonstrated in only few taxonomic groups and therefore is considered an exception. Specifically, only few examples exist for sympatric speciation in insects, despite the fact that this mode of speciation could explain their large diversity. Parasitoid wasps are extremely species rich, which demonstrates that speciation is common in this group. We studied the evidence for sympatric speciation in a local population of *Nasonia vitripennis* (Walker 1836) (Chalcidoidea: Pteromalidae), a hymenopterous parasitoid of fly pupae. We collected *N. vitripennis* in bird nests and from carcasses of dead mice in the Hohenheim Park. In behavioral essays, wasps from nests and carcasses reacted stronger to the odors of their habitat. Furthermore, wasps from carcasses laid significantly more eggs in pupae of carcass flies than wasps from bird nests. In crossing experiments in the lab there was no sexual prezygotic or intrinsic postzygotic isolation between strains from the two habitats. Nevertheless, microsatellite analyses revealed a separation of individuals from nests and carcasses. In addition, wasps from Hohenheim and another population in Regensburg are closer related to each other as compared to two populations from North Germany and The Netherlands. Together, these data indicate the sympatric emergence in Southern Germany of different types of *N. vitripennis*, which are reproductively isolated due to their ecology. This could provide the basis for sympatric speciation in this species.

Evolution of transcription factor networks in primate brains

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Complex phenotypes are determined by many genes and can well be investigated using network methods. Hence, to study the evolution of complex phenotypes, comparative network approaches are very promising. Here we aim to shed light on the evolution of cognitive abilities in humans. To this end, we used transcriptome data from pre-frontal cortex samples of humans, chimpanzees, and rhesus macaques to calculate transcription factor (TF) co-expression networks. We revealed an overall increase in connectivity on the human lineage and that several TFs that are known to be involved in brain development or cognitive disorders have turned into hubs specifically in the human networks. These TFs are good candidates for further experimental studies on the evolution of cognition. We developed several methods to facilitate comparative network analyses, among them a statistical framework to combine similar networks into consensus networks of high confidence, to assign p-values to links, and to define conserved, species-specific, and diverged links. Our methods are publicly available via two R packages, wTO and CoDINA, and come along with sophisticated interactive visualization. We hope them to be useful for other evolutionary network studies.

Explaining evolution: models go first

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Various evolutionary research programs are contending for priority and explanatory superiority of their theories, e.g., evo-devo and adaptationism, extended evolutionary synthesis and modern synthesis. Thus, the impression of a plethora of mutually incompatible evolutionary theories arises. The aim of my talk is to challenge this picture by showing that it misses a proper distinction between research programs and theories, and that it rests on an outdated concept of scientific theories, which conceives them as being defined by their general assumptions. This concept of a theory might hold in fundamental physics. Most scientific theories outside this particular field, however, are better understood as sets of overlapping models. Consequently, I take theory in evolutionary biology as consisting in the explanatory models that the different research programs contribute: models of the evolution of novel traits, of inheritance, of plasticity etc. So, models go first, theory just results and thus develops. Different research programs can differ with respect to their success to contribute explanatory models to evolutionary theory, but, in principle, all programs can contribute models.

Nevertheless, a specific model originating from one research program may be incompatible with a model from another program, so that only one of them can become part of the theory. But the choice between competing models can often be based on the criterion of empirical adequacy of the models in question, as it should be in empirical science. Background assumptions are not required for this decision. The fundamental assumptions have other functions than defining a theory. They form the heuristics of a research program and warrant its integrity.

Comparative analyses suggest reduced DNA methylation levels in Holometabola

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DNA methylation is a taxonomically widespread epigenetic modification, involved in key processes including gene expression regulation and transposable element control. Genomic levels and patterns of DNA methylation seem to considerably vary across major evolutionary lineages. For example, most studied vertebrates present a global pattern of DNA methylation, denoting that the vast majority of CG dinucleotides is methylated regardless of the genomic context. In contrast, insects exhibit comparatively low levels of DNA methylation, which is predominantly targeted to protein-coding exons. This observation has led to the hypothesis suggesting that DNA methylation may have been reduced in the last common ancestor of insects. However, DNA methylation studies on insects have largely focused on holometabolous species. To overcome this bias, we used computational methods to trace signatures of DNA methylation across insects by analyzing transcriptomic and genomic sequence data from all currently recognized insect orders. We found that holometabolous insects display signs of lower DNA methylation levels in protein-

coding sequences compared to hemimetabolous insects, suggesting a reduction of DNA methylation levels in the last common ancestor of Holometabola. Scrutinizing our dataset, we draw three additional conclusions: 1) DNA methylation is lost or extremely reduced in species belonging to springtails (Collembola), flies and relatives (Diptera), and twisted-winged parasites (Strepsiptera). 2) A functional methylation system relying exclusively on DNA methyltransferase 1 may be widespread across insects. 3) Evolutionarily conserved insect genes associated with housekeeping functions tend to show signs of heavy DNA methylation compared to the genomic/transcriptomic background. Our study provides the basis for experimental comparative analyses required to gain a deeper understanding on the evolution of DNA methylation in insects.

Approaching 'Old Friends' with a new model: how pathogen diversity shaped the adaptation of *Astyanax mexicanus* to the cave

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Host-parasite interactions are one of the major driving forces in evolution. The loss of parasite diversity in modern societies in the last 200 years, however, strongly correlates with an increase of autoimmune diseases caused by immune-regulatory defects in humans. This indicates that the interactions between host and parasite not only created a co-evolutionary dynamic, but also represent a necessity for a vertebrate host to develop a functional immune phenotype. So far, this 'Old Friends' hypothesis is largely based on descriptive data from humans since there are no suitable model organisms available that adapted to an environment with low parasite diversity. Here, we introduce *Astyanax mexicanus* as a new model organism for host-parasite interactions to specifically shed light on the question of how the loss of parasite diversity influences the evolution of the vertebrate immune system. We found that not only key innate immunological functions like phagocytosis are strongly decreased in cave populations of *A. mexicanus*, but inflammatory responses towards bacterial antigens are increased. Furthermore, we found striking differences in the organization of immune cell populations between cave dwelling and surface *A. mexicanus*. Future investigation in this direction will not only provide important insights into the immune system of the emerging model organism *A. mexicanus* in general, but will also help to elucidate the evolutionary trajectory of vertebrate hosts in an environment with low parasite diversity.

Antibiotic combination efficacy (ACE) networks in *Pseudomonas aeruginosa*

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Fundamental evolutionary principles are key to alleviate the pressing challenge of antibiotic resistance. Rather than engaging in an open-ended arms race between compound discovery and resistance evolution, evolutionary thinking assists developing empirically-informed approaches with the double aim of minimizing resistance and extending the life span of existing drugs. Due to its enhanced potency and likelihood to reduce drug resistance evolution, the WHO has endorsed combination therapy as the first-line strategy to treat tuberculosis, malaria, or HIV. Yet for bacterial infections, current clinical guidelines do not factor in likely evolutionary trajectories towards resistance during treatment. Several novel antibiotic combination strategies, based on collateral sensitivities, high resistance costs, or antagonistic drug interactions, have been proposed recently to better mitigate resistance. We systematically assessed these by performing over 1800 evolution experiments complemented with network analysis. Our data indicates that combinations specifically composed by aminoglycosides and penicillins are consistently constraining antibiotic resistance evolution due to their strong synergistic interaction and the reciprocal collateral sensitivity among their components. Altogether our approach identified relevant evolutionary factors that enhance the predictability of drug resistance evolution.

Existence of a major control locus for basic behavioral traits

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Mate choice strategy is one of the behavioral traits which can play an important role in the life history of organisms. A previous study had shown that mate choice preference between two populations of the Western house mouse (*M. m. domesticus*) is influenced by the genetic background of the fathers. Transcriptome analysis in a follow up study revealed an imprinted cluster on Chromosome 7, known as Prader-Willi Syndrome (PWS) region, is highly differentiated between mouse populations and therefore have been suggested as potential regions which may regulate this paternal preference in the house mouse. Here for the first time, we found that two paternally imprinted tandemly repeated regulatory RNA coding genes (SNORD115 and SNORD116) in PWS region are of special interest. Our study showed that the copy number variation in these genes highly correlates with behavioral measures, collectively termed 'personality'. Molecular analysis showed that this occurs by influencing the expression of more than 130 genes, which are themselves known to be involved in a variety of pathways including serotonin regulation, metabolism, cognitive ability, vocalization and craniofacial feature development. Hence, my data can nicely explain the coevolution of personality and other traits such as metabolism, cognitive ability, vocalization and craniofacial feature. The fast evolution through copy number variation of the SNORD115/116 genes suggests a mechanism for divergence of mating preferences and population differentiation. This finding is very unexpected, since it suggests the existence of a major control locus for basic behavioral traits, with an inbuilt mechanism to ensure variance in behavioral strategies within a population. This finding could open new windows not only in evolutionary biology but also in other fields such as zoology, behavioral biology, molecular biology, genetics, neurobiology and medicine.

A social niche is a “*set of social environments in which the focal individual has nonzero inclusive fitness*” (Saltz et al (2016)). Social niche construction is therefore any behavior that changes the social environment of an individual analogous to niche construction where traits of an organism determine the environment that it experiences. A similar logic applies to social niche choice where for example individuals vary in their preference for group size and probability to accept and cooperate with other individuals. An ideal system to study the genetic architecture of niche choice and construction should show consistent intraspecific variation for both of these processes. We have studied several populations of the harvester ant *Pogonomyrmex californicus* and *Myrmecocystus mendax* in Arizona and California for the last 10 years and documented alternate social phenotypes of queens founding nests either alone (haplometrosis) or in groups of unrelated yet cooperative individuals (pleometrosis). We documented individual behavior of queens from different populations in a variety of social contexts and followed the development of these founding colonies into mature colonies. Different populations show different but consistent frequencies of founding types, gyny rates (number of reproductive individuals), and individual queen behavior which led to the construction of different social niches, primary and secondary monogyny/polygyny. Queen number and colony founding strategy seems to be a very flexible trait that evolves rapidly both within and between species.

POSTER ABSTRACTS (ALPHABETICAL ORDER)

(1) A glimpse behind the mask: resolving the phylogeny of stick and leaf insects (Phasmatodea)

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Stick and leaf insects (Phasmatodea) are large terrestrial herbivores known for masquerading as plant parts such as bark, twigs and leaves. Their vast morphological diversity is represented by more than 3000 described species with the number of new species discovered steadily growing even for well-explored regions. The unmethodical classification over the last century resulted in a highly chaotic taxonomy with a third of the approximately 480 genera being monotypic. The recently observed trend that the resemblance among phasmatodean taxa may be rather the consequence of convergently evolved traits than of common ancestry was highly underestimated in the past. With the advent of molecular phylogenetics, efforts have been made to revise the traditional classification and substantiate the taxonomic groups. Generally refusing the traditional concept, some taxa have been found to coincide according to a geographical pattern rather than morphological resemblance. The phylogenetic analyses of major lineages continue to reveal discordant results probably due to incomparable usage of molecular markers as well as insufficient sample size. This clearly demonstrates the need of a profound inference and reassessment of the phylogenetic relationships of Phasmatodea which seem to remain one of the last big insect orders lacking a robust phylogeny. For our phylogenetic analysis, we seek to combine all molecular markers used in previous studies comprising in total three nuclear and four mitochondrial genes. In order to increase the species coverage for each major clade, especially underrepresented lineages as well as taxa from insufficiently sampled regions are added to our taxon sample. A well resolved phylogeny provides better insight not only into the phylogenetic relationships but also into biogeographical issues and evolutionary processes including adaptive radiation and convergent evolution. It also allows us to make assumptions on the evolution of significant traits such as body size, asexual reproduction and the capacity for flight.

(2) Eco-evolutionary agriculture: a model in crop rotations

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Since its origins thousands of years ago, agriculture has been challenged by the presence of plant pathogens. Current practices, facing the challenge of food supply in a fast growing population, have started relying on computational tools to design efficient prospective planning. However, such approaches often neglect the evolutionary component: pathogen evolution. In this project, we aim to design a cultivating strategy optimal for eradication of pathogens, able to integrate both the criteria traditionally used on crop rotations, and the analysis of host-parasite coevolution systems where artificial selection for host phenotypes has been applied.

In order to evaluate different cropping strategies, we conceive a crop rotation optimization model using analogous concepts from evolutionary theory. The model optimizes a population of rotation sequences depending on assigned beneficial attributes. Accordingly, we are able to distinguish patterns associated to yield improvement. Next, we switch to a

scenario of pathogen infection and, by considering knowledge acquired from plant-pathogen population dynamics, we adjust the previous optimality to the presence of pests. Finally, we implement evolution of the pathogen following an adapted gene for gene model, and reexamine resistance patterns. The results provide new insights on agricultural practices, as a novel application of mathematical biology tools.

(3) Catch me if you can: role of motility, adhesion, chemical signaling, and relatedness as partner choice mechanisms during nanotube formation

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In nature, bacteria live in multispecies communities in which nutritional interactions, also known as metabolic cross-feeding, are very common. Bacteria can exchange metabolites by diffusion through extracellular environment or directly through cell-cell connections. Contact-dependent metabolic exchange is more advantageous, since it prevents the loss of metabolites to the extracellular environment and also helps to direct metabolites specifically to intended partners.

Recently, we showed for the first time that amino acid auxotrophies can trigger the formation of intercellular nanotubes that auxotrophic recipient cells use to derive cytoplasmic amino acids from other con- or heterospecific bacterial cell. However, how auxotrophic bacteria find their interaction partners and which factors govern the selection of suitable host cells to establish such intercellular connections remains elusive.

In order to determine the molecular underpinnings of partner choice during nanotube formation, genes related to motility, chemotaxis, adhesiveness, and quorum sensing were tested for their role in the establishment of cross-feeding interactions in *Escherichia coli*. Our results indicate that flagella-mediated active motility, chemotaxis, and quorum sensing are not required to find metabolically complementary partners, suggesting that passive attachment through cell surface adhesive structures is sufficient to initiate the formation of such intercellular connections. However, we also found that the absence of major bacterial extracellular matrix components like flagella, fimbriae, curli, and poly N-acetylglucosamine in isolation did not negatively affect initiation of the cross-feeding process. Nonetheless, extracellular DNA, which has been recently described as one of the main components of bacterial extracellular matrix, is liberated in high amounts under nanotube-forming conditions, suggesting a likely role as the major adhesive structure in establishing nanotube-mediated interaction. Additionally, we were able to show that neither phylogeny nor genome based metabolic capabilities determine the choice of suitable host cells during cross-feeding interactions. Together, our results demonstrate how auxotrophic recipient cells develop contact-based strategies to adhere to complementary donor cells under shaking liquid environment to reciprocally exchange beneficial functions.

(4) A functional study of random coding sequences in *Escherichia coli*

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Genomes very often have been seen acquiring functional genes in response to the changing environment. Of all the established mechanisms for evolution of new genes, *de novo* gene evolution is the least studied. It is well-known that *de novo* genes arise from non-coding regions in the genomes of eukaryotes but there is limited evidence in prokaryotes. Some studies have shown that prokaryotes gain new genes from various unknown DNA sources. There are other studies which show that random sequences can eventually become functional *in vivo* by forming stable secondary structures acting as templates for *de novo* gene evolution. I am studying the fitness consequences of a few selected random sequences expressed in *Escherichia coli*. Whether random sequences can act as templates for *de novo* gene emergence in *E. coli* can be understood by studying the functions of these individual sequences.

Previously in our lab, a library of random sequences each containing about 150 random nucleotides was designed and expressed in a plasmid vector. The transformed library gave rise to a single population of *E. coli* expressing the entire library of random sequences. They further looked at the trajectory of each of the sequences over time (1 - 4 days of transfer into fresh growth medium) and observed that a fraction of sequences was depleted, a fraction was enriched while others remained at the same initial number. This dynamic was indeed very interesting to look at closely and now we are trying to understand handful of sequences in greater details in order to shed some light on their individual effects on the fitness of bacteria.

(5) Evolutionary feedbacks between insect sociality and microbial management

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Collaborative defenses against microbes have often been considered a by-product of social evolution in insects. Here, we take the view that both defense against microbial pathogens and promotion of beneficial symbionts are major drivers of social behaviours in many insect systems — ranging from aggregation to eusociality. By supporting our view with examples from a variety of taxa, we propose evolutionary feedbacks between the insect sociality and microbial communities. We identified variation in habitat stability — as determined by breeding site predictability and ephemerality — as a main ecological factor that constrains these feedbacks. To test this hypothesis, we suggest following the evolution of insect social traits upon experimental manipulation of habitat stability and microbial consortia.

(6) Evolution of the eye and head gene regulatory network between closely related *Drosophila* species

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Insect compound eyes are highly complex organs that are composed of individual subunits, so called ommatidia. We have recently shown that closely related *Drosophila* species show remarkable differences in eye size and head shape. The eye size differences between *D. melanogaster* and *D. mauritiana* are a result of differences in the number of ommatidia. We use this model to identify the molecular changes underlying the observed morphological variation in adult structures and try to understand how gene regulatory networks (GRN) in closely related species evolve.

A comparative developmental transcriptome dataset combined with a transcription factor binding analysis showed that the GATA factor *Pannier* (*Pnr*) regulates many genes that are differentially expressed between *D. melanogaster* and *D. mauritiana*. We found that the transcript of *pnr* itself is differentially expressed during eye development. Additionally, we could show that *U-shaped* (*ush*), coding for a co-factor of Pnr, follows the same expression dynamics as observed for *pnr*. This suggests that the regulatory module composed of *Pnr* and *Ush* may represent a flexible node in the eye and head developmental GRN. In order to reveal, how the regulation of *pnr* and *ush* is coordinated and co-evolves, we generated a comparative ATAC-seq dataset that allowed us to dissect the gene regulatory regions of both genes in more detail.

Predictions about potential transcriptional regulators of these two genes based on the identified regulatory regions in combination with the identification of downstream targets will eventually allow us to contribute to a better understanding about the evolution of highly conserved GRN between closely related species.

(7) Desiccation resistance and climate adaptation: conserved cuticular hydrocarbon signatures in invasive Argentine ant super colonies over vast geographic distances

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Cuticular hydrocarbons (CHC), the dominant fraction of the insects' epicuticle, form the basis for a wide array of different chemical signaling systems while primarily functioning as desiccation barrier. In eusocial insects, CHC have been shown to be the main mediators of nestmate recognition, with CHC profile uniformity appearing to be a key factor for maintaining colony identity. In our study system, the unicolonial Argentine ant *Linepithema humile*, a recent unparalleled invasive expansion has led to cooperation between vast super colonies partially spanning multiple continents, whose individual colony members retain the capability to recognize each other as nestmates. CHC uniformity as basis for this vastly extended nestmate recognition behavior would largely conflict with the considerable flexibility expected for CHC profiles as desiccation barrier adapting to the fundamentally different environmental conditions these populations encounter in their expanded range. To shed light on these seemingly contradictory selective pressures (stabilizing vs. diversifying), we attempt to decipher the particular CHC profile properties enabling constant nestmate recognition over vast geographical distances from the more flexible CHC signatures ensuring desiccation resistance despite considerable environmental fluctuations. Integrating chemical, genetic and behavioral studies, intriguing similarities in

signaling patterns begin to emerge hinting at the underlying mechanisms governing a common, unambiguous and universally accepted chemical language within super-colonies while simultaneously providing sufficient flexibility for successfully adapting to a wide range of different habitats.

(8) Rapid evolution in novel environment: a multispecies approach

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In the course of climate change, it is becoming increasingly important to understand rapid evolution that allows organisms to adapt to new environment. This is especially valid in plants, since their ability to migrate is mostly limited to seed dispersal. Here we study rapid evolution across many plant species. As a model system, we use propagation of wild plant for restoration purposes. Specialized companies collect seeds of native species in multiple wild populations with proven natural origin, mix them to ensure high genetic diversity and establish monocultures for seed production. Parts of the seeds harvested from these farms are then sold, while another part is used for establishing the next generation for seed production. After the transfer from natural populations to on-farm propagation, plants face novel environment with new selection pressures. For instance, intraspecific competition replaces interspecific competition, resource stress is not as severe and heterogeneous as in nature due to fertilization and watering, there is usually pest control, and fitness is ultimately determined by the number of seeds at the time of harvest, rather than across the entire life cycle as in the wild. These conditions might lead to plant adaptation within few generations. Commercial cultivation of native plants for seed production thus represents an unintended real-time evolutionary experiment. We use the seeds of generations F0 to F4 to grow plants of these different generations side-by-side in a common garden. As these plants will all experience the same environmental conditions, this will allow us to compare heritable phenotypes, and thus to infer evolutionary changes that may have taken place across generations.

(9) The influence of sex composition of a social group on individual boldness in sticklebacks

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Animal personalities, i.e. individual behavioral differences that are consistent over time and/or across situations, have now been demonstrated in a wide range of animal species, and often show great variation within and among population. However, it is often unclear what maintains variability, and whether different personalities are adaptive. Although it has been illustrated that animal personalities are affected by recent social conditions, little attention has been paid yet to a potential influence of the sex composition of social groups on the expression of personality types.

We hypothesised that a personality trait, namely boldness, will change when individuals are transferred to groups that consist of only males or only females. We investigated the boldness behaviour of three-spined sticklebacks, *Gasterosteus aculeatus*, in individual boldness assays (open field test). After this, the sticklebacks were housed in social groups consisting of only one or both sexes. Each individuals' boldness was then tested seven times

over seven weeks. Individuals from groups consisting of both sexes displayed a wider variation in the boldness compared to mono-sex groups. Males displayed bolder behaviour than females within these groups. The mono-sex groups illustrated that the boldness displayed by females seem to be less influenced by the sex composition of the group than that of males. Females did neither increase nor decrease their boldness display after being moved into a mono-sex group, while males decreased their boldness display in mono-sex groups.

This study is one of the first to illustrate the importance of the sex composition of social groups for the expression and potentially the evolution of personality types. While female sticklebacks seem to be more stable in the personality trait tested here, males adjusted their boldness in response to the gender composition of the environment, possibly to minimize social conflicts and aggression among males.

(10) Ecology of symbiont management in ambrosia beetles

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Ambrosia beetles (Coleoptera: Curculionidae: Scolytidae) live in association with mutualistic 'ambrosia fungi' (Ophiostomatales, Ascomycetes). These yeast-like fungi produce asexual fruiting structures and serve as the near-exclusive food source of the beetles. Ambrosia beetles are extraordinary, as they evolved sociality and the fungus mutualism in a close feedback as successful farming is apparently only successful within cooperative groups. Besides the ambrosia fungi the symbiont community of the beetles also contains fungal pathogens and competitors, which need to be managed by the beetles. It was shown, that as long as the beetles are active, and the ambrosia fungus is in full vigor these other 'weeds' cannot spread. Here we aim to test if ambrosia beetles can actively control their fungus garden communities. First, we will collect field nests and determine how much variation in the composition of the garden communities there is in nature and if these communities are influenced by age of the nest. Fungus garden communities are identified by metabarcoding. Second, by experimental removal of foundresses from laboratory nests we will check if and how strongly garden communities and their succession are affected by the presence of beetles. We expect the fungus garden communities of control nests to contain ambrosia fungi at higher abundance and over longer times. Field nests, on the other hand, are expected to show a higher species diversity than laboratory nests. Overall, this project will help to clarify if the co-evolution of fungiculture and social behaviour in ambrosia beetles is a result of better fungal management in groups with division of labour.

(11) Molecular markers for large-scale genomic data analysis

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Modularity is a keystone of molecular evolution and the reutilisation of independent units facilitates evolutionary innovation without the need for reinventing components from scratch. At the protein level such units are represented by protein domains, structural and functional building blocks of proteins, which alter protein functionality, when combined in a different context.

Ancestral reconstruction of domain arrangements allows to examine different rearrangement events along phylogenies and therefore can provide new insights into the evolutionary history of different species or whole clades.

At the same time the clock-like behavior of rearrangement events can be used to infer phylogenetic relations between species and help eliminating problems like contradictory gene trees.

That means, the gained knowledge can not just be used to answer questions about development and varying evolutionary mechanisms in different branches of life, but also to complement existing methods and overcome their restrictions.

A still remaining challenge is homology detection for deep phylogenies or, in general, for highly diverged sequences. Protein domains offer a very conserved signal and can act therefore as molecular markers, which facilitate remote homology detection and help to decide between conflicting topologies of phylogenetic trees.

An example for how to practically use the different domain contents between proteomes or transcriptomes is DOGMA, a fast and efficient program informing users about the reliability and completeness of huge sequence data sets.

(12) Origin and evolution of novel genes in humans and other primates

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Humans and other great apes are genetically remarkably similar. Despite this, recent analyses show that many genes are restricted to a single or several closely related species. Species-specific genes have been shown to be essential for biological processes and may be responsible for species-specific adaptations and traits. Several mechanisms have been proposed to explain the origin of novel genes in living organisms. These include duplication of pre-existing genes and transfer from distantly related organisms such as viruses. One intriguing explanation for the origin of species-specific genes is their emergence *de novo* from ancestrally non-coding DNA. Why these *de novo* genes initially arise, spread through a population, and evolve beneficial functions is currently unknown. Here, we analyze transcriptomes of humans and five other primate species. We identify novel transcripts arising from non-coding DNA and assign approximate ages allowing us to observe the evolution of *de novo* genes over ~30 million years of primate evolution. We analyze the sequence properties of putative *de novo* genes and their predicted protein products. Our preliminary results suggest that recent *de novo* genes code for short structurally ordered proteins and that protein disorder is a derived state which increases over evolutionary time.

(13) Ancestral reconstruction and experimental testing of evolvability using the AP-superfamily as a model system

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Evolutionary pathways by which proteins have evolved in nature over billions of years have resulted in an impressive diversity of structures that carry out many functions with unrivaled efficiency. Laboratory protein evolution in a test tube can emulate natural evolution, but is often limited by low hit rates and small improvements during evolutionary cycles. Furthermore, the combination of mutations that is needed for large improvements cannot always be reached by one-by-one introduction of mutations due to the occurrence of epistatic ratchets or general loss-of-function. The question then arises how evolutionary dead ends can be avoided or overcome. Important parameters that shape these fitness landscapes are e.g. stability and catalytic activity/specificity. We have reconstructed ancestral sequences inferred from phylogenetic relationships between members of the

Alkaline Phosphatase (AP) superfamily. Mapping of substrate specificity profiles on the genetic relationships allowed the identification of the ancestral nodes between which transitions in primary function occur. This transition in primary function is one of the key processes in evolution of new functions. The substrate specificity profiles of the current enzymes suggest that the change in primary function is the result of a shift in substrate preference of a promiscuous enzyme rather than evolution towards a complete *de novo* function. The main aim of this project is to explore sequence space these ancestral and extant AP-superfamily enzymes (with special focus on the aryl sulfatase clade) using laboratory evolution methods. Connecting the 'fitness parameters' i.e. the intricate interplay of activity, stability and epistatic effects, of the ancestral and extant enzymes to the shape of the local fitness landscape (the effect of mutations on activity and (thermo)stability) should provide quantitative insight into which properties are most important in determining the robustness and evolvability of enzymes.

(14) Origin, evolution and global transmission of *Staphylococcus aureus* ST45

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Aim: *Staphylococcus aureus* ST45 is one of the major *S. aureus* lineages comprising some highly pathogenic methicillin-resistant clones such as USA600. Although it has been described as one of the predominant strains globally, little is known about its evolutionary history. Our aim was to trace back the lineage's molecular evolution and global spread.

Methods: We investigated a collection of 304 genetically diverse *S. aureus* ST45 isolates from 23 countries sampled between 1970 and 2017 using whole genome sequencing. The *de novo*-assembled genomes were analyzed using the Ridom SeqSphere+ software version 4 (Ridom GmbH, Münster, Germany) and in depth phylogenetic investigations were performed using the BEAST software package.

Results: Genome sequence analysis of the 304 isolates revealed a deep split separating the population into two genotypically distinct clades, each comprising two major sublineages named European (EU) and North American (NA) (clade 1) and African (AFR) and Australian (AUS) (clade 2) sublineage. The groups differed in core genome- as well as resistance- and virulence-associated genes including *agr*-type. The most recent common ancestor likely emerged in the mid-13th century in Northern Europe from where it was brought to North America in the 1940s. Clade 2 isolates were transferred to Australia from where they occasionally spread to Asia. They were also carried over to Africa where the AFR sublineage emerged.

Conclusion: In summary, *S. aureus* ST45 turned out to be a genetically diverse lineage with an ancient origin. Although it is distributed globally, several genotypically and regionally distinct sublineages have evolved within this ST.

(15) Aggression and appeasement in nest founding strategies in Californian harvester ants

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Social insects are typically most vulnerable in the nest founding phase. In Californian harvester ants (*Pogonomyrmex californicus*), virgin gynes (=queens without offspring) mate on the wing and then start digging a nest on their own (haplometrotic nest founding). When encountering other nest foundresses, they act aggressive, and if both gynes enter the same nest cavity, eventually lethal fights occur or one gyne evicts the other gyne from the nest. The survival rate of these young queens is low. However, in a few populations in California, newly mated gynes cooperate in digging a nest and provisioning the brood (pleometrotic nest founding). The pleometrotic gynes are typically more docile, actively seek joining others, and are more successful in the first phase of colony development. In mixed pairs, these pleometrotic gynes appease the more aggressive haplometrotic gynes at least for a while.

It is unknown what governs these striking differences in behaviour. Since there are no discernible differences in environment between these populations, and also mixed populations occur, it seems likely that these behavioural patterns are hard-wired. We are currently investigating population genomics that might underlie these behavioural differences. In the future, we will also investigate whether differences in DNA methylation, histone modifications, small non-coding RNA, or Juvenile Hormone (JH) titer are linked to different behavioural strategies. If we find differences in hormone levels and/or gene expression levels, we will manipulate behaviour via RNAi and methoprene application, respectively. Together, these investigations will shed light on the evolution of alternative reproductive strategies that might eventually lead to speciation.

(16) Understanding *de novo* gene evolution from random sequences expressed in *E. coli*

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De novo gene birth refers to the emergence of new genes from previously non-coding sequences, such as introns or intergenic regions. It has been shown in recent years that this mechanism of gene birth, previously thought to be very unlikely, is frequently found in nature. Examples of *de novo* genes have been identified and characterized in several different species of organisms, from bacteria, to plants and metazoans. There are many unanswered questions about how these genes arise from practically random sequences of nucleotides in the genome, including the frequency at which they appear, how does selection act upon them and how are they integrated into, sometimes critical, pre-existing regulatory and metabolic networks. A publication last year (Neme et al, 2017) made a first attempt to quantitatively study the effects of 150bp-long random sequences expressed in bacteria *in vitro*. The surprising, and somewhat controversial, results showed that a large fraction of the full-length random sequences increased in frequency in the bacteria population, hinting at a positive effect on bacterial fitness caused by their expression. In our project, we are delving further into the data generated from this, and similar experiments

expanding the study to include shorter sequences, and analyses of selection coefficients to understand their actual effect on fitness. As a result, we are getting a better understanding of the dynamics of selection and evolution of *de novo* genes, and will contribute to the interesting discussion initiated by this publication.

(17) Experimental evolution of immunological specificity in the red flour beetle, *Tribolium castaneum*

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Contrary to prior believe, recent studies indicate that all animals possess forms of acquired immunity, such as immune priming in insects, which can even be specific. However, we know little about the evolution of basic characteristics of these forms of immunity. We thus addressed the question whether the specificity of immune priming can evolve rapidly, and to what extent the evolved phenotypes are linked to transcriptomic responses. The red flour beetle *Tribolium castaneum* as a host was confronted with different bacterial priming-challenge scenarios thereby creating experimental evolution conditions selecting for specific vs. unspecific (i.e. broad spectrum) acquired immunity. We measured the specificity of priming after 14 host generations. Intriguingly, specificity of priming was not universally higher in the lines selected for specificity and rather depended on the bacterial species and strains used for priming and challenge. Priming was strongest for the virulent insect pathogen *Bacillus thuringiensis*, indicating that evolution of host immunity depends on the type of interaction. Astonishingly, we could not observe any costs of this evolved acquired protection in form of developmental delay nor adult fecundity. Finally, these phenotypic results are mirrored in the transcriptomic response as well. While we could identify a universal set of genes induced by all kinds of priming, expression patterns specific to *B. thuringiensis* priming differed markedly between the experimental evolution treatments.

(18) Migrating concepts from biological to cultural evolution: a case for caution

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Cultural evolution is a rapidly escalating and distinctly interdisciplinary field of studies. As the label suggests, it applies the evolutionary conceptual toolkit first developed for the biological sciences to the study of culture, both in human and nonhuman animals.

While there is a strong case to be made about the validity of such approach, caution must be applied to the direct transfer of notions and hypotheses from one field to the other. I suggest indeed that such prudent attitude should become more endemic and systematic than it regularly is.

In support of this claim, I illustrate how the familiar notion of high-fidelity transmission of hereditary information, gradualism and cumulative adaptations in biology has led to a spectacularly muddled conceptual landscapes in cultural evolution studies.

(19) Poeciliids playing tiddlywinks – sex and species differences in color discrimination and reversal learning

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Behavioral flexibility' is the ability to adapt own behavior in order to better cope with changing environmental contingencies or unreliable access to resources. For instance, behavioral flexibility requires an animal to rapidly abandon a no longer profitable strategy to cope with certain stimuli, while at the same time it must develop a novel strategy in order to attain new associations when environmental demands change. Previous studies investigating primates, rodents and domestic fowl suggested reduced behavioral flexibility and greater behavioral persistence in male individuals. We investigated behavioral flexibility across species and sexes by comparing males and females of two closely related poeciliid species (mollies; *Poecilia latipinna*, *P. mexicana*) with more distantly related guppies (*P. reticulata*) in a visual reversal learning task. Males and females were first trained in a simple color discrimination task. Although guppies of both sexes were found to learn the task within equal time frames in a previous study, male individuals in the present study were unable to solve the task despite continuous training over more than 40 training sessions. Conversely, female guppies were well able to inhibit the previous response and gradually reduce the number of errors over consecutive experiments. Here, we ask what will happen when mollies will be given the same tasks? Are there differences between sexes and/or species? Do closer related mollies differ from a more distantly related species, the guppy? We hypothesize that (a) sex differences in behavioral flexibility in poeciliids can be explained in terms of the different roles that males and females play in reproduction and (b) the observed differences between species may reflect an ability status that arose phylogenetically in unison with the traits that lead to the formation of the examined species.

(20) Variation in reproductive traits among different simultaneously hermaphroditic flatworm species of the genus *Macrostomum*

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The *Macrostomum* clade contains a variety of hermaphroditic flatworm species exhibiting substantial diversity in reproductive mode and subsequently in several morphological and behavioral traits relevant to reproduction. We here illustrate this tremendous variation as well as the role of mating system in its evolution and maintenance by presenting the results of a series of comparable experiments across several *Macrostomum* species that differ in reproductive mode. Our dataset contains data from preferentially selfing, obligately outcrossing and preferentially outcrossing species.

(21) The choice of the environmental covariate affects the power to detect variation in reaction norm slopes

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Many traits are phenotypically plastic, i.e. the same genotype expresses different phenotypes depending on the environment. Individuals and genotypes can vary in this response to the environment and this individual (IxE) and genetic variation in reaction norm slopes (GxE) can have important ecological or evolutionary consequences. Studies on variation in plasticity often fail to show IxE or GxE; this can indicate a genuine absence or simply a lack of power. There is, however, another factor that could potentially affect the power to detect IxE or GxE: the choice of the environmental variable included in the analysis. Identifying the genuine environmental driver of phenotypic plasticity will mostly be impossible and hence only a proxy is included in the analysis. However, if this proxy is too weakly correlated with the real driver of plasticity, this will bias IxE and GxE downwards, could lead to spurious negative results and invalid conclusions. As the mean phenotype in a given environment captures all environmental effects on the phenotype, using it as 'environment' in the analysis should increase the power to detect IxE or GxE. Using simulations, I here showed that using weakly correlated proxies indeed biased estimates downwards but that when using the environment-specific means this was not the case. Using environment-specific means as a covariate has been commonly used in animal and plant breeding but rarely used outside these fields despite its potential usefulness as 'yardstick' to test whether IxE or GxE is present or absent in the phenotype of interest.

(22) Vocal learning and evolution of acoustic diversity in passerines

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Vocal learning in oscines is thought to give rise to a broad range of acoustic features. Neuromuscular control of sound frequency, as well as independent use of two sound sources enables oscines to generate broad frequency ranges in their songs. *Tyrannid suboscines*, in contrast appear to use respiratory pressure to modulate frequency. How this difference in frequency control is manifested in various frequency-related characteristics of song is not known. We analyzed song from tyrannids and emberizids and compared frequency features across many species. Whereas as a group, frequency range did not differ between the two families, emberizid species had a significantly higher mean frequency range in their songs than tyrannids. However, both mechanisms for generating frequency modulation achieve similar maximal modulation rates. The results illustrate how vocal learning has enhanced the range of acoustic features in oscines. At the same time, these data show that oscines and suboscines went different evolutionary paths toward generating similar acoustic features.

(23) Crispr/cas9-mediated knock-out of candidate genes for cold adaptation in South-East-Asian populations of *Drosophila ananassae*

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About 18,000 years ago, *Drosophila ananassae* expanded from its tropical home range in South-East Asia and colonized temperate regions where temperatures can drop down to 0°C. Using a test for chill coma recovery time (CCRT), we compared the cold tolerance phenotypes of an ancestral, tropical population from Bangkok, Thailand to a derived, temperate population Kathmandu, Nepal, and found evidence for local adaptation to cold in the derived population. To uncover the underlying genetic basis, we analyzed differential gene expression in response to cold stress. Further, we created a mapping population of recombinant inbred advanced intercross lines (RIAILs) from a cold tolerant and a cold sensitive founder strain. We combined ddRAD-sequencing and Haley-Knott-regression to map the genomic regions associated with stronger cold hardiness. Overall, we identified several candidate genes for cold adaptation in *D. ananassae*. However, genetic tools to functionally validate these candidates, such as RNA-interference, are not established in this species. Therefore, we introduced a germline-specific Cas9 construct into the wild-type founder strains which will allow the efficient manipulation of the candidate genes and enable us to directly link different genetic variants to the segregating cold-tolerance phenotypes.

(24) Trade-off and adaptive cost of insecticide resistance in the invasive potato tuber moth *Tecia solanivora*

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Resistance to pesticides is an evolutionary process that entails, in most cases, substantial consequences to the biology of the resistant populations. Regardless of the underlying genetic or metabolic mechanism of pesticide resistance, this phenomenon is usually associated with fitness costs resulting from physiological and/or life history changes. In this study we focus in life history and reproductive traits of the potato tuber moth *Tecia solanivora*, an invasive and voracious pest for which resistance to insecticides was recently reported.

A susceptible and a resistant population were selected from the initial sampling of insects collected from eight localities in Colombia. The Siachoque population exhibited a 42-fold resistance to the carbamate insecticide carbofuran, and low levels of resistance to chlorpyrifos, trend observed in six of the eight tested populations.

The carbofuran resistant population exhibited a 3.8-days shorter developmental time than the susceptible population, but with higher larval mortality. The peak of egg-laying was delayed in the resistant population in nine days, but without significant impact on the fecundity. Nonetheless, the population growth rate was higher for the susceptible population, a likely cost associated with insecticide resistance.

We hypothesize that the short developmental time of the resistant population may be an adaptation to minimize exposure to insecticides, which are applied to the soil, at the expense of survival. This adaptation is likely to require the surviving adults to compensate

the smaller nutrient amounts accumulated by the larvae in investing part of its adult life in securing the necessary resources for a late-life egg production.

(25) Polarization of ancestor relations reveals the order of traits in the evolution of cyanobacterial multicellularity

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Understanding the events during the evolution from unicellular organisms to multicellularity is a long-standing challenge. The first known transition to multicellularity occurred more than 3 billion years ago in cyanobacteria. This is a monophyletic phylum that nowadays still includes unicellular and filamentous genera, some of which represent the peak of prokaryotic complexity. Previous research on the evolution of multicellularity in this phylum has been hampered by the lack of knowledge on the phylogenetic relations among unicellular and filamentous genera. We present a novel approach that does not depend on previous knowledge of phylogenetic relationships but infers ancestor-descendent relations of ancestral nodes in phylogenetic trees. Combining the method with the assignment of phenotypic traits to ancestral nodes enable the inference of pairwise relative priority, without the need to postulate a species tree. Applying our approach to 199 cyanobacterial genomes yields a temporal sorting of traits. Our results reveal, for example, that the formation of filaments co-occurred with the ability to fix nitrogen before higher complexity evolved. This finding is in line with theory that predicts the trade-off between oxygen-producing photosynthesis and oxygen-sensitive nitrogen fixation to be the main driving force for multicellularity in this phylum.

(26) What are the factors that promote gut microbiome differentiation of closely related species? A case study on the young adaptive radiation of Nicaraguan Midas cichlid fishes

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Advances in culture-independent sequencing techniques have tremendously improved the understanding of microbial communities, first and foremost of the gut from numerous vertebrate species. Now, it is well known that a diverse set of factors, particularly diet and host genetics, influence the composition of gut microbiomes. However, the relative contributions of these factors remain a matter of debate. Further, it is commonly not clear whether gut microbiome composition promotes or is the consequence of trophic diversification. The young adaptive radiation of Nicaraguan Midas cichlids represents an excellent system to tackle these questions since divergence times are short and species occurring in sympatry within small crater lakes strongly differ in trophic ecology. To this end, we investigated gut microbiomes of multiple species of Midas cichlids by sequencing the V4 region of the 16S rRNA gene. Here, we show that bacterial community composition of Midas cichlids' guts differs among species from distinct environments and, more interestingly, also among trophically divergent species within one young crater lake but not within another. These results suggest that trophic divergence occurs first and entails subsequent changes

of the gut microbiome. However, we further found a strong correlation between pairwise distances of diet and bacterial community composition among sympatric species, which indicates changes in diet and gut microbiome might rather co-occur. Notably, there were convergent changes in bacterial community composition in limnetic species that independently evolved in two crater lakes, emphasizing that adaptation to novel food sources implies similar changes of the gut microbiome. Moreover, interspecific gut microbiome differences were maintained when fish were reared in a common environment, indicating that these differences are, at least to some extent, determined by host genetics.

(27) Social and anti-social cockroaches

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Blattodea is an enormously diverse clade, including over 4000 cockroach species that occupy a broad range of habitats across the globe. Several major innovations have occurred within this order, including vivipary (e.g. *Diploptera punctata*), wood feeding (several taxa) and different levels of sociality, including the eusocial termites. Cockroach genomes belong to the largest known among insects, ranging from 2 - 5 Gb (termites: 0.5 - 2 Gb), including a high level of transposable elements. With comparative genomic and transcriptomic analyses, we aim to better understand the molecular basis of the large diversity and success of this group. We have so far found massive expansions in several gene families but no contractions in the large genome of the omnivorous pest species, *B. germanica*. Many of these expansions help explain their success in harsh, unsanitary conditions, allowing them, for instance, to develop multiple insecticide and pathogen resistance. Many of these gene families are contracted again within the termites, related to their much more specialist and less septic lifestyles. We have also found evidence for transposable element assisted gene family expansions along with the evolution of termites. A rewiring of important developmental pathways, strong changes in expression patterns and adaptive evolution of genes involved in chemical communication assisted this major transition to eusociality.

(28) De novo gene emergence in *Drosophila*

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The field of *de novo* gene emergence has experienced rapid growth in recent years, and looks to characterize the appearance of new protein-coding genes from previously non-coding genetic material. Such a scenario is intuitively unlikely, given the vastness of sequence space and the apparent rarity of functional proteins within it. However, genes from a range of eukaryotic organisms have recently been found to have emerged from both intergenic and intronic regions. Comparative genomic approaches have further indicated the ubiquity of this mechanism and described the general sequence properties of *de novo* emerged genes. Furthermore, in *Drosophila* species, novel genes frequently show testis-biased expression and have been shown to play a crucial role in male-fertility – but to date no *de novo* protein has been fully characterized, leaving a gap in our understanding of their likely structural and functional properties. We aim to functionally and structurally characterize a number of *de novo* proteins. This will hopefully shed some light on the early evolutionary steps taken by these newly born genes, as well as the properties of the 'random' sequences from which they emerge. Additionally, a better understanding of this category of proteins may help inform future protein engineering strategies: recently

emerged proteins may represent especially evolvable starting points for directed evolution efforts, opening the door to exploration of previously inaccessible functionalities by means of directed evolution.

(29) What a difference a day makes - behaviour is less predictable near ovulation

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'Animal personalities' have been shown to exist in many species. Yet, fluctuations in the stability of these inter-individual behavioural differences are not well understood. Against this background, we wondered whether behavioural consistency over time is affected by the reproductive cycle. Female mice were tested twice at an interval of eight weeks in four paradigms assessing social interest as well as anxiety-like behaviour and exploratory locomotion. Twenty-two individuals were tested repeatedly near ovulation, whereas another twenty-two were tested repeatedly in the non-receptive phase. While we found no major behavioural effects at the group level, the reproductive state indeed had profound effects on behavioural stability over time: social interest as well as anxiety-like behaviour proved to be significantly less predictable near ovulation. It is generally believed that phenotypic plasticity is limited due to the costs it brings about. In this context, our data indicate that females accept higher costs in phases directly related to fitness maximization.

(30) Colors don't matter!

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Colorful plumage ornaments may evolve because they play a role in mate choice or in intrasexual competition, acting as signals of species identity or of individual quality. The zebra finch (*Taeniopygia guttata*) is a model organism for the study of mate choice and its colorful plumage ornaments are thought to be used in both of these contexts. Numerous genetic color variants have been described for this species, but they are rare in the wild. This raises the question whether discrimination against deviant phenotypes maintains the species' uniform plumage color (rare-mate disadvantage). Furthermore, comparison to closely related species suggests that the lack of colorful ornaments in female zebra finches is a derived condition. Male preferences for less-ornamented females may have led to sexual dichromatism in the zebra finch. Here, we test the role of plumage ornaments experimentally by altering male and female coloration to mimic 2 types of naturally occurring genetic color variants. We estimated effects on social dominance and reproductive success in large breeding aviaries in one domesticated and 2 recently wild-

derived populations. Hypotheses, methods, and analyses were preregistered to ensure maximal objectivity of the results presented. Despite a fairly drastic manipulation and a powerful experimental design, we found no effect of the treatment on social dominance or on reproductive success. Our results suggest that mate choice is not the mechanism that maintains homogeneity of zebra finch plumage coloration, or that can explain the loss of ornaments in females.

(31) Gene regulatory network architecture in different developmental contexts influences the genetic basis of morphological evolution

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Convergent phenotypic evolution is often caused by recurrent changes at particular nodes in the underlying gene regulatory networks (GRNs). The genes at such evolutionary 'hotspots' are thought to maximally affect the phenotype with minimal pleiotropic consequences. This has led to the suggestion that if a GRN is understood in sufficient detail, the path of evolution may be predictable. The repeated loss of larval trichomes among *Drosophila* species is caused by the loss of *shavenbaby* (*svb*) expression. *svb* is also required for development of leg trichomes, but the evolutionary gain of trichomes in the 'naked valley' on T2 femurs in *Drosophila melanogaster* is caused by the loss *microRNA-92a* (*miR-92a*) expression rather than changes in *svb*. We compared the architecture of the larval and leg trichome GRNs to investigate why the genetic basis of trichome pattern evolution differs in these developmental contexts. We found key differences between these two networks in both the genes employed, and in the regulation and function of common genes. These differences in the GRNs reveal why mutations in *svb* are unlikely to contribute to leg trichome evolution and how instead *miR-92a* represents the key evolutionary switch in this context. Our work shows that differences in the components and wiring of GRNs in different developmental contexts, as well as whether a morphological feature is lost versus gained, influences the nodes at which a GRN evolves to cause morphological change. Therefore, our findings have important implications for understanding the pathways and predictability of evolution.

(32) Robustness against translational readthrough by intrinsically disordered C-termini

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During protein synthesis genetic instructions are passed from DNA via mRNA to the ribosome to assemble a protein chain. Occasionally, stop codons in the mRNA are bypassed and translation continues into the untranslated region (3'-UTR). This process, called translational readthrough (TR), yields a protein chain that becomes longer than would be predicted from the DNA sequence alone.

Protein sequences vary in propensity for translational errors, which may yield evolutionarily constraints by limiting evolutionary paths.

Making use of ribosome profiling data, we have detected TR in baker's yeast and closely related species, for which comparative analyses of proteins that are prone to TR have been conducted. For baker's yeast, we have found that a relatively high frequency (5%) of genes undergo TR, including ribosomal subunit proteins. Moreover, proteins undergoing TR are highly expressed and have intrinsically disordered C-termini. I will discuss whether highly expressed proteins may compensate for the deleterious effects of TR by having intrinsically

disordered C-termini, which may provide a conformational flexibility without distorting folding. I will also present the comparative work of different yeast species, and discuss whether increasing robustness, by minimizing deleterious effects of TR, is enabling exploration of the phenotypic landscape of protein isoforms.

(33) *Tribolium castaneum* and *E. coli* Nissle 1917 - a novel experimental system for studying probiotics and host-parasite interactions

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Experimental studies of the interactions of probiotic bacteria with their hosts and the resulting fitness effects can provide important insight into host-microbiome evolution. *Escherichia coli* Nissle 1917 (EcN) is a nonpathogenic *E. coli* strain, used as a probiotic for treatment of various intestinal disorders in humans. This strain does not express pathogenicity factors such as adhesins or toxins. It is not invasive and not uropathogenic, but rapidly killed by non-specific defense factors of blood serum and has antagonistic activities against other microorganisms. Several traits contribute to this strain's probiotic character, incl. its anti-inflammatory activity, enforcement of the intestinal epithelial barrier, promotion of colonic motility and induction of the gut immune response. For large-scale experimental approaches, the availability of a simple invertebrate model host would be ideal, but is currently not available. We here introduce the red flour beetle *Tribolium castaneum*, a well-established model organism for studies of evolution and infections, as a suitable experimental host for the probiotic strain EcN. Our preliminary experiments have shown that EcN colonizes the gut of the beetles when added to the diet. We will analyze effects of EcN on the fitness and life span of the beetles after successful colonization of their gut. Importantly, making use of an established oral infection protocol with the entomopathogen *Bacillus thuringiensis*, we will investigate the evolution of this pathogen in interaction with the probiotic bacterium in the gut. This novel experimental system will also enable to further investigate evolution of EcN and give insight into its behavior in different host organisms.

(34) The effect of predation on cooperative cross-feeding in bacteria

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Predation by protists acts as an important selective agent that shapes bacterial evolution and has prompted various antipredator adaptations like e.g. microcolony formation in diverse bacterial species. However, the effect of predation on cooperative cross-feeding bacteria as largely been neglected. To fill this gap, we use a cooperative system of two *E. coli* strains that had been engineered to reciprocally exchange essential amino acids: the first strain being auxotrophic for tryptophan but overproducing histidine, the second strain being the exact complement. Both strains exchange their cytoplasmic constituents via membrane-derived nanotubes. A significant fitness advantage of this obligate cross-feeding system relative to a metabolically autonomous wildtype strain had been demonstrated. However, in the presence of *Tetrahymena thermophila* - a predatory protist - the cross-feeding bacteria (CF) are at a clear disadvantage: compared to non-CF their fitness is significantly decreased. Since the CF are supposed to be interconnected via nanotubes, thus forming cell aggregates that are more difficult to be grazed upon by the predators, the observed fitness cost is in contrast to recent theories of antipredator adaptations in

bacteria. A possible explanation for this discrepancy might be a trade-off between optimal aggregate sizes for cross-feeding versus grazing resistance.

(35) Is the glass half full or half empty? New tools to assess cognitive judgement bias in mice

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In natural habitats, individuals are constantly confronted with environmental cues they have to react to appropriately. This requires fine-tuned decision-making, especially when the environmental information is ambiguous. Investigating factors that influence such processes and thereby lead to optimistic or pessimistic judgement biases is of great interest for both behavioural ecology and evolutionary medicine. The first necessary step within this framework is to develop test paradigms for the accurate assessment of judgement biases in the species of interest. Using two separate approaches, the aim of this study was to develop a cognitive judgement bias test for mice.

Each approach comprised an independent test paradigm. Both were based on a discrimination task, in which mice had to learn to correctly respond to a positive and a negative reference cue. Cues differed between paradigms and were either constituted by tunnels of different lengths or bars displayed at different positions on a touchscreen. Upon successful discrimination learning, the animals' judgement bias was assessed during ambiguous probe trials, in which they were confronted with intermediate tunnel lengths or bars at intermediate positions. Responses according to the positive reference cue were rated as optimistic choices, while pessimistic choices were assumed for responses according to the negative reference cue.

As expected, in both projects, animals showed a graded response curve, with highest optimism scores for the positive reference cue and the ambiguous cue nearby. Scores were lowest for the negative reference cue and the adjacent ambiguous one. Provided that being successfully validated in the future, both paradigms can be implemented to assess cognitive judgement bias in mice.

(36) *Agouti-related peptide 2* drives convergent evolution of stripe patterns across cichlid fish radiations

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The color patterns of African cichlid fishes provide striking examples of convergence, the recurrent evolution of phenotypic similarities. For instance, across the more than 1,200 species of the East African Rift Lakes of Victoria, Malawi and Tanganyika, melanic horizontal stripes have evolved numerous times. Here, we discovered that the same locus accounts for this evolutionarily labile trait. Regulatory changes of *agouti-related peptide-2* (*agr2*) act as a molecular switch controlling the presence of horizontal stripes. In Lake Victoria

cichlids, we identified a skin-specific ~1 kb *cis*-regulatory element that modulates *agrp2* expression.

However, underlying mutations are not conserved across cichlid radiations, indicating that different regulatory mechanisms affect *agrp2* expression and thereby stripe patterns in other cichlid species flocks. Using CRISPR-Cas9, we demonstrate that *agrp2* acts as a repressor of stripes and its knockout reconstitutes stripes in a non-striped cichlid, *Pundamilia nyererei*. Thus, we identify *agrp2* as a major regulator of color pattern convergence and diversification in cichlids.

(37) RNA structures shaping evolutionary pathways

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RNA is a versatile molecule involved in a variety of processes related to gene expression and protein synthesis. Due to the diversity in functions they perform, there are numerous different types of RNA, including mRNA, tRNA, miRNA. RNA forms so-called hairpin loop structures. Generally, RNAs are able to form several suboptimal structures in addition to their most stable and therefore most likely structure. The probability of a structure is being determined through the Minimum Free Energy (MFE). Some RNAs switch back and forward between stable structures, leading to bistability. Bistability and consequently bifunctionality can promote evolution of new functions. Especially after gene duplication removes selective constraints to maintain both functions. Using bioinformatical methods we investigate the structures and their probabilities of pre-miRNAs and mature miRNAs. Furthermore, we want to investigate the effects of mutations on structure stability and structure itself. Here, we hope to identify bistable RNAs, their function, and traits of both their structures to gather insights on the role of bistability and bifunctionality in evolution.

(38) The ability to survive frost is better explained by microenvironment than by altitude in *Arabidopsis thaliana*

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Strong vegetation changes along elevation gradients are a result of many simultaneously changing environmental variables among which decreasing average temperature plays a prominent role. Therefore, high altitude populations often show enhanced frost tolerance compared to low altitude populations. However, changes in slope, soil depth and exposition are known to strongly affect microenvironmental conditions which may counteract average effects of altitude. We tested winter frost hardiness of *Arabidopsis thaliana* accessions originating from 12 sites along an altitude gradient in the South Tyrol and Trento provinces of Italy in a common garden experiment over 3 years and collected high-resolution temperature data from 8 of these sites during two years. Our results show that frost-hardiness on average increased with altitude which is consistent with adaptation to higher frost frequency at higher altitudes. However, this correlation was primarily observed for the lower part of the gradient. From about 900 m.a.s.l. the correlation disappeared due to strong scattering. Indeed, the variance across populations for the number of frost days increased strongly with altitude. Including the temperature data in the model revealed a better association of frost-hardiness with the number of frost days than with altitude. These results suggest that a strong microenvironment effect may partly overrule effects of altitude

allowing a range of differently adapted populations to survive at high elevations. These results demonstrate that the southern alpine mountain regions may not only serve as a refuge for rare species but also function as a refuge for high functional diversity within a species.

(39) Experimental characterization of the putative *de novo* gene *Goddard* from *Drosophila melanogaster*

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Over the last five years, there has been an increasing amount of evidence for the *de novo* emergence of protein-coding genes from non-coding DNA, rather than by gene duplication. Most of these studies are based on identification and verification of *de novo* emerged-genes. So far, putative *de novo* genes have been identified in mouse, fruit flies, sticklebacks, apes, and humans. But how these genes emerge is still unclear. There are two theories: ORF-first or transcription first, but up until now neither of these two principles has been proven to be correct.

One of the greatest obstacles for the field of *de novo* genes is the lack of high-quality genomic data with very short divergence times which could help to precisely pin down their location. Another problem is that most studies have examined longer evolutionary time scales and rarely considered protein structural properties. As a result, it remains unclear how these properties are shaped by evolution, depend on genetic mechanisms and influence gene survival. Taken together, it seems that *de novo* genes resemble frozen accidents of randomly emerged ORFs which survived initial purging, likely because they are selectively neutral or beneficial for the organism.

To date, only a few experiments have attempted to characterize the structure and function of *de novo* protein-coding genes. In *Drosophila melanogaster* a potential *de novo* gene named *Goddard* has been identified. It plays an important role in the spermatogenesis of male fruit flies, but the characteristics and interaction partners of the protein remain unknown. Here we present the characterization of this *de novo* protein. First structural experiments indicate a highly disordered protein, having only a helix as a secondary structural element. It is remarkable that a mainly disordered protein plays such an essential role in shaping the evolution of male reproductive traits.

(40) Physiology of key symbionts and their interactions in the fungus-farming mutualism of ambrosia beetles

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Fungal agriculture by insects evolved 20-100 million years before human agriculture in three groups: attine ants, macrotermites and wood-boring weevils, the so-called ambrosia beetles (Scolytinae and Platypodinae). Latter are characterized by boring tunnel systems into nutrient- poor sapwood of recently dead trees, wherein they actively farm species-specific fungal mutualists. These ambrosia fungi line the tunnel walls with their nutritional fruiting structures. Unknown is how the fruiting is induced and what physiological capabilities the ambrosia fungi have.

Here we aim to explore (i) the mechanisms used by the beetles to trigger the fruiting and (ii) the wood degrading potential of their ambrosia fungi. Our first results show that in our

main model system *Xyleborinus saxesenii* symbiotic *Pseudomonas* bacteria are responsible for the induction of fruiting in the *Raffaelea sulphurea* ambrosia fungus. Preliminary data about the specificity of this effect and the underlying chemical mechanisms will be presented. Bacteria induction of nutritional structures is unique among fungus-farming insects and shows that this farming mutualism is a complex, multi-partite system.

Second, we present first data on the enzymatic capabilities of ambrosia fungi. We show that ambrosia fungi primarily target hemicelluloses (e.g. xylan: endo-1-1,4-xylanase) followed by a lower preference for celluloses (e.g. endo-1-1,4-glucanase), which indicates that they are poor degraders of structural components in wood.

Overall this project, which is still at the beginning, will provide novel insights into the physiology and interactions between the major microbial symbionts in the poorly understood ambrosia beetle-fungus symbioses.

(41) Plasticity and evolution of the expression of the chitinase enzyme, a virulence factor of *Bacillus thuringiensis*

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Gut-infecting bacteria infect their hosts with the help of powerful virulence factors. The production of virulence factors is costly for the bacteria, which may result in trade-offs, but they can also act in synergy. Most strains of *Bacillus thuringiensis* (*Bt*) are entomopathogenic bacteria, i.e. natural pathogens of insect species. Until recently, research on the virulence of *Bt* has mostly focused on the well characterised crystal (Cry) toxin proteins. When spores are ingested, Cry leads to the formation of pores in the midgut epithelial cells. However, for a full understanding of the interactions between host and pathogen it is crucial to also study the importance of other virulence factors, such as chitinases. Chitinases degrade chitin, which is a major component of the peritrophic membrane of the insect gut. Penetration of this chitin- rich barrier facilitates access of Cry toxins to the gut epithelial cells.

In this project, we first analyzed the expression pattern of chitinase in *Bt tenebrionis*, a beetle-infecting strain. In particular, we asked whether chitin expression is modified in response to chitin in the growth medium, and whether this has an effect on Cry toxin expression. Using a serial passage experiment, we will then study whether chitin expression shows microevolutionary change in response to environmental chitin, how this impacts on Cry toxin expression, and finally, whether it affects virulence in its beetle hosts, *Tribolium castaneum* and *Tenebrio molitor*. This study thus aims to deepen our understanding of interactions, plasticity and evolution of crucial bacterial virulence factors.

(42) Cause and consequence: The identification of the molecular basis underlying eye size differences between *Drosophila melanogaster* and *D. mauritiana*

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The size and shape of adult organs is controlled by developmental gene products, which are organized in gene regulatory networks (GRNs). To reveal the molecular basis of natural variation in complex trait morphology, the architecture of such GRNs needs to be considered. We study the evolution of compound eye size and head shape in different *Drosophila* species. As previous studies have shown, the size of the head cuticle and the

eyes are negatively correlated in various *Drosophila* species. Compared to *D. melanogaster*, *D. mauritiana* has larger eyes which form at the expense of head cuticle.

The larger eyes are a result of more ommatidia. Ongoing work has shown that the GATA family transcription factor *Pannier* (*Pnr*) represents a flexible node in the GRN. However, genetic tests suggest that the causative genomic changes lie upstream of the *pnr* locus. We combine various datasets to identify putative evolving regulators of *pnr*: 1) Based on a transcriptome dataset, we identified several candidates that bind to regulatory elements of *pnr* (e.g. *Mad*, *Jim*, *Zen*). 2) Previously published quantitative genetics datasets aiming at revealing candidate changes responsible for intra-specific head cuticle variation revealed genes that may be involved in the observed interspecific variation (e.g. *jim*, *Fasciclin 3*, *Reticulon-like1*). To test which of these candidates is indeed responsible for morphological differences between we combine reciprocal hemizyosity tests based on CRISPR/Cas9 mutagenesis with developmental genetics approaches. Eventually, we aim at unveiling the role of the putative regulators in the GRN of head formation in *Drosophila*.

(43) Enzymes involved in cuticular hydrocarbon (CHC) biosynthesis: insights from an extraordinary case of intrasexual CHC profile dimorphism in a mason wasp

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Cuticular hydrocarbons (CHC) diversity has been intensively studied over the last decades as have CHC behavioral effects. CHCs play two essential roles for insects: CHCs act as anti-desiccation agents and they are exploited for intra- and interspecific communication (e.g., as sex, territorial, and epideictic pheromones, and for caste and species recognition). Yet, only few genes involved in their biosynthesis have been identified. By studying an exceptional case of intrasexual CHC profile dimorphism in the spiny mason wasp, *Odynerus spinipes* (Hymenoptera: Vespidae), we are able to shed light on the biosynthesis of CHCs. *O. spinipes* females express two CHC profiles (chemotypes) that differ in more than 70 compounds qualitatively from each other. Females seem to differ exclusively in this specific trait and keep their chemotype during their entire lifespan. We searched for genes that are systematically differentially expressed in females of the two chemotypes. By doing so, we readily identified 16 candidate genes likely involved in CHC biosynthesis (i.e., desaturases, fatty acid synthases, elongases, and reductases). We currently seek to validate the function of these genes via RNAi-mediated knockdown experiments on *O. spinipes* and on the honey bee, *Apis mellifera*. The exceptional CHC dimorphism of *O. spinipes* females not only prove to be an intriguing gateway for shedding light in the genetics of CHC diversity, but also raises the question why and how this dimorphism evolved in the first place. The CHC dimorphism seems to be the result of intraspecific and interspecific kleptoparasitism. *O. spinipes* females steal weevil (Coleoptera: Curculionidae) prey from the nests of other *O. spinipes* females or they take the ownership of the nest of other *O. spinipes* females expressing the same chemotype. Furthermore, two cuckoo wasps (Hymenoptera: Chrysididae) that each chemically mimic one of the two *O. spinipes* CHC profiles kleptoparasitize *O. spinipes* nests.

(44) Adaptive reshaping of neuroendocrine profiles beyond adolescence

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

(45) Plastic expression of seminal fluid protein genes at different sperm competition levels

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Seminal fluid proteins (SFPs) are a crucial and dynamic component of the ejaculate. They affect sperm motility, mated females' physiology, and even the fitness of offspring. To optimize the benefits from SFPs transferred, males are expected to adjust SFP production depending on the situation they face. For example, the numbers of potential mates and rivals are well-supported variables that males use to assess the risk of sperm competition. We tested if the great pond snail *Lymnaea stagnalis* alters SFP production depending on mate availability, by estimating the expression level of SFP genes. We kept snails isolated, paired and in groups of five individuals for nine weeks. Based on qPCR expression analyses for five SFP genes, we found that mate availability indeed alters SFP gene expression – (1) isolated snails showed reduced SFP gene expression, and (2) the paired and grouped showed elevated levels of SFP gene expression, but did not differ from each other. Based on these results, we argue the scenario that, at the phase of SFP production, being fully ready for sperm competition in the presence of mating partners is the best strategy. Overall, our research contributes the understanding of post-copulatory reproductive strategies.

(46) Gathering plant knowledge: children's social learning about plants in a naturalistic garden setting

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Although plant knowledge seems peripheral to daily life in modern environments, throughout evolutionary history plants have been an essential part of human life. Humans relied on the benefits extracted from plants (e.g., food resources, raw materials for artifact construction) but were vulnerable to the dangers plants pose. All plants produce toxic chemical defenses against herbivores and some have physical defenses as well (e.g., thorns), making trial-and-error learning a costly proposition. It was therefore predicted that social learning strategies would evolve to transmit plant knowledge from one generation to another.

Consistent with this proposal, recent developmental studies have shown that infants possess behavioral avoidance strategies to protect them from the harm plants can inflict. Further, infants differentially seek out social information from others when confronted with plants and selectively learn about plant edibility using social cues from adults.

However, much is still unknown how children do acquire and retain knowledge about plants, particularly outside of a laboratory setting. The present study uses a naturalistic garden setting to explore (i) the underlying processes of social learning abilities about plant properties, and (ii) whether young children retain this acquired knowledge over long periods of time. In a series of tasks over a three-year longitudinal study, we tested children's knowledge about plants and their capacity to recall what they have learned in a gardening program. Results show that learning about plants in a naturalistic setting improves children's recognition of and memory for properties of plants encountered during the gardening program, especially visual and olfactory properties. Detailed coding of their behavior during the sessions will help to understand more about the learning processes at place and ultimately give insights into the evolutionary trajectory of human-plant interaction during human history.

(47) Seminal fluid mediates sexual conflict over the fate of male ejaculate

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In polyandrous species, sexual selection continues after mating as sperm compete with each other and/or female choose their preferred sperm to fertilize eggs. The variety of male adaptations to sperm competition and cryptic female choice may frequently give rise to sexual conflict, as male-benefit traits can be costly to females, triggering cycles of sexually antagonistic adaptation and counter-adaptation. Seminal fluid proteins (SFPs) transferred together with sperm during mating are likely to be key mediators of post-mating sexual selection and conflict but it is often difficult to identify such antagonistic adaptations in seminal fluid because of its complex and functionally redundant nature. Here we used a novel systematic investigation for establishing the function of SFPs through a combination of quantitative genetics, RNA interference and behavioural assays in the simultaneously hermaphroditic flatworm *Macrostomum lignano*. We hypothesized that if any seminal fluid component influences partner that received ejaculate, this should manifest itself as genetic correlations between expression of SFPs and post-mating behaviour of partners. Therefore, we first determined genetic correlations between expression of SF transcripts in sperm

donors and subsequent mating behavior of recipients, namely suck behaviour, that is to remove the received ejaculate. We identified six candidate genes having strong negative genetic correlations with propensity of suck behaviour. We then used RNAi to knock down these candidate gene products and found that lacking gene products of two candidates substantially increase the suck propensity of mating partners. Our study demonstrated the utility of genetic correlations to investigate transcriptional function of candidate genes and provided valuable insight to understand genetic architecture of seminal fluid with new evidence for potential adaptations that could be driven by post-mating sexual selection and sexual conflict.

(48) Chemoreceptor diversity in solitary apoid wasps – did eusociality drive the expansion of OR genes?

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Chemoreceptors allow organisms to identify chemical components of their environment. For most insects they play a major role in localizing and evaluating the quality of food, oviposition sites and mating partners, and they are crucial for social insect to establish their communities. Three different chemoreceptor families evolved in the ancestors of pterygote insects: gustatory receptors (Grs), olfactory receptors (Ors) and ionotropic receptors (Irs). While the amino acid sequences of Irs are highly conserved among all insects, Grs and Ors possess a high diversity of amino acid sequences. Consequently, identifying Grs and Ors poses a challenge and our knowledge of chemoreceptor repertoires is restricted to few annotated species groups. Recent investigations revealed that Or and Gr lineages were extraordinarily expanded within the Hymenoptera (i.e. wasps, ants and bees), most notably in ants. However, also solitary Hymenoptera, such as the parasitoids *Nasonia vitripennis* and *Microplitis demolitor*, possess a high number of Ors and Grs. We are generating antennal transcriptomes in order to study chemoreceptor diversification patterns among lineages of Aculeata (i.e. stinging Hymenoptera) and collected specimens that reflect the predominant lifestyles found in this insect order. Specifically, we sampled specimens from various solitary and eusocial lineages and of predators, herbivores, cleptoparasitic, and parasitoid species. We aim to answer these key research questions:

- (1) Can we reconstruct the chemoreceptor repertoire of the last common ancestor of Aculeata?
- (2) Do solitary and social lineages systematically differ in the amount and properties of chemoreceptors?
- (3) Do females express the same diversity of chemoreceptors as males?

(49) What is evolution? A deflationary answer

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

My purpose, in this talk, is precisely to (briefly) offer an original answer to the issue of what evolution is, on the basis of a certain neo-Aristotelian view on what change is. Furthermore, I argue that my view on what evolution is remains empirically realizable.

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

Within the huge philosophical literature on the notion of change, a preliminary distinction between accidental change and substantial change is often drawn; how to understand this distinction is a matter of considerable scholarly controversy.

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

(50) Lake Malawi in the pantry: Surprising diversity of cryptic species in a parasitoid of household pests

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Generally, the emergence of a high number of species within a taxonomic group is associated with an ecologically diverse habitat, a prominent example being the speciation of Cichlids in Central American and African lakes. We studied *Lariophagus distinguendus* (Förster) (Hymenoptera: Pteromalidae), a parasitoid wasp of larvae of various beetle species, which are often pests on stored products. Earlier studies revealed that *L. distinguendus* in fact consists of two distinct species separated by a number of different barriers, including sexual isolation and different host preferences and habitats. They are referred to as 'granary weevil species' and 'drugstore beetle species' according to their preferred hosts. A collection of strains of the drugstore beetle species in the area of Stuttgart revealed a high diversity. All strains can be divided into four groups that are separated by a difference in the cytochrome oxidase 1 of two percent. Since they all were collected on drugstore beetles as host, they seem to occupy the same ecological niche, namely pantries and other storage places in households. Thus, ecological separation does not seem to have been the driving force for their emergence. We studied the isolation between these four groups, focusing on the following questions:

Are the four groups separate species?

Which isolating barriers act between the groups?

Is cytoplasmic incompatibility involved in the isolation?

(51) Evolution of eye size and head morphology between *Drosophila americana* and *D. novamexicana*

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The insect head harbors major sensory organs, such as the eyes. Alterations in size and shape of those traits likely represent functional adaptations to an ever-changing environment. Different sources of variation in head morphology, and in particular in eye size, have been shown for species of the *Drosophila melanogaster* group. While the molecular basis for these differences is being revealed, it remains unclear whether similar diversifications are common and governed by similar or different molecular mechanisms over longer timescales. Species of the virilis group, *D. americana* and *D. novamexicana*, represent an excellent model to address these issues, since they have been diverging from *D. melanogaster* for at least 40 million years. Additionally, they show remarkable differences in head morphology and eye size with the latter being smaller in *D. novamexicana*. In order to reveal the major genomic regions responsible for the observed differences we have used a combination of geometrics morphometrics and genome-wide quantitative genetics. Our results show that variation in normalized eye size and head shape are mainly caused by genes located on the 2nd, 3rd and 4th chromosomes. Additional characterization of the dynamics of eye-antennal disc growth throughout larval development revealed that the eye primordium starts to become significantly bigger in *D. americana* in mid-L3 stages. RNA-seq and ATAC-seq data of different developmental stages is currently being generated to identify the responsible changes in the gene regulatory network underlying head development. Further functional validation will provide valuable information about the molecular mechanisms responsible for morphological diversification throughout evolution.

(52) Sexual dimorphism in immunity and parental investment

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Sexual dimorphism also applies to immunity. Higher immunocompetence in one sex leads to increased longevity for that sex (in comparison with the other sex). Studies performed on humans and other species with female pregnancy show that females, who provide major parental investment, tend to have increased longevity.

In the family Syngnathidae (that consists of seahorses, pipefishes), males get pregnant and studies show that they have higher immunocompetence. Data from several pipefish species with varying levels of male pregnancy, show that increase in parental investment brings a rise in immunocompetence in males i.e. more sexual dimorphism in immunity. Developing theoretical models informed by experimental data, we seek to provide a theoretical support for the patterns observed in the experiments, predict under what conditions sexual dimorphism in immunity can occur and in what circumstances can an increase in parental investment also lead to a rise in immunocompetence. Our work will provide a generalised idea about how immunocompetence depends, in a certain sex, on the amount of parental investment it gives and not to the sex itself.

(53) Cognitive flexibility and mate assessment behavior in female three-spined sticklebacks (*Gasterosteus aculeatus*)

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Sexual selection has resulted in the evolution of traits that signal male quality, but females often vary in their preference for these traits. Intrinsic factors such as cognitive ability, personality, and body condition likely influence the perception of sexual signals, resulting in differences in individual preference among the choosy sex for sexually-selected traits. Cognitive flexibility can be measured as the ability to inhibit a previously-learned behavior in a reversal learning task, and coping styles theory predicts that more cognitively-flexible individuals collect more information from the environment than inflexible individuals. When viewed in the context of mate choice, we hypothesized that cognitively-flexible individuals would acquire more information about potential mates and be choosier. We used female three-spined sticklebacks as a model species to examine the influence of cognitive ability using a simple activity-based reversal learning task in a foraging context for a single male trait which has been heavily studied in this species (red vs. orange throat coloration). Here we show that mate assessment is not independent from other cognitive traits. We found that females that spent more time assessing potential mates learned a reversal task in fewer trials despite being more persistent in continuing to search for the food reward in the previously rewarded location. This suggests that these females that are highly responsive when evaluating potential mates rapidly formed strict routines when foraging. Females that were highly responsive to the male stimuli also made faster correct decisions and more quickly reversed incorrect decisions in the learning experiment. Overall, these are among the first results to connect intrinsic factors such as cognitive style to mate choice behaviors. This highlights the importance of examining how these intrinsic factors drive the mating decisions of the choosy sex.

(54) Ecological pleiotropy and evolution of jasmonic acid signaling networks

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Plants live in a complex and dynamic environment and have to adapt to multiple kinds of stresses. Therefore, when a gene or trait is involved in multiple stress responses, their evolution is constrained by ecological pleiotropy. A classic example is the jasmonic acid (JA) pathway, which is known for its various roles in the interaction with herbivores, pathogens and pollinators (flower development). This raises the question to what extent the different modules of the JA network are shared among different plant-environment interactions and whether the evolution of the JA signaling network is constrained by ecological pleiotropy. To investigate this, we analyze a group of genetically diverse tomato plants and analyze three different functionalities of the JA pathway – flower development, herbivory response and mycorrhizal interaction. The plants include the cultivated tomato *Solanum lycopersicum*, wild tomato species (7 represented by each 3-4 accessions) and plants whose JA pathway has been genetically manipulated. We will combine transcriptome analysis and

metabolite profiling to construct co-expression networks and characterize the JA dependency, level of pleiotropy and evolution for each of the JA signaling networks. The results from this project will help us to systematically understand the role of ecological pleiotropy for the evolution of adaptive traits and how synergisms and antagonisms among environmental stresses shape the adaptation processes in nature.

(55) Linking personality, parasite-induced behavioural manipulation and immunity in two populations of three-spined sticklebacks (*Gasterosteus aculeatus*)

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Many parasite species manipulate behaviors of their hosts to facilitate transmission to the next host. Accordingly, animal behavioral types (personality) might change upon parasite infection. On the other hand, host infection probability might vary with behavioural type and certain personalities might be more prone to infection. We wanted to address these questions and used the infection of three-spined sticklebacks (*Gasterosteus aculeatus*) with the cestode *Schistocephalus solidus* as a model. This parasite makes its stickleback host bolder, to facilitate its transmission to the final host, a fish eating bird. We used sticklebacks from an Icelandic origin with high and a German origin with low *S. solidus* infection pressure. We assessed individual behavioral responses of the sticklebacks in the context of confinement stress, activity, aggression and boldness four times during the course of six months. We exposed the sticklebacks to *S. solidus* halfway through the experiment. After the last observation we assessed basic immune functions.

If the *S. solidus* infection developed, sticklebacks from both origins developed higher boldness. However, sticklebacks from Iceland were generally bolder and got infected less often with *S. solidus* than sticklebacks from the German origin. In fact, about one third of Icelandic sticklebacks even refused to eat copepods, and female Icelandic sticklebacks particularly avoided copepods harboring their sympatric *S. solidus*. Male Icelandic stickleback, which had ingested infected copepods, were more likely to defend the infection if they had high boldness and low aggression scores before the parasite exposure. Thus, for Icelandic male sticklebacks we could predict future probability of becoming infected with *S. solidus* by their behavioral profile.

Our data suggest that expression of behavioral types and susceptibility/resistance to parasite infections might be connected. In the Icelandic population, higher infection success of *S. solidus* in shy individuals might drive selection towards higher boldness.

(56) Pleistocene climate cycling and host plant association shaped the demographic history of the bark beetle *Pityogenes chalcographus*

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The present distribution and genetic structure of organisms were shaped by past climatic oscillations, e.g., during the Pleistocene. During glaciation events survival of many organisms was only possible in glacial refugia. The European spruce bark beetle, *Pityogenes chalcographus*, is an insect with a life cycle closely associated with its main host tree Norway spruce. It is hypothesized that both species shared the same glacial refugia. Postglacial warming led to range expansion and recolonization of Europe, and reestablishment of gene flow via secondary contact.

We assessed the glacial and postglacial history of *P. chalcographus* by studying individuals from a huge part of the beetle's range. We applied ddRADSeq to disentangle the present genetic population structure and to infer glacial and postglacial processes. We confirmed and re-evaluated three glacial refugia in the Italian-Dinaric region, in the Carpathian Mountains and in the Russian plain. Present genetic structure was strongly influenced by secondary contact during warm periods and the insect's reproductive and dispersal behavior. Population structure analyses revealed a high level of gene flow across populations leading to a shallow genetic structure and a low level of population differentiation.

(57) Which waterway did the Iberian amphipod *Echinogammarus berilloni* took to East Westphalia/Germany, and was adaption necessary to establish in this area?

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Aquatic invasions are becoming quite normal in our globalised world, partly equalizing many habitats that had distinct biotic communities before. We are studying one of the rare aquatic invaders from south - west Europe, the amphipod *Echinogammarus berilloni*. This species has been reported in Germany from 1924 on, partly having displaced the native amphipod fauna. The northernmost invasion front of *E. berilloni* is a karstic region, the Paderborn plateau in North Rhine-Westphalia, characterised by seasonal flow intermittency in the mid-stream reaches of the river. We observed the spreading of this amphipod in this area for now more than a decade and have noticed a yearly upstream movement and continuous displacement of the native relatives. The intermittent reaches act as a strong barrier yet was overcome by the invader.

9 years ago, population genetic data of the species with 9 microsatellite loci was compiled from sample sites in this area, revealing that the intermittent stream sections had a strong isolation effect. A recent microsatellite analysis with the same set is currently performed,

to see in how far the genetic structure of this species at these sites altered and to observe if there is upstream migration, if inbreeding is getting higher or if the genetic structure probably shifts by adaption processes. First results, analysed with Reynolds' as well as Nei's genetic distance, revealed that the upstream populations still have a high genetic distance to the downstream sites and that genetic drift or mutation occurred within the 9 years. To proof for adaption pressure that might arise by the factor temperature, as the eurytherm amphipod establishing closer to the colder headwaters, temperature experiments are conducted. Here we test for mortality, oxygen consumption and activity also with specimen from warmer sample sites.

Last, we were interested to unravel the invasion route with the transition zones between the river basins and the propagule pressure of *E. berilloni*. Thus, the current set of sample sites comprise besides the resampling additional sample sites from four drainage basins.

(58) Comparative analysis of genomic repeat content in acridid grasshoppers: phylogenetic similarities and differences

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Large parts of eukaryotic genomes consist of repetitive elements and the repeat content is variable among species and correlates tightly with genome variation. Genome size varies tremendously across species with similar level of cellular and developmental complexity and effects fitness-related traits such as gene expression, metabolic rate and cell and body size. Furthermore, it has also been suggested that rate of genome size evolution is proportional to genome size, with the fastest rates occurring in the largest genomes. This phenomenon has been insufficiently examined in insects.

The highly diverse orthopteran group exhibits genome gigantism amongst the insects. However, it was not known what may contribute to this phenomenon. The recently published *Locusta migratoria* genome revealed that repetitive elements constituted about 60% of the assembled genome, of which DNA transposons and LINE retrotransposons where the most abundant elements.

Recent genomic repeat content analysis of the acridid grasshopper, *Gomphocerus sibiricus*, suggests that satellite DNA dominates (estimated 9-10%) the genome as the largest single repeat class with an estimated genomic repeat content of about 86-89%. This distribution of repeat elements differs substantially from other published distributions. This existence of one predominant class of repeats argues for a recent expansion of this repeat sequence type. However, this pattern does not hold for other acrididae grasshoppers. We investigated 6 acrididae grasshopper species (*Pseudochorthippus parallelus*, *Aeropedellus variegatus*, *Gomphocerippus rufus*, *Chorthippus biguttulus*, *Gomphocerus sibiricus* and *Stauroderus scalaris*) for potential gains and losses of repeat elements. Our preliminary results suggest that estimated repeat content strongly correlates with estimated genome size, with estimated genome content ranging from 79-94%. Here, we provide evidence of satellite DNA to the likely driver of genome expansions in the observed genomic gigantism in specific Acridid grasshoppers.

(59) Demographic perspectives to population dynamics

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Population change and associated evolutionary processes are driven by simple demographic events, the reproduction and survival of individuals. Heterogeneity among individuals in survival and reproduction is not only driven by genetics and the environment, but — often not quantified — stochastic events. In parameterizing population models using data from controlled plant and single cell bacteria experiments. I will show how large amounts of neutral individual heterogeneity can be generated by stochastic events. Such large amounts of neutral variability influence ecological and evolutionary processes by slowing adaptive processes. I will end with discussing open questions how such neutral heterogeneity might have evolved and how it might be maintained.

(60) Metadata modeling in phylogenetic software to increase data reuse and reproducibility

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Phylogenetics, phylogenomics and related fields have become data-intensive due to increasingly cheaper high-throughput sequencing technologies, the digitization of large biological collections or data contributions from citizen science. An increasing number of computationally accessible methods for analyses that produce derived data, like phylogenetic trees, further contribute to the production of large quantities of potentially reusable data. This opens up new opportunities for data-intense studies, but also creates new challenges for cyberinfrastructure and method development such as meaningful and ideally machine-interpretable annotation of published data to allow easy reuse and automated large-scale data collection.

Here we present new functionality of our phylogenetic tree editor, TreeGraph 2, to store, edit and visualize any type of metadata attached to phylogenetic trees or their nodes and branches. TreeGraph 2 has become widely used since its first release in 2008 and offers versatile editing and formatting features in a user-friendly graphical user interface. It now supports the metadata model of NeXML that is based on the Resource Description Framework (RDF) and allows unambiguously describing the relation of metadata to phylogenetic data. The new functionality simplifies necessary metadata annotation of phylogenetic trees to allow their optimal reuse, to document the workflow used to infer them, and to link respective raw data.

A similar extension of the metadata model of our multiple sequence alignment editor PhyDE is currently underway. In combination, PhyDE and TreeGraph 2 provide necessary annotation functionality for all major datatypes of phylogenetics. The new functionality is based on our software libraries JPhyloIO and LibrAlign that exhibit their functionality to third-party applications.

(61) Diversification in Midas cichlid visual system: opsin gene expression divergence is mediated by differential thyroid hormone signaling

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Thyroid hormone (TH) is a messenger molecule of major importance in vertebrates, inducing a cascade of regulatory mechanisms substantially altering gene expression patterns in target cells. One recently proposed target of TH is opsin gene expression in vertebrate's retinae. Many teleosts show an ontogenetic change in the pattern of opsins expression, shifting as development progress from expressing an opsin set that confers maximum sensitivity at short wavelength to a set most sensitive at longer wavelengths. Artificially increasing TH circulating levels in juveniles alters this ontogenetic pattern, upregulating long wavelength sensitive opsins and downregulating the short wavelength sensitive opsins that characterize early timepoints in development. Nicaraguan Midas cichlids (*Amphilophus cf. citrinellus*) have recently (<2000 generations ago) colonized crater lakes from great lakes. These lakes differ drastically in their light conditions, with crater lakes being enriched in short wavelength light compared to great lakes. Midas cichlids inhabiting crater lakes have adaptively diverged from their source populations by having a short wavelength sensitive visual system resembling juveniles from the turbid great lakes. Additionally, crater lake Midas cichlids have lower circulating TH levels than populations from the ancestral great lakes. Thus, we hypothesize that TH might have played a role in the adaptive diversification of the visual system of Nicaraguan Midas cichlids (*Amphilophus cf. citrinellus*). In this study we provide evidence for a TH concentration dependent regulation of opsin gene expression in Midas cichlids. We found that increasing TH levels results in a shift in visual sensitivities toward longer wavelengths. We additionally show that artificially decreasing TH levels alters opsin gene expression resulting with sensitivities shifted toward shorter wavelengths. Our results provide evidence that TH signaling might have facilitated adaptation to the novel light environment in the crater lakes by inducing an ontogenetic shift in development that resulted in a paedomorphic phenotype.

(62) Molecular exaptation: can selective pressure toward increased sulfatase activity lift phosphoesterase activity to a selectable level?

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Adaptation toward new functions often occurs via duplication of an existing protein-coding gene and subsequent accumulation of adaptive mutations in one of the gene copies. *De novo* emergence of a completely novel function in an existing protein is highly unlikely. Therefore the 'new' function is typically already present at low levels in the 'old' protein prior to the gene duplication event. The latter principle requires that the 'new' function can emerge while the 'old' function is initially maintained or decreases only slightly, i.e. the trade-off between the increased activity and decreased specificity for the primary function

is initially low. Recent specificity profiles recorded by us for several existing sulfatases show constant specificity across increasing levels of primary sulfatase activity. The latter suggests there is no trade-off between catalytic performance for the primary sulfatase activity and its specificity toward sulfoesters relative to the secondary phosphoester substrates. As a result, selection pressure for increased sulfoesterase activity could be accompanied by an equal increase in phosphoesterase activity. We are currently testing if we can use this trade-off free molecular exaptation principle to increase phosphoesterase activity of a moderately proficient sulfatase by adapting it toward improved sulfatase activity using laboratory evolution. For this purpose, we have successfully established a lysis-free assay system to screen for increased sulfatase activity using micro-droplet based high-throughput screening technology, resulting in up to 6.3-fold increased sulfatase activity after only one round of laboratory evolution.

(63) Thermo-plasticity of Programmed DNA Elimination in *Paramecium tetraurelia*

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Background: During the biogenesis of somatic nuclei, Internal Eliminated Sequences (IESs) must be efficiently and reproducibly excised via Programmed DNA Elimination (PDE) to safeguard *Paramecium*'s somatic genome integrity and preserve cellular function. To date, considerable efforts have been made to gain insight into the molecular dynamics underlying somatic development in *Paramecium*. These efforts have yielded deep mechanistic knowledge of PDE and its epigenetic regulation. However, much less consideration has been devoted to assessing the influence of environmental conditions on PDE. Understanding PDE's response to environmental changes could reveal a function for this process, which may lie beyond PDE's commonly established role in genome defense.

Purpose: Our aim is to examine the effects of growth temperature on PDE efficiency.

Methods: We allowed clonal *Paramecium tetraurelia* lines to undergo autogamy at three different temperatures, 25°C, 18°C, and 32°C. The somatic nuclei of both parental (25F0) and F1 lines (25F1, 18F1 and 32F1) were isolated and the macronuclear DNA (MAC) subjected to whole genome Illumina-sequencing. IES Retention Scores (IRSS) were computed using ParTIES. Genome-wide analysis of IES retention was performed via statistical comparison of F0-F1 IRSSs.

Results: We find a remarkable increase in the number of loci affected by erroneous IES excision at 18°C and 32°C compared to 25°C. The number of IESs that are significantly retained in somatic genomes rearranged at 18°C and 32°C dramatically increases relative to 25°C; ~12-fold and ~ 17-fold, respectively. An excess of these IESs are epigenetically regulated, thus these alternative splicing events are potentially transmittable to successive sexual generations even in the absence of genetic changes. Finally, hundreds of the IESs that are significantly retained in response to sub-optimal growth temperatures lie in exons, potentially disrupting open reading frames or diversifying protein sequences.

Conclusions: Sub-optimal growth temperatures during autogamy significantly impact the efficiency of PDE in *P. tetraurelia*. The increased levels of alternative DNA splicing may serve to modulate gene expression and/or increase the diversity of proteins encoded by the *Paramecium* genome.

(64) Gene-knockdown of putative seminal fluid proteins in a simultaneously hermaphroditic flatworm

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Seminal fluid proteins (Sfps) are thought to play a key role mediating post-mating sexual selection, by potentially modulating recipients' behavior and physiology in ways that influence reproduction, as well as in sexual conflict. Despite the importance of Sfps for the reproductive physiology and behavior of the ejaculate recipient and the fertilizing ability of the donor, the identification and characterization of seminal fluid proteins has to date focused on just a few animal groups and mainly on species with separate sexes. In an *in situ* hybridization screen we identified 76 transcripts with prostate-gland limited expression as expected for Sfps in the simultaneously hermaphroditic flatworm *Macrostomum lignano*. Here we report RNAi knockdown experiments for 19 seminal fluid candidates to probe the function of this putative seminal fluid proteome, with diverse predicted roles impacting behavior, fertility and competitive fertilization success.

(65) Analysis tools for German plant DNA barcode data

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DNA barcoding allows to identify species using predefined target genes. It is especially useful when samples are degraded, fragmented or consist of hard to identify parts, e. g. larval stages of insects or seeds and roots of plants. The German Barcode of Life (GBOL) project aims to create a database of all plants, animals and fungi in Germany and develop applications of DNA barcoding.

A database-backed web application was developed for GBOL5, the sub-project working on barcoding the approximately 4,800 German land plant species, to allow scientists from all involved research groups to work on the same data and to automate common workflows. Sequence reads can be uploaded and are then automatically assembled to generate barcodes for the four GBOL5 marker genes. A taxonomy-driven quality assessment is then conducted in order to find misidentified or contaminated samples. Various analysis methods allow for statistical testing of biological hypotheses and are directly accessible within the app, including intra- and infraspecific variation, regional differences and an assessment of species boundaries.

(66) Between exonization and exaptation: alternatives in molecular evolution

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Exonization is the acquisition of novel exons by inclusion of mostly non-protein-coding sequences such as intronic inserted transposed elements. Here we present an analysis of more than 150 Alu Short Interspersed Element (SINE) exonizations and describe their gradual contributions to primate gene evolution, including cryptic and major splice variants and constitutive expression. Multi-genome comparisons and transcriptome data from phylo-comparative analyses enabled us to very precisely reconstruct ancient, stepwise events leading to new splice forms of genes. In the relatively young Alu exonizations, reversals to the original splice variant were frequent and indicate cases where selection pressure on alternatives is still less profound. Our study paves the way for future studies on

potential exaptations of alternative exon compositions of genes during gene and species evolution.

(67) Catching retrogene transposition in act: characterization of genomewide retrogene polymorphism landscape in natural populations of the house mouse

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Evolution of new genes can come about by various mechanisms, of which retrogene transpositions are a major factor. While retrogenes have been amply studied in between species comparisons, less attention has been paid to population level polymorphisms, which are the ultimate source of all new adaptations. Taking advantage of the excellent NGS genomic sequencing data resource and well-defined evolutionary history of house mouse populations/subspecies, we developed an efficient computational pipeline to detect retrotransposition event based on next-generation sequencing dataset, and characterized the genome-wide retrogene polymorphism landscape in natural populations of the house mouse with this pipeline. This result would help us to better understand the evolutionary dynamics and functional consequence of retrotransposed genes in their very early population segregating stage before fixation within species.

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