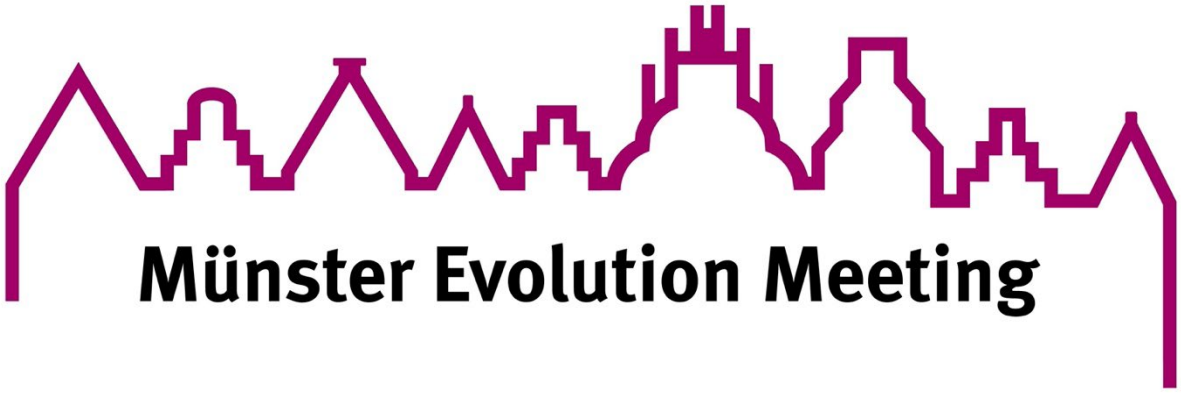

2023

ABSTRACT BOOK

TALKS

Münster Evolution Meeting

13th MARCH, 2023

Münster Evolution Meeting

MEYER, Axel

Time: 14:15 -14:45
Room: Aula

On the origin of species in sympatry - genetics of speciation, adaptations, and homoploid hybrid speciation in crater lake cichlid fishes

The transition from 'well-marked varieties' of a single species into 'well-defined species'—especially in the absence of geographic barriers to gene flow (sympatric speciation)—has puzzled evolutionary biologists ever since Darwin. Gene flow is expected to counteract the buildup of genome-wide differentiation through the evolution of irreversible reproductive barriers (incompatibilities) that complete the process of speciation. Theory predicts that the genetic architecture of divergently selected traits can influence whether sympatric speciation occurs, but empirical tests of this theory are scant because comprehensive data are difficult to collect and synthesize. Within a young species complex of Neotropical cichlid fishes we analyzed genomic divergence among populations and species across several crater lakes in Nicaragua where repeatedly and parallel several species originated in these isolated small lakes. Also, several adaptations such as hypertrophied lips, differences in dentition, coloration and body shapes evolved convergently in theses lakes. By generating a new genome assembly and re-sequencing >500 genomes, we uncovered the repeated genetic architecture of traits, that have been suggested to be important for divergence. Species that differ in monogenic or oligogenic traits that affect ecological performance and/or mate choice show remarkably localized genomic differentiation. By contrast, differentiation among species that have diverged in polygenic traits is genomically widespread and much higher overall, consistent with the evolution of genome-wide barriers to gene flow. Simple trait architectures might not always be conducive to sympatric speciation, but polygenic architectures can promote rapid speciation in sympatry. We also discovered a case of homoploid hybrid speciation (i.e., hybrid speciation without a change in ploidy). Only few accepted empirical examples of homoploid hybrid speciation exist, and in only one previous case was it convincingly shown that this process occurred in complete sympatry. Here, we report an instance of sympatric homoploid hybrid speciation in cichlid fishes in Crater Lake Xiloá. The hybrid lineage, albeit at an early stage of speciation, has genomically and phenotypically diverged from both of its two parental species. Together with a distinct stable isotope signature this suggests that this hybrid lineages occupies a different trophic niche compared to the other sympatric Midas cichlid species.

Münster Evolution Meeting

MAZZONI, Camila

Time: 14:45 -15:15
Room: Aula

Evolution at a small pace: what has Genomics already revealed about sea turtles and their highly conserved genomes?

Turtle genomes have gone through a deceleration of evolutionary rates. Among them, sea turtles (Chelonioidea) are the only group to have fully adapted to the marine environment approximately 100 million years ago. Despite their deep phylogenetic splits, all seven extant sea turtle species present the same chromosome number (2n=56) and high levels of conservation and collinearity in their genomes, placing sea turtles as a particularly interesting and potentially unique model of evolution. The genome conservation is such that a few species with over 30 million years of divergence still undergo hybridization and introgression. The first comparative analysis of reference quality genomes between the two extant sea turtle families revealed that most of the structural differences are often associated with the presence of multicopy and fast evolving olfactory receptors and immune gene families. Chromosome-wide analyses showed that the smallest microchromosomes accumulate higher levels of interspecific divergence and intraspecific genetic diversity in association with a higher accumulation of genes. In order to further understand the mechanisms of genome evolution and environment adaptation, we are in the process of assembling and analysing the reference quality, chromosome-level and almost completely phased genomes of the remaining five sea turtle species. Unveiling the genomic basis for their anatomical, physiological and ecological differences and the process of genetic variation associated with those should help us understand the potential of recovery for the highly pressured populations of sea turtles across the globe. The genomic variation already revealed very different demographic histories between species, and the combination of functional analysis and demographic predictions is an important next step to inform how conservation efforts may support the survival of sea turtles in a changing world.

Münster Evolution Meeting

CARRANZA PINEDO, Victor Rafael

Time: 15:20 -15:35
Room: Aula (session 1)

The fitness effects of animals' emotions: the case of affective dominance

It has been proposed that discrete emotion categories (e.g., sadness, fear, joy, etc.) have been selected by evolutionary processes because they trigger adaptive behaviors that help organisms successfully deal with recurrent life tasks or situations (e.g., fighting, falling in love, responding to the death of family members, etc.) (Plutchik 1980, Tooby and Cosmides 1980). However, it is unclear whether emotions can, in turn, shape the natural selection pressures working on organisms during their development. In this presentation, I propose to address this question by shifting from discrete to dimensional characterizations of emotional states (i.e., by classifying emotions in terms of valence, arousal, and dominance, see Mehrabian and Russell 1974) and from a cognitive to a situated perspective (e.g, by characterizing emotions as involving a skill-full, goal-oriented engagement with the environment, see Griffiths and Scarantino 2005). As a case study, I will focus on the dominance dimension, which refers to the extent to which organisms feel behaviorally constrained with respect to other organisms or the environment, and which clearly illustrates the extent to which some emotions are scaffolded by the natural context in which they occur. Then, I will briefly discuss the potential effects of the dominance dimension on i) dominance hierarchies and ii) landscapes of fear, and argue that these phenomena may constitute evidence in favour of the hypothesis that emotions are not only selected but constitute causal starting points in evolutionary trajectories.

ZEMELLA, Alex

Time: 15:35 -15:50
Room: Aula (session 1)

Gene regulation of aggression and courtship in a three'morph mating shorebird

The ruff (*Calidris pugnax*) is a migratory shorebird that exhibits distinct morphs known as Independent, Satellite, and Faeder, which are genetically determined by a 4.5 Mb autosomal inversion harbouring approximately 100 genes. During the breeding season, these morphs display alternative reproductive strategies and differ in circulating androgens concentrations and aggression levels. To investigate the molecular mechanisms underlying these differences, we applied RNA-Seq methods to quantify gene expression profiles, measure allelic imbalance in the inversion genes, and identify networks of genes showing similar co-expression patterns in four body tissues involved in steroidogenesis and nine brain areas. Through this approach, the HSD17B2 gene, located within the inversion, has been identified as a key mediator of the aforementioned differences. The gene encodes the enzyme that converts testosterone to androstenedione, highlighting the role of steroid hormones in regulating aggression and courtship in this species. Steroid hormones can bind to different types of receptors within cells, and each type of receptor can have different, complex effects on gene expression by influencing the activity of other transcription factors and co-activators or co-repressors. In the central nervous system, brain-derived steroid hormones can operate as behavioural neuromodulators by binding to receptors on the surface of neurons and altering their electrical activity, leading to changes in neural signaling and behaviour. Our findings indicate a correlation between fine-scale regulation of HSD17B2 expression in the brain and decreased levels of dopamine, serotonin, and GABA receptors, as well as a lower expression of genes associated with aggressive and mating behaviour. Moreover, in the morphs carrying the autosomal inversion polymorphism, inversion genes consistently feature in our results and the majority of them are under cis-regulation. These findings provide insight into the genetic mechanisms underlying the evolution of alternative reproductive strategies in shorebirds.

Münster Evolution Meeting

METZGER, Lukas

Time: 15:20 -15:35
Room: S1 (session 2: SPP- RAPID ADAPTATION SYMPOSIUM)

Inference of host-parasite interaction matrices using genome-wide polymorphism data

Coevolution is driven by genotype x genotype (G x G) interactions between hosts and their symbionts. Recent developments in joint genome wide association analysis of host and pathogen polymorphism data greatly advanced the identification of the genes underlying these interactions. However, deciphering the specific form and magnitude of these GxG interactions has proven difficult and currently relies on experimental approaches. Based on a theoretical model of host-parasite interactions, we first derive four statistics to complement joint genome wide association studies. We demonstrate the efficiency of these indices in discriminating various GxG interaction matrices in simulated data sets by numerical estimation integrated into an ad hoc Approximate Bayesian Computation method. The indices are based on extracting relevant information from polymorphism data of randomly sampled uninfected hosts and randomly sampled infected host and their respective parasite strains. Second, we apply our method to a SNP data set of 451 European humans and their infecting HCV virus strains supplemented by polymorphism data from the 1000 genomes project. Our model based approach recaptures ca. 180 significant interactions previously found. By applying our inference framework, we show, that these significant interactions between MHC-genes and HCV genes seem not to follow matching-alleles interactions but rather gene-for-gene interactions. We speculate that this relationship is due to an only recent expansion of HCV population in Europe and the low prevalence of HCV in the human population.

ELDON, Bjarki

Time: 15:35 -15:50
Room: S1 (session 2: SPP- RAPID ADAPTATION SYMPOSIUM)

Sweepstakes reproduction facilitates rapid adaptation

Adaptation enables natural populations to survive in a changing environment. Understanding the mechanics of adaptation is therefore crucial for learning about the evolution and ecology of natural populations, and for better conservation and management of natural resources such as fish stocks. Here, we focus on the impact of random sweepstakes on selection in highly fecund haploid and diploid populations partitioned into two genetic types, with one type conferring selective advantage. For the diploid populations we incorporate various dominance mechanisms. Furthermore, we assume that the populations may experience recurrent bottlenecks. In random sweepstakes the distribution of individual recruitment success is highly skewed, resulting in a huge variance in the number of offspring contributed by the individuals present in any given generation. Using extensive computer simulations, we investigate the joint effects of random sweepstakes, recurrent bottlenecks, and dominance mechanisms on selection. In our framework, bottlenecks allow random sweepstakes to have an effect on the time to fixation, and in diploid populations the effect of random sweepstakes depends on the dominance mechanism. We also analyze selective sweepstakes which are well approximated by recurrent selective sweeps of strongly beneficial allelic types arising by mutation. We demonstrate that both types of sweepstakes reproduction may facilitate rapid adaptation (as defined based on the average time to fixation of a type conferring selective advantage conditioned on fixation of the type). However, whether random sweepstakes cause rapid adaptation depends also on their interactions with environmental factors (such as bottlenecks) and genetic mechanisms (e.g. dominance mechanisms). Finally, we review a case study (Arnason et al, 2023; eLife, to appear) in which a model of recurrent selective sweeps is shown to essentially explain population genomic data of the highly fecund Atlantic cod, with implications for studying the evolution and ecology of highly fecund populations across domains of life.

REICH, Marlis

Time: 16:20 -16:50
Room: Aula

The role of marine fungi in the oceanic carbon turnover

The ocean plays a central role in the long-term storage of carbon. The photosynthetic activity of phytoplankton alone already binds 50 Gt of atmospheric carbon in the form of biomass. Whether this carbon is respired, enters the marine food chain or is stored long-term depends on the heterotrophic microbial degradation activities within the microbial loop. The organismal diversity herein is large and leads to different forms of organismal interaction. Although marine fungi are ubiquitously represented in pelagic microbial communities, their importance for oceanic carbon turnover is still largely unexplored. Whether and how fungi interact with other organisms in the microbial loop and food webs influences the efficiency of marine carbon conversion. Therefore, important variables and mechanisms that influence fungal carbon turnover need to be identified including cell numbers, biomass, interaction partners and degradation capacities.
In two consecutive studies we linked the classification of mycoplankton communities sampled from a marine time series station in the North Sea with tag sequencing and CARD-FISH counting, and modelled the interactions of fungi with other plankton groups via complex network analyses. In a large-scale isolation campaign, individual members of the fungal community were isolated and their degradation capacity was investigated in targeted growth experiments on different organic food sources. Genome analyses of individual model organisms accompanied these experiments. Both, fungal cell numbers and biomass, reached ecologically relevant values. In the case of the parasitic fungi, the results suggest that they form a shortcut within the food chain by passing the carbon obtained from the decomposition of phytoplankton directly to the zooplankton without involving the microbial community. In terms of saprotrophic fungi, the fungal cell number in- crease over the phytoplankton bloom exceeded that of bacteria. The accumulation of ecologically relevant biomass is an indication that fungi are competitive with other microbes and metabolise carbon substantially. Subsequent growth experiments and genomic data from isolates showed that fungi are not limited in their degradation capacity relative to the most prominent pelagic organic sources and that the fungal niche is probably defined much more by organismal interactions than by the availability of carbon sources.

Münster Evolution Meeting

MENZEL, Florian

Time: 17:00 -17:15
Room: Aula (session 1)

Cuticular hydrocarbons in ants: Do communication and waterproofing interfere with each other?

Organismal traits may experience conflicting selection pressures if they fulfil different functions simultaneously. This can be ameliorated by functional separation between elements of the trait. An important multifunctional trait in insects is the cuticular hydrocarbon (CHCs) layer. CHCs protect against desiccation and serve as signals for communication and (in social insects) nestmate recognition. To maintain their waterproofing function, insects change the physical properties of the CHC layer by adjusting the chemical CHC composition to current temperatures. However, these changes might affect their information content. Here, we studied how acclimatory CHC changes affect nestmate recognition in two species of *Lasius* (Formicidae). We analysed behaviour towards same and differently acclimated conspecifics, and determined which CHCs were related to acclimatory changes, colony differences, and inter-individual aggression. Indeed, differential acclimation increased aggression among former nestmates. Interestingly, few compounds sufficed to explain inter-individual aggression, suggesting that ants use only some CHCs for nestmate recognition. The contribution of individual CHCs to colony differences and to acclimatory changes were negatively correlated, especially in *Lasius platythorax* but less so in *L. niger*. Several CHC classes were involved in both functions. We conclude that the two functions are somewhat separated, but cannot be optimised without affecting each other. The degree of functional separation differs between species, and might be linked to the need to separate functions, which itself may depend on species-specific life-history traits such as polydomy or the microclimatic variability.

FELDMEYER, Barbara

Time: 17:15 -17:30
Room: Aula (session 1)

Species-specific phenotypic responses after acclimation to different temperature regimes

Climate is one of the most important abiotic variables to which organisms must adapt. Ectothermic organisms in particular are highly dependent on ambient temperature as everything from development to survival is affected. Many ectothermic organisms, especially insects, are highly susceptible to desiccation due to their low surface-to-volume ratio. Insects carry cuticular hydrocarbons (CHCs) on their cuticle as desiccation barrier. Here we study the acclimation response of three ant species, occupying different temperature niches, in two constant and one fluctuating temperature treatments. We examine changes in the CHC profile, differences in gene expression, and measured their survival probability under drought. The results were similar for two species. Acclimation to low temperature led to significantly lower survival probability at high temperature than acclimation at higher and also fluctuating temperature. The similarity between high and fluctuating temperature was also reflected in the number of differentially expressed genes. In the third species, there were neither large differences in gene expression nor in survival rate. The chain length of n-alkanes as well as the CHC quantity showed contrasting patterns between the two species with similar survival and similar numbers of differentially expressed genes and the third species. Our results thus indicate that adaptation to different niches provides limited information about the acclimation potential of species, and that there are strong species-specific patterns.

BÜLLESBACH, Jan

Time: 17:30 -17:45
Room: Aula (session 1)

Genetic and genomic architecture of species-specific cuticular hydrocarbon variation in the jewel wasp *Nasonia*

Cuticular hydrocarbon (CHC) profiles play two fundamental roles in insects: protection against desiccation and chemical signaling. This pivotal dual functionality renders this complex trait essential for insect survival, diversity, reproductive success, and adaptation. Curiously though, most research on the biosynthesis and genetics of CHCs has been restricted to the Dipteran model species *Drosophila melanogaster*. However, how exactly this knowledge can be transferred to other insect taxa, for instance the economically and ecologically important Hymenoptera, remains poorly understood. Focusing on *Nasonia*, a genus of parasitoid jewel wasps suitable as a Hymenopteran model organism for genomic research, we investigated the genetics governing CHC biosynthesis and variation. Taking advantage of their haplo-diploid sex determination and cross-species fertility, we mapped quantitative trait loci (QTL) for CHC variation in recombinant F2 hybrid males from interspecific crosses between different *Nasonia* species. We complemented the QTL mapping with identifying and localizing orthologs of *Drosophila* CHC biosynthesis genes in the *Nasonia* genome. We discovered multiple genomic "hotspots" governing CHC variation between the different *Nasonia* species. Intriguingly, these hotspots coincide spatially with the genomic location of various CHC biosynthesis candidate genes. Our results particularly shed light on the so far little-known genetic underpinnings of the variation in methyl-branched alkanes, the most wide-spread and diverse CHC compound class in our investigated taxa. These findings also have considerable implications on how these fundamental complex traits can be governed, produced and maintained in Hymenoptera in general.

Münster Evolution Meeting

SUN, Weizhao

Time: 17:45 -18:00
Room: Aula (session 1)

Genetic and chemical basis of species-specific sexual communication in the parasitoid wasp genus *Nasonia*

The evolution and maintenance of intraspecific sexual signaling is essential for successful reproduction. In insects, sexual signals are often based on semiochemicals, which commonly exibit high species specificity. However, our understanding of how exactly sexual signals are chemically encoded, as well as the genetic basis that generate and maintain species-specific chemical patterns is comparatively limited. To bridge those knowledge gaps, we utilized the parasitoid wasp genus *Nasonia* as model system, in which female cuticular hydrocarbons (CHCs) can function as species-specific sexual cues, eliciting preference and attraction in conspecific males. Firstly, we performed a quantitative trait locus (QTL) study on two closely related endemic *Nasonia* species, where males of one species exibit a strong preference towards conspecific female CHC profiles. Exploiting the haplo-diploid sex determination of *Nasonia*, we generated haploid males with recombinant genotypes, which were then backcrossed to both parental species to produce diploid female offspring with chimeric CHC phenotypes. By further associating the chimeric CHC profiles of the female offspring from the backcrosses with species-specific mate preference, we narrowed down several single methyl-branched alkane compounds either positively or negatively correlated to higher courtship frequencies from males. Secondly, we characterized a fatty acid synthase gene in a cosmopolitan *Nasonia* species, which systematically up- and down-regulates specific methyl- branching components in female CHC profiles, which we discovered to be involved in female sexual attractiveness. These findings strongly suggest a coding mechanism for sexual attractiveness mediated by methyl-branched alkanes in *Nasonia*, among which several specific single compounds are potentially responsible for the species-specific mate preference.

Münster Evolution Meeting

ROTH, Olivia

Time: 17:00 -17:15
Room: S1 (session 2: SPP- RAPID ADAPTATION SYMPOSIUM)

Genome rearrangements, male pregnancy, immunological tolerance & the microbiome– the curious case of the syngnathid immune system

Evolutionary innovations are major drivers of evolutionary success as they create new ecological opportunities. The syngnathid fish group (seahorses, pipefishes and seadragons) is a fascinating lineage associated with an array of evolutionary innovations that include diverse morphologies and their unique male pregnancy. These innovations also extend to their immune systems, with a range of intriguing immunological characteristics and genomic rearrangements, which pose questions regarding their evolutionary history and immune strategies. The functional loss of the major histocompatibility complex class II pathway (MHC II) in the Syngnathus genus and related pathway components in the seahorse (Hippocampus) were two discoveries that initially piqued interest. These sparked discussions concerning immune capabilities, possible facilitative roles in advanced male pregnancy evolution through means of evoking immunological tolerance, as well as a general re-evaluation of how we interpret vertebrate immunological plasticity. With experimental approaches we have further clarified the efficacy of the syngnathid immune response and shed light on innovations and specificities regarding the pathways in play during pregnancy as well as the role of immunological inheritance and vertical microbial transfer.

Münster Evolution Meeting

WENDLING, Carolin

Time: 17:15 -17:30
Room: S1 (session 2: SPP- RAPID ADAPTATION SYMPOSIUM)

Conflicting selection pressures and social benefits maintain costly prophages in bacterial populations

Prophages, viral sequences integrated into bacterial genomes come, like plasmids, with a multitude of fitness costs and benefits for their host bacterium. However, in contrast to plasmids, prophages can kill their host. Bacteria can ameliorate this risk through prophage inactivation or prophages loss. Why then are active prophages present in as much as 83% of sequenced bacterial genomes? To understand the evolutionary forces that maintain prophages we combined experimental evolution and genomics with stochastic modelling. We found that prophage maintenance and loss is determined by environmental conditions that amplify the net fitness effect of a prophage. Prophages will be lost quickly from a population if the environment purely selects against it. This loss occurs through environment-specific sequences of selective sweeps, which can prolong prophage maintenance in the presence of conflicting selection pressures. If prophage costs outweigh prophage benefits, prophage encoded social benefits can additionally maintain prophages at low frequencies within a population. That is because their gene product can protect their phage-free kin that are likely to emerge as cheaters if selection against prophages is high. Our model suggests that the evolutionary trajectories behind prophage loss and maintenance are largely driven by environmental selection pressures rather than mutation rate Given that bacteria are constantly surrounded by prophages and exposed to changing environmental conditions, our data have important implications for our understanding of bacterial evolution.

KRAEMER, Ute

Time: 17:30 -17:45
Room: S1 (session 2: SPP- RAPID ADAPTATION SYMPOSIUM)

Introgression of a complex extreme physiological trait across a ploidy barrier?

The outcrossing stoloniferous perennial *Arabidopsis halleri* is a metal hyperaccumulator species. Accordingly, zinc and cadmium concentrations in above-ground organs can be above 3,000 µg g-1 and 100 µg g-1 leaf dry biomass, respectively, in the natural habitat, that is more than an order of magnitude above critical toxicity thresholds of ordinary plants. Metal hyperaccumulation is known in more than 700 plant species, it requires metal hypertolerance, and it is thought to act as an elemental defense against biotic stress. Although the majority of *A. halleri* populations are found on non-contaminated soils, *A. halleri* appears to have repeatedly colonized calamine metalliferous soils containing toxic levels of the heavy metals zinc, cadmium and lead. The traits of metal hyperaccumulation and metal hypertolerance are unique to *A. halleri* among a small group of species, including also *Arabidopsis arenosa*, in the sister clade of the genetic model plant *Arabidopsis thaliana*, from which it diverged between 10 and 5 mio. years ago. In a large field survey, we occasionally observed *A. halleri* and *A. arenosa* plants together at non-metalliferous and also at metalliferous sites. At a subset of these metalliferous sites, the individuals of both species grew in metalliferous soil patches. In experiments under controlled conditions, we demonstrated elevated heavy metal tolerance in both *A. halleri* and *A. arenosa* collected at metalliferous sites, when compared to plants originating from non-metalliferous sites. We also conducted genome scans based on short read genome re-sequencing data, which provided evidence for convergent evolution at some loci (1). Next, we hypothesized that there may have been introgression of metal tolerance and possibly even hyperaccumulation loci from *A. halleri* into *A. arenosa* at metalliferous sites. We confirmed that all *A. halleri* were diploid and all *A. arenosa* were tetraploid at the sites under investigation. We observed metal hyperaccumulation in a subset of *A. arenosa* populations from metalliferous soils. Genome scans for introgressions and selection, as well as analyses of gene copy number were consistent with our hypothesis and identified overlapping sets of candidate introgressed metal homeostasis genes in *A. arenosa* populations at metalliferous sites (2). Using transcriptomics we observed *A. halleri*-like expression patterns for these genes in an *A. arenosa* population from a metalliferous soil, whereas expression patterns were *A. thaliana*-like in an *A. arenosa* population originating from a non-metalliferous soil (3). Our data are consistent with the hypothesis of introgression of the metal hyperaccumulator syndrome from *A. halleri* into *A. arenosa* across a ploidy reproductive barrier and also with selection for metal hyperaccumulation on metalliferous soils. The results will be discussed and examined in the light of hypotheses on the ecological role of metal hyperaccumulation in plants.

(**1**) Preite et al. (2019) Convergent evolution in *Arabidopsis halleri* and *Arabidopsis arenosa* on calamine metalliferous soils. *Phil Trans R Soc B* **374**: 20180243.
(**2**) Hanikenne et al. (2008) Evolution of metal hyperaccumulation required *cis*-regulatory changes and copy number expansion of *HMA4*. *Nature* **453**: 391-4.
(**3**) Talke et al. (2006) Zinc-Dependent Global Transcriptional Control, Transcriptional Deregulation, and Higher Gene Copy Number for Genes in Metal Homeostasis of the Hyperaccumulator *Arabidopsis halleri*. *Plant Physiol* **142**: 148-167.

Münster Evolution Meeting

KUSCH, Stefan

Time: 17:45 -18:00
Room: S1 (session 2: SPP- RAPID ADAPTATION SYMPOSIUM)

Adaptive genome evolution of the cereal powdery mildew fungi

The cereal powdery mildews (*Blumeria* spp. of the family Erysiphaceae) are globally occurring fungal pathogens of grasses and cereals and pose a constant threat for agriculture. *Blumeria* species infect grasses and cereals in a host-specific manner. Ubiquitously distributed transposable elements make up >75% of the genomes of the cereal powdery mildews, which can be a source of genetic variation and genome instability. We study if and how *Blumeria* regulates and repurposes transposable elements to rapidly overcome host resistance. We found transcriptional activity of transposable elements in the barley powdery mildew pathogen *B. hordei* at specific stages of infection, particularly during early host cell penetration and haustoria establishment. Epigenetic profiling in conidia revealed increased 5mC methylated DNA levels in retrotransposons, while small RNA sequencing of isolated mycelia and haustoria indicated accumulation of phasiRNAs in >1,500 retrotransposon loci, suggesting dynamic control of transposon expression through epigenetic mechanisms and RNA interference. We further discovered long spliced antisense RNAs (antisense lncRNAs) at loci of transposon replication genes. These transposon antisense lncRNAs exhibit time point-dependent expression patterns as well as distinct co-expression patterns with transposons, indicative of both positive and negative regulation of transposons by antisense lncRNAs. Our findings indicate that the barley powdery mildew pathogen dynamically regulates its abundant transposable elements via epigenetic mechanisms, RNA interference, and antisense lncRNAs. Antisense lncRNAs could be a mechanism to repurpose transposable elements and give rise to novel genes. Thus, transposable elements are the likely key drivers of adaptive evolution in cereal powdery mildew fungi.

Münster Evolution Meeting

14th MARCH, 2023

HAUG, Joachim

Time: 09:00 -09:30
Room: Aula

The evolution of developmental patterns – trying to understand ’metamorphosis’, ’larva’ and ’indirect development’

Evolution can act on ontogenetic sequences. In fact, it has been hypothesised that changes in developmental timing represent a major source for evolutionary novelties. In evolutionary terms, such changes of ontogenetic sequences should be subtle, accumulating over many generations. On the contrary, the descriptive tools for addressing different patterns related to ontogeny are strongly typological and coarse. Additionally, many different terms are often treated as coupled to each other, among these the groups of terms ‘larvae-metamorphosis-indirect development’ on the one hand and ‘juveniles-gradual-direct development’ on the other hand. While this seems deeply rooted in many disciplines, a strict evolutionary frame easily reveals that: 1) there is no such coupling, hence many of these aspects of an ontogeny are in fact independent of each other, and 2) not in all fields of biology these aspects are based on the same criteria. I aim at presenting an evolutionary framework for understanding what ‘metamorphosis’, ‘larva’ and ‘indirect development’ could mean and how they could be identified. I use examples from the group Euarthropoda, especially various lineages of crustaceans including the hyperdiverse group Insecta. Representatives of Euarthropoda have the advantage that they grow by moulting and hence have pseudo-discrete steps in their ontogeny, providing an easy to grasp framework. It is therefore more easily possible to also include fossil data into such evolutionary analyses.

Münster Evolution Meeting

BARTON, Nicholas

Time: 09:30 -10:00
Room: Aula

Genetic analysis of a flower colour hybrid zone in snapdragons

The snapdragon *Antirrhinum majus* includes subspecies that differ in flower colour. In joint work with David Field (Univ. of Vienna) and Enrico Coen (John Innes Institute, Norwich), we have made an intensive study of a narrow hybrid zone that separates yellow and magenta flowers. Pooled sequence data shows that selection likely acts on just a few genes involved with flower colour, and prevents gene flow only across a very small region of genome. Sharp clines at flower colour loci allow us to estimate selection and gene flow, whilst a pedigree gives us direct estimates of dispersal and fitness. This study shows how a variety of techniques can be combined to understand a striking natural phenomenon.

Münster Evolution Meeting

REINHOLD, Klaus

Time: 10:05 -10:20
Room: Aula

Evolution of individual variation in a competitive trait: a theoretical analysis

Most theoretical studies on the evolution of competitive traits investigate the evolution of binary polymorphisms in traits, yet most trait variation in wild populations is continuous. To fill this gap, we examined the effects of resource distributions on the maintenance of continuous variation of costly competitive traits. Specifically, the shape of the frequency distribution of resource quality, as well as the ratio between the best and the worst used resources could affect qualitative changes in trait evolution and were thus varied. We used individual-based evolutionary models to test conditions that favour stable maintenance of variation and cause temporal fluctuations in trait values. This approach, inspired by contrasting outcomes of previous studies, clearly showed a decisive role of resource distributions. Under some extreme conditions, populations evolved to be uniform either for the absence of competitive traits or the evolution of strong investments into competitive traits. Some distributions led to strong temporal fluctuations on competitive trait values, whereas other distributions led to the maintenance of huge variation in competitive traits together with temporally stable trait values. Our results thus allow to predict how variation in resource distributions can explain some of the variation found in previous theoretical studies.

Münster Evolution Meeting

STEINER, Ulrich

Time: 10:20 -10:35
Room: Aula

Evolution and maintenance of individual heterogeneity

Much interest in evolutionary biology is given to understand genetic and environmental variation to explain heterogeneity among individuals, as such heterogeneity in functional traits and fitness components is what selection acts upon. Evolutionary theories predict that selection in constant environments acts against such heterogeneity. But observations reveal substantial non-genetic and also non-environmental variability in phenotypes. I examine whether there is a relationship between selection pressure and phenotypic variability by analysing structured population models based on data from a large and diverse set of species. The findings suggest that non-genetic, non- environmental variation is in general neither truly neutral, selected for, or selected against. Much variation among species and populations within species is found, with mean patterns suggesting nearly neutral evolution of life course variability. Populations that show greater diversity of life courses do not show, in general, increased or decreased population growth rates. Our analysis suggests we are only at the beginning in understanding the evolution and maintenance of non-genetic non environmental variation, even though such variation has profound influence on evolutionary processes.

Münster Evolution Meeting

WANG, Yangzi

Time: 10:05 -10:20
Room: S1 (session 2)

Population genomic insights into the evolution of facultative asexuality in plants

Many organisms, particularly plants, can reproduce sexually and asexually but vary in frequency. As variations in the mating system profoundly affect fitness and genomic diversity, evolutionary changes to asexual reproduction can also be subject to natural selection. However, the genomic basis underlying the evolution of asexuality remains largely unclear. Here, by analyzing 228 genomes of *Spirodela polyrhiza*, a facultative asexual plant, we show that while the genomic diversity in this plant is very low, it varies among populations. The variations of genomic diversity among populations were jointly determined by both demographic history and frequency of asexuality, which is associated with structural variations of MADS-box genes. The genome-wide scan revealed that candidate genes involved in female gametogenesis and embryogenesis were under positive selection, consistent with the observed facultative asexuality in this plant. Together, these results indicate novel insights into the evolution of the mating system in plants and suggest that natural selection can act on the mating system, which in turn alters the levels of genetic diversity.

STIFT, Marc

Time: 10:20 -10:35
Room: S1 (session 2)

Breakdown of self-incompatibility caused by functional disruption of a specific S-allele by a modifier unlinked to the S-locus

Self-incompatibility is a widespread adaptation to avoid self-fertilization in plants. It has a genetic basis with the so-called S-locus mediating recognition of self-pollen. Despite the advantages of out-crossing, breakdown of self-incompatibility and transition to selfing is among the most frequent evolutionary transitions. Disruptive mutations of S-locus alleles have been inferred as the likely genetic basis of the loss of self-incompatibility in several systems (including the model Arabidopsis thaliana). Here, we tested whether an alternative mechanism that could explain the breakdown of self-incompatibility in six selfing populations of the otherwise self-incompatible North American *Arabidopsis lyrata*. In this species, selfing populations consist of either S19S19 or S1S1 S-locus homozygotes. We tested whether this association is due to a functional link of these S-alleles and self-compatibility, and subsequently phenotyping and genotyping the progeny. We found this was the case. We then further tested whether this functional link was due to S-locus mutations, or may be due to an alternative mechanism. We found that cross-progeny were self-compatible if they combined S19 from the self-compatible cross-partner with recessive S1 or S3 from the self-incompatible cross-partner, but self-incompatible with dominant S-alleles. Thus, functional disruption of S19 could both be caused by a modifier or mutation causes self-compatibility. Cross- progeny combining S1 from the self-compatible cross-partner with S1 from the self-incompatible cross-partner were self-compatible, but self-incompatible with any other S-alleles. Because S1S1 homozygotes in outcrossing populations are self-incompatible, mutation of S1 cannot explain self- compatibility in our S1S1 cross-progeny. This supports the hypothesis that a modifier unlinked to the S-locus causes self-compatibility by functionally disrupting S1. Our data represent the first conclusive evidence for breakdown of self-incompatibility not caused by disruptive mutations at the S-locus.

HEIDE, Michael

Time: 11:00 -11:30
Room: Aula

Functional analysis of the role of primate-specific genes during neocortex development and evolution

The neocortex is a fascinating brain structure, as it is the seat of mammalian, and notably primate, higher cognitive abilities. In the primate lineage, different neocortex morphology, in form of size and folding differences, has evolved. The development of the neocortex, and particularly of the different neocortex morphology, depends primarily on the precise regulation of the activity and behavior of cortical neural stem and progenitor cells (cNPCs), a regulation that is mediated by genes that are specifically expressed in these cells. Previously, we identified 50 of such genes, which are specific to primates. The study of the function of these genes in primate brains has been challenging due to technical and ethical reasons. However, the establishment of the brain organoid technology allows to study brain development of traditional primate models (like rhesus macaque and common marmoset) as well as of previously experimentally inaccessible primate species (like great apes), in an ethically justifiable and less technically demanding system. In this talk, I will present a fast and cost-efficient way to genetically modify cell populations within the ventricle-like structures of primate cerebral organoids, a subtype of brain organoids. Our method combines a modified protocol for the reliable generation of cerebral organoids from human-, chimpanzee-, rhesus macaque- and common marmoset-derived induced pluripotent stem cells (iPSCs) with a microinjection and electroporation approach. Moreover, I will provide an example of how this system can be used to study primate neocortex development and evolution.

Münster Evolution Meeting

LEE, Jeong-Eun

Time: 11:35 -11:50
Room: Aula

Human ZEB2 orchestrates a network of genes with stronger contribution to neuronal development than non-human primate ZEB2

Humans differ from other primate species in many phenotypic traits. However, the protein sequences of humans and other primates are nearly identical, hence, it is rational to search for causes of the human-specific traits at other levels, e.g. transcriptional regulation. Transcription factors (TFs) form a complex gene regulatory network to regulate the gene expression pattern. Amongst TFs, ZEB2 has been suggested to play a role in human brain evolution as it is important in neuronal development and is both more highly expressed and more extensively connected with other TFs in the human compared to chimpanzee brain. Given the high conservation of the ZEB2 protein, we asked whether target genes of ZEB2 and their network might have changed on the human lineage. Our comparison of genome-wide expression patterns of human, chimpanzee, and orangutans wild-type B-lymphocytes and B-lymphocytes of the same species with ZEB2 knockdown, suggested evolutionary differences in ZEB2 target genes related to neuronal development. Additionally, our analysis of two public datasets (RNA-seq & scRNA-seq) of developing neurons of humans and other primates reveals human - specifically correlated genes of ZEB2, providing us insight into the network of ZEB2 and its target genes. Our major findings demonstrate that human ZEB2 is more associated with axonogenesis and neuronal development, independent of cell types, while ZEB2 of non-human primates is more related to gene expression processes, such as mRNA processing. These results provide insights into evolutionary differences in ZEB2 functions in primate species and suggest ZEB2 as a crucial transcription factor for human brain evolution.

Münster Evolution Meeting

FIC, Malgorzata

Time: 11:50 -12:05
Room: Aula (session 1)

Collective beliefs and trust in structured populations

Collective acceptance of narratives can catalyse cooperation in a population of selfish individuals. This effect is present even when the stories and the ensuing cultural narrative that constitute the belief lack any moralising aspect. An example of such a story is the Mâori myth of Rangi and Papa or the Slavic story of Kikimora. Such a narrative catalyst frequently involves a complex system of stories. Hence, it is unlikely to appear in society spontaneously in the same way as actions can change within a generation. Consequently, actions and beliefs can spread at different rates within a population. Besides the process itself, we consider the structure of human populations explicitly. Social and cultural identities often bias the network of interactions. Hence, we further develop this model by applying the setup assuming a heterogeneous group size and structured population. The person perpetuating a belief might have different degree of connectedness. We aim to understand the speed at which trust builds in a network when the myth originator has low or high connectedness. In this work, we explore the probability, time and dynamics of the spread of trust and beliefs on specific network structures such as a random Erdös and Rényi network, a scale-free Barabási- Albert network and a small world Watts Strogatz network. Comparing these properties across various network topologies allows us to disentangle the effect of structure, group size diversity and the evolutionary dynamics itself on the evolution of trust and belief.

Münster Evolution Meeting

HUYLMANS, Ann Kathrin

Time: 11:35 -11:50
Room: S1 (session 2)

Evolution of sex determination systems and consequences on gene regulation in non-model organisms

Sex determination systems have evolved multiple times independently across the tree of life and there is a huge diversity of both genetic and non-genetic systems. However, almost all traditional model-organisms used in biology have genetic sex determination via XY sex chromosomes. While we know quite a bit about this mode of sex determination and associated consequences on gene regulation, data on non-model organisms beyond a pure description of the sex determination systems is scarce. In addition, how and why sex chromosome systems turn over very fast in some group while they are very stable in others is still an open question.
We study genomic and gene regulatory aspects associated with reproduction and how the genome can be so plastic as to generate vastly different phenotypes such as males and females or switch between sexual and asexual reproduction. We can show that gene regulatory effects of sex chromosome evolution such as the evolution of dosage compensation mechanisms that balances gene expression between the sexes can be extended to species with ZW sex chromosomes which had previously been debated. In species with environmental sex determination, the entire genome is shared by both sexes and conflict over gene regulation is potentially even more pronounced. We study the consequences of environmental sex determination to identify the role of sex-biased gene regulation in the resolution of sexual conflict. Furthermore, we investigate the sex chromosome evolution and gene regulation in termites where we can study the interplay between different sexes and castes. This system also exhibits some species with intriguing modifications of meiosis where during spermatogenesis multiple chromosomes can segregate together with the sex chromosomes.

Münster Evolution Meeting

DARRAS, Hugo

Time: 11:50 -12:05
Room: S1 (session 2)

Obligate chimerism in male yellow crazy ants

Multicellular organisms typically develop from a single fertilized egg and therefore consist of clonal cells. We report an extraordinary mode of reproduction in the yellow crazy ant, which results in males being chimeras of haploid cells from two divergent lineages (R and W). In these males, R cells are overrepresented in somatic tissues, while W cells are overrepresented in the germline. Chimerism is established at the onset of male development, with R and W parental nuclei bypassing syngamy and dividing separately within the same egg. Our study reveals a completely new mode of reproduction in animals and demonstrates that this mode of reproduction is associated with a conflict between lineages to preferentially enter the germ line instead of the soma.

Münster Evolution Meeting

WITTMANN, Meike

Time: 14:00 -14:30
Room: Aula

Fluctuating selection and the power of dominance

Temporally fluctuating selection can be a powerful mechanism for the maintenance of genetic diversity, but only in certain scenarios. In diploids, one key parameter is the genetic dominance at the loci contributing to the trait or traits under selection. In this talk, I will illustrate this using three modeling case studies: 1) fluctuating selection with simultaneous sexually antagonistic selection, 2) fluctuating selection on a metabolic pathway, and 3) selection on plant chemical defenses through fluctuating herbivore occurrence. I will highlight common emergent results such as maintenance of variation under beneficial reversal of dominance. Compared to distributions of selection coefficients, dominance coefficients are so far much less studied. Given their potential importance for the maintenance of variation, I argue that more research effort should be devoted to them.

KERP, Hans

Time: 14:30 -15:00
Room: Aula

A Permian floristic melting pot from Jordan – phytogeography, evolution and extinction patterns

During the late Permian (254.1–252.9 myr before present) the present-day Dead Sea region was situated at a paleolatitude of c. 15°S. With over 50 taxa, the fossil flora of the Umm Irna Formation, Jordan, is the most diverse and richest Permian flora of the Middle East. Fossil-bearing rocks were deposited in a floodplain setting with meandering rivers, abandoned channels, ephemeral lakes and backswamps of various size in a warm and humid monsoonal climate with a short dry season. Each of these depositional environments is characterized by its own typical plant association. In the Permian four major floral provinces are distinguished within the supercontinent Pangea: the (sub)aequatorial Euramerican and Cathaysian provinces, the temperate Northern Hemisphere Angaran and the temperate to cool Southern Hemisphere Gondwana provinces. Mixed floras occur in border regions of two adjacent provinces. The Umm Irna flora is the only mixed flora that comprises taxa from all major floral provinces. Not only the mixed nature of this flora is of interest, but also the earliest appearances of plant lineages that were traditionally regarded as typically Mesozoic. Moreover, this flora records the last appearances of long-ranging Paleozoic groups. Associations from swampy habitats include mostly typical Cathaysian taxa. Deposits from oxbow lakes and abandoned channels typically comprise predominantly Gondwanan elements with minor proportions of Cathaysian and Angaran taxa. Lake deposits are rich in small, wind-transported conifer remains, representing Euramerican taxa that constituted the hinterland vegetation. Nearly all taxa adapted to ecologically stable conditions, both those from the permanently wet swamps and from the dry hinterland, became extinct during the end-Permian biotic crisis. They were apparently unable to cope with sudden and dramatic temperature rises and changing edaphic and hydrological conditions. In contrast, the mesic to xeric taxa that first appeared and evolved rapidly in ecologically unstable, disturbance-prone and periodically drier habitats, survived the end-Permian extinction and became major, some even dominant constituents in the early Mesozoic. The recognition of these evolutionary patterns of origination and extinction sheds a new light on the floral turnover resulting from the largest biotic crisis of the Phanerozoic.

SALEM, Hassan

Time: 15:05 -15:20
Room: Aula (session 1)

Quid pro quo: Leaf beetle propagates a phytopathogen in exchange for pupal protection

Many insects rely on microbial protection early in development. However, in contrast to symbiont- mediated defense of eggs and young instars, the role of microbes in safeguarding pupae remains relatively unexplored, despite the susceptibility of the immobile stage to antagonistic challenges. Here, we outline the importance of symbiosis in ensuring pupal protection by describing a mutualistic partnership between the ascomycete *Fusarium oxysporum* and *Chelymorpha alternans*, a leaf beetle. The symbiont rapidly proliferates at the onset of pupation, extensively and conspicuously coating *C. alternans* during metamorphosis. The fungus confers defense against predation as symbiont elimination results in reduced pupal survivorship. In exchange, eclosing beetles vector *Fusarium* to their host plants, resulting in a systemic infection. By causing wilt disease, the fungus retained its phytopathogenic capacity in light of its symbiosis with *C. alternans*. Despite possessing a relatively reduced genome, *Fusarium* encodes metabolic pathways that reflect its dual lifestyle as a plant pathogen and a defensive insect symbiont. These include virulence factors underlying plant colonization, along with mycotoxins that upgrade the defensive biochemistry of the insect host. Collectively, our findings shed light on a mutualism predicated on pupal protection of an herbivorous beetle in exchange for symbiont dissemination and propagation.

MYRIE, Ameka

Time: 15:20 -15:35
Room: Aula (session 1)

Cohabiting Coffee Berry Borers

The Coffee Berry Borer (*Hypothenemus hampei*, Scolytinae, Curculionidae) has invaded all major coffee-producing areas in the world, causing an estimated economic loss of US$500 million annually. A single female beetle typically infests one coffee berry, which her offspring consume over the course of development. Her female and male offspring then engage in sib-mating before daughters fly off to infest a new berry. Across different localities in Jamaica cohabitation of beetles is common, 3.21-16.25% of infested berries are infested by two females, correlating with overall infestation levels. This suggests that beetles preferentially breed alone and indicates potential conflict between co-habiting female beetles. Little is known about the behavior of these calamitous insect pests because they spend their lifecycle entirely inside the coffee berry. An artificial habitat was used to study the beetle's behavior in the laboratory. Adult females pushed and pulled other adult females, pushed late-stage larvae, and were protective of galleries containing eggs. Touching was most frequent weeks after habitat infestation, however, both females spent majority of the time digging and making their respective galleries. Cohabitation seems to affect the productivity of beetles under limited and ad libitum conditions, as one female beetle produced more offspring per capita than two females. All developmental stages were faster in setups with single females than in setups with cohabiting females after 5 weeks, indicating that there is a disadvantage to cohabitation in the Coffee Berry Borers. Finally, when given the opportunity to stay within their maternal berry or to infest a new berry, adult daughters tended to leave. This suggests that social behavior in this species is largely limited to parental care, in contrast to the eusocial behavior that evolved in other bark beetles (the fungus-farming Platypodinae and ambrosia beetles).

Münster Evolution Meeting

MIKHAILOVA, Alina

Time: 15:05 -15:20
Room: S1 (session 2: MGSE SYMPOSIUM)

Major changes in domain arrangements are associated with the evolution of termite castes

Domains as functional protein units and their rearrangements along the phylogeny can shed light on the functional changes of proteomes with the evolution of complex traits like eusociality. It has been hypothesized that, while mainly regulatory changes are expected during the early stages of social evolution, greater functional changes occur in more advanced stages of sociality. Moreover, the functional changes are also expected to occur with the emergence of new phenotypes such as distinct castes. One of the groups of organisms that evolved eusociality is termites. While the available genomes of termites show a reduction of the proteome size and more common gene family contractions, the functional novelty could be acquired by changes in the existing proteins. Analyzing the domain rearrangements in the proteomes of three solitary cockroaches and five eusocial termites, we observed more than 5000 rearrangements over the phylogeny of Blattodea. The novel domains that emerged in the origin of termites were related to metabolic and regulatory processes, mitochondrial function, cation binding, and chromatin assembly. Interestingly, we observed an enrichment of the GO terms related to post-translational modifications on three inner nodes leading to the termites exclusively. Also, we observed a significant enrichment of genes with caste-biased expression and alternative splicing among the genes with domain rearrangements in several termite species which could be related to the evolution of termite castes. The genes with domain rearrangements also show higher methylation in termites compared to non-rearranged genes which indicates differences in their regulation. Moreover, we observed depletion of transposable elements in the close proximity of the genes rearranged in the origin of termites and sterile workers which might be related to the potential functional importance of the rearranged genes and selection against TE insertions acting on them. The findings suggest different patterns of expression, methylation and selection for genes with domain rearrangements and altogether show for the first time the involvement of domain rearrangements with the emergence of eusociality.

Münster Evolution Meeting

MANSKE, Felix

Time: 15:20 -15:35
Room: S1 (session 2: MGSE SYMPOSIUM)

uORFdb: A central resource for translational regulation by upstream open reading frames

Upstream open reading frames (uORFs) are defined by an AUG or near-cognate start codon in the transcript leader sequence (TLS) of the mRNA. Since the uORF start codon is located upstream of the coding sequence (CDS), it is usually recognized first by the scanning ribosome and translation is attempted. This can in some cases lead to functional proteins (uPeptides). Mainly, however, it leads to the depletion of essential co-factors from the translating ribosome which need to be replenished before subsequent translation events can occur. Depending on the location of the uORF and its nucleotide context, the ribosome may not have enough time to replenish before encountering the CDS start codon, resulting in reduced expression of the main protein. As uORF translational control can respond to cellular conditions, it is part of a regulatory network which, for example, controls the translation of transcription factors. Moreover, variations at uORF positions have been attributed to several diseases, including cancer. We have designed uORFdb (https://www.bioinformatics.uni-muenster.de/tools/uorfdb) to serve as a central hub for uORF research. With currently 1,049 manually curated publications, more than 6.6 million predicted uORF sequences from 13 animals (including humans), and uORF-related somatic variants from whole-genome sequencing analysis of 6 major cancer types, it is the most comprehensive uORF database. The data are presented in an accessible and modern web interface, which contains streamlined visualizations, automatic notifications about new publications, and links to external resources such as dbSNP and ClinVar. Consequently, it allows users to predict uORF functions in a fraction of the time needed for fully manual data aggregation.

Münster Evolution Meeting

BECKS, Lutz

Time: 16:05 -16:20
Room: Aula (session 1)

Repeated evolution of cell groups under predation

One major transition in the organization of life is the one from unicellular to multicellular life where cells are differentiated and arranged into functioning tissue ("soma and germ") within an integrated organism. This transition is one of the most important as well as one of the least understood transitions in the organization of life, particularly at the ecological and genomic level. The formation of aggregated cell groups is the first major steps involved in this transition. One important condition that could facilitate the shift from undifferentiated cells within a group to differentiated soma and germ cells is an increasing cost associated with increasing cell group size. We present results from an experimental evolution study with the single celled green algae *Chlamydomonas reinhardtii* comparing the evolution of cell groups in the presence and absence of predators. We found that predation selects for cell groups and that survival and reproduction evolve with a concave trade-off curve, where individuals either optimize survival or reproduction. Evidence from phenotypic assays and from the comparison of transcriptome data in different environmental conditions suggests that the changes in survival and reproduction are heritable. We further compared genomic changes between isolates of cell groups and single cells to identify mutations that potentially underlie the phenotypic changes. Surprisingly, identical mutations evolve in all cell group isolates. These mutations were linked to survival. This fairly high degree of repeatability and the small number of generations suggest some degree of determinism for the phenotypic and genomic response in *C. reinhardtii* to predation pressure.

Münster Evolution Meeting

ONA BUBACH, Leonardo

Time: 16:20 -16:35
Room: Aula (session 1)

Cooperation enhances resilience to ecological perturbations in microbial networks

Microorganisms are typically found in intricate networks of ecological relationships. Despite the fact that the growth and survival of these organisms often rely on the exchange of vital metabolites, it can be challenging to understand how these communities can endure despite the disruption caused by ecological disturbance. Our study uses a population dynamics model to investigate this issue. Unlike prior research that indicates the possibility of obligate interaction networks is limited, we discovered the opposite trend: ecological disturbance favors certain network configurations and cooperation among community members. These findings indicate that environmental disturbances play a crucial role in shaping the structure of microbial interaction networks.

Münster Evolution Meeting

PAULI, Benedikt

Time: 16:35 -16:50
Room: Aula (session 1)

Obligate mutualistic cooperation limits the evolvability of bacterial consortia

Bacterial communities are characterized by a tremendous diversity of different ecological interactions among its constituents, which can dramatically affect the fitness of the individuals involved. An important and widespread type of interaction is obligate mutualistic cooperation, in which two or more genotypes reciprocally exchange essential metabolites. As a consequence, the fitness of the individuals that are involved in this type of interaction is not only determined by the information that is encoded in their own genome, but also by the traits and capabilities of their respective interaction partner. How does this affect evolutionary adaptation relative to physiologically autonomous cells? To address this question, we used auxotrophic strains of Escherichia coli that had previously evolved a bidirectional exchange of costly amino acids. Monocultures and cocultures of these cooperative strains were subjected to a long-term evolution experiment, in which they were exposed to a stepwise increase of the antibiotic concentration in their growth environment. It was found that metabolically interdependent bacteria were generally more susceptible to antibiotic treatments than physiologically autonomous strains. Moreover, bacteria engaging in an obligate mutualism showed an increased probability to revert to a prototrophic phenotype, thus either resulting in a loss of the corresponding other partner or a conversion of the bidirectional mutualism into a unidirectional cross-feeding interaction. Together, our results demonstrate that obligate mutualistic interactions can limit the ability of the entire consortium to adapt to stressful conditions.

Münster Evolution Meeting

SCHMITZ, Jürgen

Time: 16:05 -16:20
Room: S1 (session 2: MGSE SYMPOSIUM)

Jumping genes in phylogeny and genome evolution

Jumping genes or transposed elements (TEs) significantly influence genome architecture. They can also increase the substrate for adaptive evolution. Besides, they are suspected of causing disease, changing behavior and lifestyle, impacting sex determination, and modifying genes. We identified, extracted, and analyzed TEs for their diagnostic power in phylogeny and adaptation in vertebrates. However, the once sparse sequence information increased dramatically in the new era of Next Generation Sequencing and opened new horizons in understanding the impact of jumps in the genome but also challenged the development of new informatic tools in biology. In phylogeny, jumping genes are nearly perfect neutral presence/absence markers. The same genomic presence site in two species marks a relationship as long as the insertion was fixed before speciation and is absent in more distant relatives. To handle genome data, we recently developed and successfully applied “2-n-way,” a comparative analysis suite that detects, sorts, and extracts TE loci and other insertions or deletions, e.g., intron loss, at the multi-species genome level without the need for bioinformatics or high-performance computing. To apply 2-n-way, the user selects/uploads their genome sequence and chooses a target reference genome plus one or more query genomes. The 2-way module generates complete pairwise genome alignments. It transfers the coordinates to the n-way module to design a multi-species, comparative, presence/absence table for the selected elements by combining all associated 2-way genome alignment information in record time. The resulting presence/absence table and sequences can be sorted, modified, and downloaded. Under likelihood criteria, the statistical significance of diagnostic phylogenetic insertion is evaluated with a 4-lineage statistical suite. One example of the power of phylogenetically diagnostic jumping genes is the recent reunion of Australasian possums. Autonomous jumping genes can co-retrotranspose mRNAs as intron-less retropseudogenes. Latter often recombines with genes and removes introns. We follow such evolutionary relevant processes using 2-n-way from humans to the earliest representatives of vertebrates. Jumping genes may also directly influence the evolution of genes. We developed user-friendly tools to measure gene evolution. For example, we applied parallelized selection analyses on 1151 proven cases of novel exons.

Münster Evolution Meeting

RINKE, Janina

Time: 16:20 -16:35
Room: S1 (session 2: MGSE SYMPOSIUM)

Recurrent horizontal gene transfer from bacteria into ants

Bacteria have profoundly influenced animal evolution either as parasites, commensals, or beneficial symbionts. In addition, bacteria have been important sources for new genetic material via horizontal gene transfer (HGT). While the impact of HGTs on the evolution of phenotypic innovations and environmental adaptations is well documented in many insects, the extent of HGTs in ants, one of the most successful insect families, remains largely unknown. In this study, we systematically screened for HGTs in over 160 ant genomes from 12 subfamilies, which were sequenced by the Global Ant Genomics Alliance (GAGA). Among several hundred HGT candidates that contain expressed and potentially functional genes, we identified cases of ancient HGTs conserved across a specific clade of ants as well as cases of species-specific HGTs. Moreover, we discovered over 200 horizontal transfers of *Wolbachia* derived ankyrin repeat proteins spread across 34 species from eight different clades. In general, HGTs in ants are derived predominantly from intracellular endosymbionts, likely due to their intimate association with the germ line of their eukaryotic hosts. Our study builds the foundation for understanding the impact of HGTs in the evolution of ants and their origins. It may furthermore help explain aspects of their ecological success and niche adaptations.

Münster Evolution Meeting

KORSA, Ana

Time: 16:35 -16:50
Room: S1 (session 2: MGSE SYMPOSIUM)

How host immune priming affects pathogen evolution

Due to their enormous genomic plasticity and fast microevolutionary processes, bacterial pathogens have the potential to evolve rapidly. On the other hand, flexible immune systems enable hosts to adapt and respond to pathogens by forming immunological memory (or 'priming' in insects) of a previous encounter. Studies in the red flour beetle have shown that a previous priming of the immune system leads to increased survival upon infection with *Bacillus thuringiensis* (Bt). However, it remains unclear how such improved host immunity affects pathogen adaptation. We performed one - sided experimental evolution of Bt in beetles with different immune status (primed and non- primed) hypothesizing priming could drive faster pathogen adaptation. Experimental evolution of *B. thuringiensis* via 8 serial passages resulted in a drastic variation of bacterial virulence (i.e., host killing) in particular in the replicate lines that evolved in primed hosts. Additionally, evolution in primed hosts in tendency increased the correlation between host mortality and pathogen load. Whole genome resequencing of the evolved bacteria revealed some genomic changes, particularly in the plasmid that carries Cry toxin genes. Taken together, our study provides urgently needed, but rare knowledge about the relevance of the host immune response for the evolution of pathogen virulence.

ERRBII, Mohammed

Time: 17:00 -17:15
Room: Aula (session 1)

The genetic basis of social polymorphism in the ant *Pogonomyrmex californicus*

Social insects vary considerably in their social organization both between and within species. In the California harvester ant, *Pogonomyrmex californicus*, colonies are commonly founded and headed by a single queen (haplometrosis, primary monogyny). However, in some populations, unrelated queens cooperate in founding and leading the colony (pleometrosis, primary polygyny). The genetic and evolutionary basis of this social polymorphism (haplometrosis vs pleometrosis) has remained unknown. Using population genomics, linkage mapping, and demographic modeling we investigate the genomic basis and evolutionary history of this trait. Our investigations led to the discovery of an approximately 8 Mb non-recombining region segregating with the observed social polymorphism, showing characteristics similar to those of supergenes underlying social organization in other ant species. However, in contrast to previously described systems, we identified additional loci showing signatures of selection, segregating with the haplometrotic and pleometrotic social forms of this species. This includes genes involved in epigenetic regulation through histone modification (*chameau*) and DNA methylation (*dnmt1*). Together, our results suggest that social morph in *P. californicus* is a polygenic trait including a young supergene that evolved less than 0.2 million years ago, allowing us to study and explore the origin of supergenes.

Münster Evolution Meeting

LIN, Silu

Time: 17:15 -17:30
Room: Aula (session 1)

Effect of food restriction on survival and reproduction of a termite

Food availability affects the trade-off between maintenance and reproduction in a wide range of organisms, but its effects on social insects remain poorly understood. In social insects, the maintenance-reproduction trade-off seems to be absent in individuals but may appear at the colony level, although this is rarely investigated. In this study, we restricted food availability in a termite species to test how it affects survival and reproduction, both at the individual and colony level. Using Bayesian multivariate response models, we found very minor effects of food restriction on the survival of queens, individual workers or on the colonies. In contrast, queen fecundity was significantly reduced while colony-level fecundity (i.e., the number of dispersing alates, future reproductives) increased under food restriction as workers gave up cooperation within the colony and became alates that dispersed. Our study shows that life history trade-offs can be mitigated by individuals' social behaviours in social organisms.

Münster Evolution Meeting

SCHULTNER, Eva

Time: 17:30 -17:45
Room: Aula (session 1)

Regulation of caste polyphenism in an ant with a sterile worker caste

Division of labor between reproductive queen and non-reproductive worker castes forms the basis of superorganismality, thereby permitting one of the major transitions in evolution. A century of research on caste determination and differentiation in social insects has revealed a complex picture of how these developmental processes are regulated across the range of queen-worker polyphenism. Today, advances in molecular methods are paving the way toward the identification of common patterns across species, bringing us closer to a unified concept of caste development. I will give an overview of the current state of knowledge on caste polyphenism in social Hymenoptera and present new results on the regulation of embryonic caste development in *Cardiocondyla obscurior*, an ant with an obligately sterile worker caste.

Münster Evolution Meeting

ALTINOK, Ozan Altan

Time: 17:00 -17:15
Room: S1 (session 2: MGSE SYMPOSIUM)

Evolutionary medicine at the face of multiple environment of evolutionary adaptedness based on epigenetic inheritance mechanisms, which direction to go to?

In this talk, I will briefly summarize the history and current accounts of Evolutionary Medicine (EM) following the analysis and distinctions made by Zamperi (2009) and Méthot (2011). I will show that EM, in its current forms, is using an evolutionary understanding that carries the explanatory framework, as well as explanatory limits, of the Modern Synthesis (MS) of which structure has been criticized due to its limitations (Gould, S. J., & Lewontin, R. C. (1979, Ahouse, 1998)) to argue that the current form of EM of Williams & Nesse (1991) and Nesse (2019), is strongly related to Environment of Evolutionary Adaptiveness (EEA) of Bowlby (1969). Based on the previous work (Altinok, forthcoming) I will criticize one common critique of EM is of its claimed irrelevance clinic (Courneya & Kennedy (2014), Courneya (2018). I will address that this is mostly based on the proximate – ultimate distinction drawn by the main framework of MS and is embedded in the work of Mayr (1961). Upon the established understanding of MS, I will then point out some essential elements that need to be seen as limiting factors within EM and analyze the limitations that are brought about by the MS understanding of it. On this basis, I will argue that if the latest developments in evolutionary theory are considered – in particular, those pertaining to the inheritance mechanisms highlighted by the Extended Evolutionary Synthesis (EES) (Uller et. al. 2014, Laland et. al. 2014), particularly epigenetics (Jablonka & Lamb 2014, Jablonka & Lamb 2020) the relationship between what is inherited, inheritance mechanisms and the environment will change drastically in the making of evolutionary histories of populations. I will claim that this will allow us to create multiple EEA points within the history of the individual and social groups (Altinok, 2022), making us able to create more clinically interventionist evolutionary explanations, which are easier fitting for the purposes of clinicians. Although as addressed above, the multiplicity of mechanisms, as well as relevance to the making of research programmes are getting more central in the making of research agendas of EM, most imaginaries of EEA seem to follow some very unfiltered, and even ideological assumptions. After pointing out the strength of the previous work about the possibility of the many different reasons and possible research programmes within EM, I will critique the limited perspectives of EM in relationship to other possible domains of expertise within scientific research. I will claim that the political economy of reasons being framed – if not shaped – by the modern synthesis not only at the structural level but at the level of agenda setting, is the leading structural force with respect to the making of the research programs of evolutionary medicine.

Münster Evolution Meeting

TEMME, Imke

Time: 17:15 -17:30
Room: S1 (session 2: MGSE SYMPOSIUM)

Insights into aerobic and anaerobic carbon utilization of hybrid STEC/UPEC

The number of pathogenic *Escherichia coli* isolated and identified as hybrids has increased strongly within the last decade. However, their adaptation, virulence, and outbreak potential remain largely unknown. Hybrid Shiga toxin-producing and uropathogenic *E. coli* (STEC/UPEC) serogroup O2:H6 phylogenetically align between Shiga toxin-producing (STEC) and uropathogenic (UPEC). Besides their ability to cause both diarrhea and urinary tract infections, STEC/UPEC hybrids showed adaptation to both the colonic and bladder environment during phenotype analysis of virulence-associated traits. The carbon source utilization of hybrid STEC/UPEC was tested to further investigate the adaptation to both intestinal and extraintestinal milieu. For this, a Phenotype MicroArray screening of 95 carbon compounds was done under aerobic and anaerobic conditions. Besides the O2:H6 hybrid strains, the commensal K-12 MG1655, the canonical UPEC strain 536, and EHEC strains B2F1 and Sakai were tested. Analysis of the aerobic and anaerobic growth patterns shows significant differences between the two environments. Not only is the overall growth capacity of all strains significantly reduced under anaerobic conditions, but also the range of utilized carbon sources is lowered. Most significant is the reduction in utilization of amino acids and peptides under anaerobic conditions and a clear focus on the anaerobic niches of all strains on sugar compounds. Interestingly, under aerobic conditions, the hybrid strains show overall high similarities to UPEC strain 536. While STEC strain B2F1 is also similar to the hybrids and 536 the utilization of the urine-specific compound D-Serine suggests an extraintestinal metabolic background for the STEC/UPEC hybrids. During anaerobic growth, the similarities between all strains and the overall focus on sugar compound utilization show the adaptation of all groups to the colonic environment which is considered anaerobe and serves as the main reservoir milieu for all tested strains. In contrast, the observed differences during aerobic growth show a metabolic background of extraintestinal pathogens for the hybrid O2:H6 strains. Overall, this supports an adaptation to both the colonic and bladder environment but a uropathogenic origin of the hybrid STEC/UPEC.

KEIZERS, Marla

Time: 17:30 -17:45
Room: S1 (session 2: MGSE SYMPOSIUM)

The loss of the lsr operon in Escherichia coli of the phylogroup B2 may lead to a fitness advantage during long-term bladder colonization

Gram-positive and Gram-negative bacteria shed and react to the inter-species quorum sensing molecule autoinducer-2 (AI-2). In *Escherichia coli* (*E. coli*), AI-2 is incorporated and processed by proteins encoded by the *lsr* operon. Epidemiological studies have shown that *E. coli* strains that cause extraintestinal diseases, such as urinary tract infections, are frequently part of the phylogroup B2. Interestingly, most *E. coli* strains of the phylogroup B2 have lost the *lsr* operon during evolution. We therefore hypothesize that the loss of AI-2 dependent quorum sensing has led to an extraintestinal fitness gain in *E. coli* of the phylogroup B2, e.g., during long-term bladder colonization. To test our hypothesis, we use the B2 strain 83972, isolated from an asymptomatic bacteriuria case, that also lacks the *lsr* operon. We complemented the *E. coli* strain 83972 with a full-length *lsr* operon and analyzed phenotypes that are crucial for efficient long-term bladder colonization. Amongst others, the frequent void of urine and the attack by neutrophils that use reactive oxygen species to combat bacterial infections display mechanisms to which bacteria had to adapt. We tested the growth behavior and resistance to hydrogen peroxide (H2O2) of *E. coli* 83972 and the complemented, *lsr* positive, *E. coli* 83972 *attB::lsr*. The complemented strain showed a significantly longer lag phase and a slower growth rate, resulting in complete loss of the complemented strain in direct competition experiments. Also, the complemented strain was significantly less resistant to 20 mM H2O than the wild type strain during mid-log growth. We therefore used RNA-Seq to screen for differentially expressed genes (DEGs) that may be involved in the observed phenotypes. We found 199 significantly DEGs, including an outer membrane protein that may be involved in H2O2 resistance, a toxin-antitoxin system that may contribute to a reversible growth arrest, as well as genes related to metabolism and motility. To summarize, we have identified phenotypes suggesting that the loss of the *lsr* operon in *E. coli* could constitute an evolutionary advantage for bladder colonization. Further experiments are necessary to clarify if the *lsr*-dependent deregulation of these genes indeed contributes to the extraintestinal fitness of *E. coli* 83972.

Münster Evolution Meeting

15th MARCH, 2023

Münster Evolution Meeting

WIDDIG, Anja

Time: 09:00 -09:30
Room: Aula

The impact of realized relatedness on the evolution of primate sociality based on WGS data

Most primate species live in permanent groups consisting of several adult males and females. Males usually disperse from their birth group around puberty to breed elsewhere, and females mainly raise their offspring alone, with males sometimes providing protection and access to resources. Given that males and females mate promiscuously, paternity is expected to be confused to males. Past research has shown that complex social systems have evolved across primate species, with genetic relatedness being one major driver shaping primate sociality. However, we still understand little about how the variation in relatedness leads to differences in sociality within and across species. For example, across macaques, a genus of 23 species living under diverse ecological conditions, variation in genetic relatedness and kin structure within groups has promoted the evolution of considerable differences in social dynamics. This ranges from pronounced and stable bonds mainly with close kin in highly despotic and intolerant societies, as presented by rhesus macaques (*Macaca mulatta*), to relaxed and flexible bonds not limited to close kin in egalitarian and tolerant societies, for example in crested macaques (*M. nigra*). In the first part of my talk, I show which factors shape patterns of relatedness in primate groups contrasting these two macaque species. Furthermore, I demonstrate evidence of kin preference in social behavior, focusing on paternal kin bias (here father-offspring and paternal sibling dyads) and introduce likely mechanisms and cues of paternal kin recognition. In the last part of talk, I present data from an ongoing project producing whole genome sequencing data of 800 individual rhesus macaques to assess dyadic realized relatedness (identity-by-descent or IBD). The results suggest that IBD provides more accurate estimates of relatedness than pedigrees as they reveal the theoretically expected gradient in relatedness (with variation within and between kin classes) compared to the categorical mean values of pedigrees. I will discuss the implication of this gradient in relatedness for our understanding of the impact of realized relatedness on the evolution of primate sociality.

SCHLÖTTERER, Christian

Time: 09:30 -10:00
Room: Aula

Incipient speciation from standing genetic variation

Ecological speciation and mutation-order speciation are two different mechanisms of adaptation-driven speciation. Both mechanisms predict different patterns of reproductive isolation for replicate populations adapting to the same environment. With ecological speciation, barriers to gene flow emerge between populations from different environments, but not among replicate populations from the same environment. Mutation-order speciation predicts reproductive isolation among populations adapted to the same environment. We demonstrate that both speciation processes occurred within about 100 generations when replicate *Drosophila simulans* populations adapted to a novel, hot environment. Gene expression analysis identified the underlying molecular mechanisms. Premating ecological speciation is the byproduct of an altered lipid metabolism, which also changed the cuticular hydrocarbon (CHC) composition in hot-evolved flies. Postmating reproductive isolation supports mutation-order speciation most likely driven by co-evolution of reproduction-associated genes. Adaptation processes can rapidly induce incipient speciation and different speciation mechanisms affect pre- and postmating reproductive isolation. We propose that the definition of mutation- order speciation should be expanded to account for polygenic processes from standing genetic variation.

Münster Evolution Meeting

GROESCHEL, Matthias

Time: 10:00 -10:20
Room: Aula (session 1)

Host-pathogen Co-evolution shapes susceptibility to infection with *M. tuberculosis*

The obligate human pathogen of the Mycobacterium tuberculosis complex (Mtbc) separates genetically into nine lineages with distinct patterns of geographical distribution that in some cases parallel that of human subpopulations. Based on these observations, geographically restricted Mtbc lineages have been hypothesized to be niche specialists that preferentially infect particular human subpopulations, but this is yet to be confirmed while controlling for social networks and risk of disease among exposed hosts. Here we show that strains of specialist (spec) Mtbc lineages L1, L2spec, L3, L4spec, L5, L6 are intrinsically less transmissible than generalist Mtbc lineages (L2gen, L4gen) across Western European and North American cosmopolitan populations. Comparing transmissibility between sympatric and allopatric host-pathogen pairs, we found the first controlled evidence for co-adaptation between Mtbc strains and their human hosts; allopatric host- pathogen exposures had a 32% decrease in the odds of infection among contacts compared with sympatric exposures. We measured 10-fold decreased phagocytosis and growth rates of L6 specialist strains compared to L4gen in in vitro allopatric macrophage infections. Long-term co-evolution between Mtbc strains and humans has resulted in differential transmissibility between allopatric and sympatric hosts for the specialist lineages. Understanding the specific genetic and immunological underpinnings of this co-evolution may inform rational vaccine design and TB control.

WOHLLEBEN, Anika

Time: 10:20 -10:35
Room: Aula (session 1)

Comparison of Gene Expression upon Infection with the cestode *Schistocephalus solidus* in Two Alaskan Stickleback (*Gasterosteus aculeatus*) populations

Helminths are common parasites that often drastically reduce host survival and reproductive success, and therefore impose strong selection pressure on the hosts to evolve countermeasures (e.g., immune response, behavioral changes). The study of the host-parasite interaction between the three spine stickleback fish (*Gasterosteus aculeatus*) and the cestode *Schistocephalus solidus* offers a unique view into the mechanisms underlying the influence of these countermeasures at the population level. When oceanic stickleback populations independently invaded freshwater habitats after the last glacial maximum, they first encountered *S. solidus* which led to different stickleback freshwater populations evolving different strategies to manage infection pressure. To identify genetic mechanisms underlying differences in *S. solidus* susceptibility we used TagSeq to compare gene expression between two Alaskan stickleback populations that differ in their natural infection prevalence: One high-infection and one low-infection population. We hypothesized gene expression would differ between infected and uninfected stickleback and between fish from the two populations. In the high-infection population, we found numerous (immune) genes to be differentially expressed between infection statuses, specifically genes of the cellular innate immune response and the complement cascade were up-regulated during infection. In contrast, in the low-infection population only a few genes were differentially expressed as a result of infection status. Finally, when comparing baseline gene expression in uninfected fish, we found expression of innate immune genes was higher in the low-infection population compared to the high-infection population. Our findings provide new insight into the genetic mechanisms underlying the evolution of resistance upon exposure to a novel parasite.

HECKENHAUER, Jacqueline

Time: 10:05 -10:20
Room: S1 (session 2: SPP-GEvol SYMPOSIUM)

Characterization of primary structure of the major silk gene, h-fibroin, across caddisfly suborders (Trichoptera)

Larvae of Trichoptera produce silk to build various underwater structures allowing them to exploit a wide range of aquatic environments. The heavy chain fibroin (h-fibroin) gene encodes the primary protein component of their silk. Studies on this long (>20 kbp) and highly repetitive gene have been limited by difficulties in its sequence assembly. Recently, high-quality long-read sequencing techniques have been successfully applied to obtain the full-length h-fibroin sequence. We used three new and five previously published genomes to identify eight full-length h-fibroin gene and protein sequences of h-fibroin across the order Trichoptera covering various endpoints of the diversity of ecological silk use in caddisflies. We analyze these together with four existing high- quality h-fibroin sequences. Across the order, we observed conserved patterns in h-fibroin (high similarity of amino(n)-/carboxyl(c)-termini, presence of characteristic repeating structural modules). However, the sequence, number, and arrangement of these repeating modules varied across clades with increasing structural complexity of h-fibroin in fixed retreat and tube-case builders compared to cocoon-builders. We also found a higher percentage of proline in fixed-retreat makers. This study provides characterizations of the primary structure of h-fibroin from a diverse set of caddisflies. The interplay of conserved termini and basic motif structure with high variation in repeating modules as well as the variation in the percentage of proline might be linked to differences in mechanical properties (i.e., tensile strength, toughness) related to the different silk usage. This sets a starting point for future studies to screen and correlate amino acid motifs and other sequence features with quantifiable silk properties.

Münster Evolution Meeting

DOHMEN, Elias

Time: 10:20 -10:35
Room: S1 (session 2: SPP-GEvol SYMPOSIUM)

On the Tracks of Functional and Regulatory Adaptations towards Eusociality

The evolution of eusociality and with it the questions of how a single genome can encode for several alternative phenotypes of such great disparity fascinates and is up to this day not fully understood. It is astonishing that such a complex trait, involving among others the development of reproductive and completely sterile castes within the same species, evolved multiple times independently as for example in bees, wasps and ants. At the same time, the multiplicity of similar and different evolutionary solutions to the same problem offers an opportunity to study the molecular fundamentals of eusociality. We identify some of these fundamentals in the form of functional and regulatory adaptations through comparative analyses of gene co-expression networks combined with machine learning models. This way, we get insights beyond classical differential expression or principal component analyses. For this purpose, we generated an RNAseq data set of *Apis mellifera* (honeybee) samples of queens and workers at different age. The results are evaluated in the light of current knowledge about drivers of evolution of eusociality as well as compared to other species to identify the genetic fundamentals next to species-specific functional and regulatory adaptations.

Münster Evolution Meeting

EDISON, Alitha

Time: 11:05 -11:20
Room: Aula (session 1)

The role of behaviour in insecticide resistance in the Colorado potato beetle

Rapid evolution of resistance to insecticides is a huge threat to sustainable global food production. Despite employing biochemical and/or physiological mechanisms of resistance, agricultural pests can develop behavioural resistance to insecticides via choosing to feed or oviposit exclusively on insecticide-free hosts. As young offspring have relatively low mobility, oviposition preferences of female adults may play a critical role in shaping the evolutionary trajectory of pest populations. While oviposition avoidance of insecticide-treated hosts was found in different agriculture pests, it remains unclear whether female adults actively choose to occupy insecticide-free hosts. To address this question, we investigated feeding and oviposition preferences to imidacloprid in the Colorado Potato Beetle (CPB, *Leptinotarsa decemlineata* (Say)), a major potato pest. First, we performed toxicity assays on five different strains of CPB using the neonicotinoid insecticide, imidacloprid. Using two of those strains that were relatively more resistant and relatively more susceptible to imidacloprid, we investigated feeding and oviposition preferences in behavioural choice assays. We identified a strain that chooses to feed from the insecticide-free plants than the insecticide- treated plants. We found that the females of this strain prefer to lay more eggs on the insecticide- free plants. If this avoidance behaviour has a genetic basis, mapping the corresponding regions to the CPB reference genome will significantly advance the relatively unexplored field of behavioural resistance to insecticides. In order to do this, we generated an F3 population by crossing five CPB strains. Then we pooled individuals with extreme phenotypes for the traits of interest and sequenced the pools. We will use the cost-effective bulked segregant analysis approach to map the genomic regions associated with the avoidance and survival traits.

Münster Evolution Meeting

RAJENDRA, Dharanish

Time: 11:20 -11:35
Room: Aula (session 1)

From Replicator Dynamics to Reinforcement Learning: Understanding the Evolution of *Clunio*

Clunio is a genus of marine midges living in intertidal zones across the globe. They have evolved to take in environmental cues such as waves during the tides and moonlight to coordinate their emergence from the pupal stage to adulthood in order to maximize the chance of finding a mate and reproducing. Further, several strains of *Clunio* show distinct emergence patterns, such as emergence around full moon, around new moon, or both. We use evolutionary game theory, replicator dynamics, and provide a novel outlook at the evolution of emergence times in *Clunio*, reinforcement learning, to understand the conditions that might have led to the current behavior of *Clunio*, its different strains, and their coexistences. The models tell us that the arrhythmic strains could have arisen due to weak selection and sufficiently high mutation rates. The monomorphic populations could be a result of strong selection and low mutation. On the other hand, the polymorphic populations could result from lower selection strengths and similar mutation rates. The reinforcement learning framework gives more attention to individual behaviors and gives us more insight into the phenomenon.

Münster Evolution Meeting

SCHULZ, Nora

Time: 11:35 -11:50
Room: Aula (session 1)

The role of niche construction for the adaptability of the red flour beetle, *Tribolium castaneum*

Niche construction is an important eco-evolutionary process, where organisms modify their ecological niches by altering the chemical, physical, or biological properties of their environment, which may promote adaptation to changing environments. In group living animals (sharing the same environment), these alterations can influence the level of pathogenic threat that their conspecifics or offspring are exposed to and thus modify the selective environment of both the niche constructors and recipients. To understand the ecological and evolutionary consequences of niche construction, we preformed experimental evolution using the red flour beetle and its naturally occurring parasite *Bacillus thuringiensis* (Bt). Adult beetles modify their environment by releasing quinone-rich secretions which alter their surrounding microflora. We tested the impact of impaired niche construction ability on host adaptation to Bt selection by inhibiting the quinone production of beetles via RNAi knockdown. After nine generations of host selection, we found that host survival was enhanced in the Bt-exposed lines and the difference in survival was larger between the selection regimes with conditioned flour than those with quinone-less flour. Furthermore, selection with Bt led to faster development and increased fecundity in lines with quinone-less flour. Finally, we combined these phenotypic data with differential gene expression analyses, to investigate if different mechanisms lead to the observed Bt resistance and how the beetles evolve under different niche construction abilities. This work provides urgently needed but rare empirical evidence on the role of niche construction for adaptation.

Münster Evolution Meeting

MENGES, Vanessa

Time: 11:50 -12:05
Room: Aula (session 1)

Temporally consistent behavioural variation between wild ant colonies is robust to strong seasonal and thermal variation

One of the key questions of evolutionary ecology is how different species or conspecifics can coexist in the same habitat. Both species-, and conspecific- coexistence depend not only on the availability of ecological niche space, but also on their degree of niche overlap and their ability to compete for resources. Therefore, overlapping niches might favour individual trait variation by promoting niche differentiation. An ecologically important aspect of trait variation is behaviour. Behavioural differences between conspecific individuals that are consistent across time are defined as 'animal personality'. Whereas animal personality traits have been described under laboratory conditions in many insects, including ants, knowledge about consistent behavioural variation in the field is scarce. Here, we conducted two field studies analysing, first, intercolonial behavioural variation in *Lasius niger* in one year. Followed by a large scale field study investigating the consistency of behavioural variation in the ant species *Lasius niger, Formica rufibarbis* and *Tetramorium caespitum* in the next year. We used standardized behavioural assays for exploration, aggression towards con- and allospecific ants, the tendency to forage at honey and the foraging activity at the nest. Each assay was repeated multiple times over the course of the season. We found consistent differences between colonies in some, but not all behavioural traits of the tested species. In the first experiment *L. niger* colonies differed consistently in exploration and aggression as well as in their foraging activity. In the second year colonies of all species showed consistent differences in aggressive behaviour against allocolonial and/or allospecific colonies. This consistency is the more remarkable as nearly all traits showed strong seasonal and temperature effects in both experiments. Thereby, these findings suggest that traits can be plastic and consistent at the same time. Our work shows that despite variable abiotic and biotic conditions, temporally consistent animal personality traits can be detected in the field underlining their importance in understanding ecological interactions and intra-, as well as inter- specific coexistence.

Münster Evolution Meeting

POSNIEN, Nico

Time: 11:05 -11:20
Room: S1 (session 2: SPP-GEvol SYMPOSIUM)

Can gene regulatory networks help us understanding the evolution of complex traits? What we can learn from natural variation in compound eye size in *Drosophila*

Natural variation in complex traits is often controlled by many genomic loci with little individual impact on the phenotypic outcome. Therefore, it is challenging to pinpoint individual genes underlying natural variation in quantitative traits. Since most genes do not act individually but are interconnected in gene regulatory networks (GRNs), the identification of variable nodes and modules within GRNs has a great potential to gaining mechanistic insights into phenotypic evolution. The formation of the insect compound eye is determined by a complex GRN composed of more than 5,000 genes and natural variation in eye size is pervasive in *Drosophila*. Therefore, we study differences in compound eye size between *D. melanogaster* and *D. mauritiana* to unravel key variable GRN modules. We integrated quantitative trait loci mapping data with functional genomics information (RNAseq, ATACseq) to reveal 67 candidate genes. An RNAi screen for these genes confirmed a function during eye development for 12 genes. GRN reconstruction allowed us predicting key variable processes underlying observed eye size differences. We confirmed some of these predictions by single-cell RNA sequencing and functional genetics analyses in *D. melanogaster*. We conclude that natural variation in the expression of genes involved in regulating the interplay between cell proliferation and differentiation plays a major role in defining eye size differences among closely related *Drosophila* species. In summary, instead of identifying individual genes underlying eye size variation, we revealed variation in a core network module that is linked to a specific developmental function.

GLASER-SCHMITT, Amanda

Time: 11:20 -11:35
Room: S1 (session 2: SPP-GEvol SYMPOSIUM)

Dynamics and stage-specificity of between-population gene expression divergence in the Drosophila melanogaster larval fat body

Gene expression variation is pervasive across all levels of organismal organization, including development. Few studies, however, have examined variation in developmental transcriptional dynamics among populations, or how it contributes to phenotypic divergence. Indeed, the evolution of gene expression dynamics when both the evolutionary and temporal timescale are comparatively short remains relatively uncharacterized. Here, we examined coding and non-coding gene expression in the fat body of an ancestral African and a derived European Drosophila melanogaster population across three developmental stages spanning ten hours of larval development. Between populations, expression divergence was largely stage-specific. We detected higher expression variation during the late wandering stage, which may be a general feature of this stage. During this stage, we also detected higher and more extensive lncRNA expression in Europe, suggesting that lncRNA expression may be more important in derived populations. Interestingly, the temporal breadth of protein-coding and lncRNA expression became more restricted in the derived population. Taken together with the signatures of potential local adaptation that we detected at the sequence level in 9–25% of candidate genes (those showing evidence of expression divergence between populations), this finding suggests that gene expression becomes more developmental stage-specific during adaptation to new environments. We further used RNAi to identify several candidate genes that likely contribute to known phenotypic divergence between these populations. Our results shed light on the evolution and dynamics of expression variation over short developmental and evolutionary timescales, and how this variation contributes to population and phenotypic divergence.

GRANDCHAMP, Anna

Time: 11:35 -11:50
Room: S1 (session 2: SPP-GEvol SYMPOSIUM)

de novo transcripts in *Drosophila melanogaster*

In most multicellular organisms, only a small fraction of the genome codes for proteins. Intriguingly though, also a large fraction of the non-genic regions are transcribed at least occasionally or under specific conditions. Transcripts emerged in only close species or inside one species are called de novo transcripts. Their facultative coding potential could be the first step in the emergence of de novo genes from previously non-coding regions. Since transcription is a necessary step in de novo gene emergence, further insight into the gain-loss dynamics of de novo genes depends on a better understanding of the gain-loss dynamics of transcripts on evolutionary short time scales. Based on a new pipeline of orthology detection, we identified de novo transcripts in 7 lines of *Drosophila melanogaster*, and studied their gain and loss processes.

CZUPPON, Peter

Time: 11:50 -12:05
Room: S1 (session 2: SPP-GEvol SYMPOSIUM)

De novo transcript evolutionary dynamics in seven *Drosophila melanogaster* populations

In many eukaryotes both gene-coding and large parts of non-genic regions of a genome are transcribed. Among the non-genic transcripts, some arise from previously non-transcribed genomic regions and are therefore referred to as de novo transcripts. The protein-coding potential of these de novo transcripts has sparked the interest of genome researchers to understand the early stages during the emergence of a novel gene. To gain insight on the time scales of the evolutionary dynamics of novel genes, it is therefore key to understand de novo transcript gain and loss rates. Here, we analyze de novo transcript data from seven *Drosophila melanogaster* populations. Based on the transcript frequency spectrum derived from this data, we estimate de novo transcript gain and loss rates. The estimated rates suggest a high turnover of de novo transcripts. Moreover, we find differences between these evolutionary rates across different genomic locations of the de novo transcripts, with the highest gain rates found in non-coding and pseudogenic regions of the genome.

Münster Evolution Meeting

KUHLWILM, Martin

Time: 14:00 -14:30
Room: Aula

Ghost admixture in great apes

A wide range of organisms including humans and other primates experienced a complex history of admixture. In humans, the availability of thousands of modern and ancient genomes allows to detect introgression with good confidence, while the genomic landscapes of introgression have not been studied as thoroughly in other species. Even though multiple introgression events have been described in other clades, a comparative analysis remains a challenge. In our closest living relatives, the great apes, it is impossible to do the same kind of analysis, hence an important path of understanding their evolution is to detect admixture without knowledge on the source population ("ghost admixture"). We have described such an event in bonobos, and compared the distribution of introgression in the genome to that in modern humans. Now, we also find evidence for an admixture event from such an external lineage into the ancestors of eastern gorillas. This introgression event took place before the split of mountain and eastern lowland gorillas, likely more than 40 thousand years ago, and may have influenced perception of bitter taste. When comparing the introgression landscapes of gorillas, humans and bonobos, we find a consistent depletion of introgressed fragments on the X chromosome across these species.

Münster Evolution Meeting

UECKER, Hildegard

Time: 14:30 -15:00
Room: Aula

Mathematical population genetics of bacteria: Evolutionary dynamics on multicopy plasmids

Mathematical models play a fundamental role in understanding evolutionary processes. In this talk, I will present population genetics theory for bacterial adaptation on plasmids. Plasmids are extra-chromosomal DNA elements and prevalent in bacteria, playing a pivotal role in bacterial evolution. For example, antibiotic resistance genes are often located on plasmids. Many plasmids are present in the cell in several copies. Alleles on plasmids are thus subject to dynamics at two hierarchical levels – the intracellular processes of plasmid replication and segregation and the processes at the level of cells, most notably cell division and death. I will present a mathematical framework to study the evolutionary dynamics of alleles on multicopy plasmids. Based on multitype branching processes, we consider the early phase of spread of beneficial mutations and determine the probability that a bacterial population adapts to a harsh environmental change, e.g. develops resistance to an antibiotic. We then characterize the full trajectory of allele fixation. A comparison of our theoretical predictions to results from in vitro evolution experiments confirms our understanding of the dynamics.

VAN ELST, Tobias

Time: 15:05 -15:20
Room: Aula (session 1)

Phylogeography of Gerp's mouse lemur highlights the importance of rivers and altitude as dispersal barriers in Madagascar's humid rainforests

Madagascar is a biodiversity hotspot with exceptionally high levels of endemic diversity. Historical variability in climate conditions likely played a crucial role in shaping the diversification and distribution of species in Madagascar by changing water and habitat availability and thus creating geographic barriers. However, the relative importance of such processes for different forest-adapted taxa in Madagascar is relatively poorly understood because empirical studies are lacking. Here, we combine RADseq-based population genomic inference, coalescent models and ecological niche modelling to reconstruct the phylogeographic history of the lowland specialist Gerp's mouse lemur (*Microcebus gerpi*; Cheirogaleidae). We identify relevant mechanisms and drivers of diversification in humid rainforests of Madagascar's east coast and show that *M. gerpi* diversified during the late Pleistocene, likely through repeated cycles of dispersal punctuated by isolation to refugia as a result of paleoclimatic fluctuations. The inferred ecological niche, patterns of gene flow and genetic differentiation in *M. gerpi* suggest that the potential for rivers to act as biogeographic barriers depended on both their size and the elevation of headwaters. For instance, populations on opposite sides of the largest river in the area with headwaters that extend far into the highlands show particularly high genetic differentiation comparable to that between its two sister species, whereas rivers with lower elevation headwaters have weaker barrier functions as indicated by higher migration rates and admixture. We present a scenario for the diversification of *M. gerpi* and argue that it serves as a model of diversification for other humid rainforest taxa that are similarly limited by geographic factors.

Münster Evolution Meeting

NIETO BLAZQUEZ, Maria Esther

Time: 15:20 -15:35
Room: Aula (session 1)

Impact of feralisation on evolutionary trajectories in the genomes of feral cat island populations

Feralisation is the understudied counterpart of domestication, and refers to the return of domestic taxa to natural habitats. Molecular genetic expectations are well documented in organisms that have undergone domestication, however, these aspects are understudied for feral taxa. In this study, we aim to study the patterns of genetic differentiation between domestic and feral cats, and explore genome-wide patterns of the independent feralisation process in two geographically distant islands. Using whole genome sequencing data of unrelated feral cats from Dirk Hartog Island (Australia) and Kaho'olawe (Hawaii), worldwide domestic cats and wildcats, we investigate the population structure, genetic differentiation (FST), genetic diversity (π), highly differentiated genes and recombination rates. Our results show that clear split between domestic-feral cats vs wildcat (PC1 explained 18.3% of the total variance). Moreover, PC2 explained 7.9% of the total variance and split between Hawaiian feral cats and the rest of Felis catus individuals. Mean genome-wide FST for feral and domestic cats was 0.056 and, FST above the 99.8% threshold for Australian and Hawaii feral cats with domestic cats (FST = 0.518 and FST = 0.618) were considered for the selection analyses. π was generally low and higher for domestic cats than feral and wildcats, as for Watterson's Theta (θW) estimator. Mean Tajima's D (TD) showed slight differences in mean values. We found 78 and 65 highly mutually differentiated genes for Australian and Hawaiian feral cat with domestic cats, respectively. For both, Australian and Hawaiian feral cats, almost 50% of these genes were related to nervous system development. Recombination rates were also higher in domestic than feral and wildcats. Finer exploration of π and TD in the divergent regions, points towards relaxed selection in the feral populations. This study shows that feralisation in cats is not a reversal of domestication, but rather an adaptation process that brings feral cats on a unique evolutionary trajectory with an open outcome most likely due to different selective pressures and environmental circumstances during the feralisation process.

Münster Evolution Meeting

KALYANARAMAN, Dhevi

Time: 15:35 -15:50
Room: Aula (session 1)

Genetic architecture of hybrid incompatibility and potential rescue mechanisms in the parasitoid wasp genus *Nasonia*

The evolution of hybrid incompatibilities is a driving force of speciation as it helps to form and maintain new species. Genes responsible for postzygotic isolation, also known as speciation genes, are only known for a handful of model organisms. We used recombinant F2 males from the cross between *Nasonia vitripennis* (Nv) x *Nasonia girault*i (Ng) to identify genes/loci underlying F2 hybrid mortality. We corroborated, that 98% of surviving recombinant F2 hybrid males from this cross with Ng cytoplasm retained a Ng allele for a marker at the previously reported incompatibility region located at the distal end of chromosome 5. The remaining 2% of males had a Nv allele at this marker. This extreme bias from the expected 50:50 segregation of parental alleles indicates that inheriting Nv alleles at this region is incompatible with Ng cytoplasm. Detailed genomic analyses of the 2% of surviving recombinant F2 *Nasonia* hybrid males carrying a Nv allele at the marker on chromosome 5 changed the transmission ratio of alleles in chromosomes 1, 3 and 4. Large regions of these chromosomes were significantly biased towards *N. girault*i alleles. This transmission bias towards Ng genotype in other chromosomes when selected for incompatible genotype in chromosome 5 indicates potential epistatic nuclear-nuclear interactions involved in rescuing these males destined to die due to the effect of having a N. vitripennis allele at the distal end of chromosome 5. Moreover, these "2% males" retained species specific genes on chromosomes 1, 2 and 4 that are present in *N. girault*i but not in *N. vitripennis* including a candidate gene (*Ndufa3*), that is coding for a protein subunit of mitochondrial complex I involved in OXPHOS pathway. One explanation is that retaining this Ng specific nuclear gene, *Ndufa3*, is important for a functional mitochondria of the F2 hybrid males having a *N. girault*i cytoplasm. Together, these results argue for a complex and dynamic set of genetic interactions, that include both nuclear-nuclear and nuclear-mitochondrial interactions, underlying the observed variation of hybrid incompatibility between *N. vitripennis* and *N. girault*i. It seems that even the strongest incompatibility can be rescued by changes of the genomic composition in other parts of the hybrid genomes.

Münster Evolution Meeting

LIEVENS, Eva

Time: 15:05 -15:20
Room: S1 (session 2)

Artificial selection reveals evolutionary constraints in a large virus

Evolutionary theory predicts that various factors can constrain adaptation, including trade-offs, mutation supply, and epistasis. We used a large lytic virus, PBCV-1 (~360kb genome), and its unicellular algal host, *Chlorella variabilis*, to investigate the impact of trade-offs and genetic background on evolution. Twelve different genotypes of PBCV-1 were exposed to two artificial selection treatments: one treatment selected for faster lysis, the second for faster lysis and higher attachment. After 16 passages, the evolved lines were phenotyped, sequenced, and compared to their ancestors. Both lysis time and attachment significantly improved in the evolved lines, but at a cost of burst size. Thus our results demonstrate a trade-off between progeny quantity on the one hand, and progeny quality and production speed on the other hand. There were clear effects of the ancestral genotype on the phenotypic and genotypic changes, suggesting that epistasis also played an important role in the evolution of this virus. Overall, we found that both trade-offs and epistasis were substantial constraints for the adaptation of this large virus.

Münster Evolution Meeting

BERRÍOS-CARO, Ernesto

Time: 15:20 -15:35
Room: S1 (session 2)

Antibiotic resistance evolution under non-mixing and mixing transfer strategies

In evolution experiments, bacterial populations are often subject to serial transfers, i.e., a fraction of the population is transferred from one well (or medium) to another. These transfers are usually performed following either non-mixing or mixing sampling strategies. In the former, bacterial populations are transferred independently of each well; in the latter, bacterial populations of each well are mixed before being transferred to other wells.

Recent evolution experiments in *Pseudomonas aeruginosa* populations conducted by Hinrich Schulenburg's group have observed that the mixing sampling strategy employed has important consequences in resistance evolution. Their findings demonstrate that mixing strategies favour the evolution of resistance compared to non-mixing strategies. This behaviour is observed in single- and double-drug therapies.

In this presentation, I will show the factors that come into play in this phenomenon. Through a mathematical model, I will quantify the effect of stochasticity in mixing and non-mixing strategies. I will explore two sources of stochasticity: demographic noise and randomness in the transfer sampling. Additionally, I will test the implications of assuming a usual birth-death process to model bacterial growth against more realistic models that consider a given distribution for the inter-division times of cells. I will show the consequences in the distribution of mutants of assuming each approach in the evolution of resistance under non-mixing and mixing strategies.

Münster Evolution Meeting

NYHOEGEN, Christin

Time: 15:35 -15:50
Room: S1 (session 2)

Mathematical models for the optimization of multi-drug treatment strategies

The rapid evolution of drug resistance frequently causes treatment failure of standard antibiotic therapies. One option to reduce the risk of resistance evolution is to increase the genetic barrier to resistance, which can, for example, be achieved by increasing the number of drugs applied throughout the treatment. Different drugs could be alternated (sequential therapy) or administered simultaneously (combination therapy). Mathematical models allow us to compare the evolutionary dynamics during the treatment of a given strategy under different conditions. We can test whether observations regarding these strategies from laboratory experiments still hold in a more 'patient-like' environment when including specific host-related factors, such as fluctuating drug concentrations due to the pharmacokinetics of the drugs or a limit of the overall drug dose to avoid toxicity. With our modelling approach, we were able to show that drug-drug interactions strongly influence the optimal cycling frequency during a sequential regimen in a patient, as doses from consecutive admirations can overlap in the body. Although laboratory experiments suggest rapid cycling frequencies, slower cycling can sometimes be preferable for patient treatment. For treatments with a limited overall dose, we observed that the simultaneous administration, in which the dose is split over multiple drugs, is not always superior to the administration of just one drug. A result which strongly depends on the drug's pharmacodynamics and the rate at which single and double resistance evolves. While the dynamics during multi-drug treatments are complex and depend on many factors, our mathematical approach helps us to disentangle where the benefits of a specific strategy arise from and how to optimize the treatment settings for potential clinical use.

Münster Evolution Meeting

ENARD, Wolfgang

Time: 16:20 -16:50
Room: Aula

Evolution of molecular circuitries in primates

To understand how genotype-phenotype relations evolve in primates is important from an evolutionary, medical and cultural perspective. I will present different approaches that we use to tackle this question. This will include how we generate and analyse induced pluripotent stem cells from different primates and how the protein sequence and regulatory sequences of TRNP1 co-evolve with cortical folding in mammals.

Münster Evolution Meeting

FELDHAAR, Heike

Time: 16:50 -17:20
Room: Aula

External immunity: The role of antimicrobial secretions in the evolution of insect immune systems

When we think of the immune system of an organism we usually picture the immune system as a complex system within an organism's body that is able to sense and react to various pathogens threatening the integrity and homeostasis of the host organism. In contrast, the application of antimicrobial secretions in the environment is not generally viewed as part of the immune system. Manipulating the microbial environment nevertheless constitutes a first barrier to pathogens. Hygienic measures ranging from the protection of oneself or conspecifics, the nesting site, to stored food may be more efficient with secreted antimicrobials. Thus antimicrobial secretions represent an extended arm of the immune system – for which we have coined the term "external immunity" - forming an underappreciated selective force in the evolution of immune systems. Integrating external immunity into the immune system and general host physiology provides an amenable concept for the understanding of immune system variation and life history trade-offs. Here I will introduce the concept and will provide examples where of the complementary or additive roles of antimicrobial secretions in relation to internal immunity in social insects.

Münster Evolution Meeting

COLGAN, Joe

Time: 17:25 -17:40
Room: Aula (session 1)

Signatures of adaptation, constraints, and potential redundancy in the immune genes of a key pollinator

All organisms require an immune system to recognise, differentiate and defend against pathogens. In general, the enormous selective pressures exerted by pathogens on their hosts has suggested that immune genes should be fast-evolving to cope with evolving pathogenic threats. However, given the functional diversity and pleiotropic nature of genes involved in the immune system, immune genes likely evolve under different types of selection. Wild insect pollinators represent a powerful and timely system to examine immune gene evolution given their observed recent declines driven, in part, by pathogen spread. However, our understanding of the genetic variation maintained within immune genes and how they are evolving in wild populations of pollinators is poor. To address this, we performed whole-genome resequencing of wild-caught *Bombus terrestris*, a common bumblebee species of ecological and commercial importance. We assessed nucleotide diversity and extended haplotype homozygosity within canonical immune genes and found that such genes are evolving under different selection pressures. For example, we found strong signatures of recent positive selection acting on antiviral defence and pathogen recognition genes, which may be possibly driven by growing pathogen spread in wild populations. However, our analysis also found genes evolving under strong purifying selection, highlighting potential constraints. Furthermore, we identified a number of immune genes carrying potential loss of function alleles suggestive of potential redundancy within the bumblebee immune system, which is surprising given their conservative immune gene repertoire. Collectively, our analysis provides novel in- sights into the recent evolutionary history of the immune system of a key pollinator, highlighting targets of selection, evolutionary constraints, as well as potential redundancy.

BAST, Jens

Time: 17:40 -17:55
Room: Aula (session 1)

Independent haplotype evolution and innovation in the long-term absence of sex in the oribatid mite *Platynothrus peltifer*

Ancient asexuals defy the scientific consensus that sex is a prerequisite for evolutionary persistence of species and how they escape their dead-end fate remains enigmatic. Here, we generated a haplotype-resolved, chromosome-scale genome of the parthenogenetic diploid oribatid mite *Platynothrus peltifer* and sampled worldwide populations. We found that large populations can contribute to maintaining effective selection and haplotypes diverge independently since the transition to asexuality at least 15 my ago. Several lines of evidence indicate conservation of one haplotype and release of evolutionary constraints in the other. Our findings imply that absence of sex can lead to novel and previously unknown routes of evolutionary innovation via haplotypic independence helping some asexual species to adapt, diversify and persist for millions of years.

Münster Evolution Meeting

GIROUD, Sylvain

Time: 17:55 -18:10
Room: Aula (session 1)

Lifelong effects of the use of energy-saving strategies during development in a small hibernator

Heterothermy, or torpor, allows individuals to save energy via metabolic depression associated with reduced body temperature. Social thermoregulation, or huddling, can be used in association with torpor to enable individuals to minimize energy needs while maintaining a relatively high body temperature necessary for growth. To date, little is known about the developmental flexibility of heterothermy and how it relates to its expression later in life. In this study, we assessed torpor patterns of juvenile garden dormice (*Eliomys quercinus*) subjected to four distinct conditions, i.e., housed singly or in groups of four individuals, and provided with food ad-libitum or intermittently-fasted. We further determined the expression of heterothermy at adulthood and measured telomere lengths, the end caps of chromosomes that are a good indicator of cellular ageing, over four years of life in individuals which expressed different levels of torpor during development; the highest (top third) or the lowest (bottom third), namely 'high torpor use' ('HT') and 'low torpor use' ('LT') respectively. We found that juvenile dormice use more frequent and longer torpor bouts when housed individually than in groups during fall, and that torpor use was stimulated by reduced food availability prior to hibernation. Interestingly, we found that HT dormice still displayed a higher torpor frequency and longer torpor duration compared to LT individuals one year later (as subadults) irrespective of food treatment. This significant difference in torpor use between HT and LT individuals remained visible among two years-old dormice (adults) fed ad- libitum, but disappeared when the latter were intermittently-fasted during the pre-hibernation fall. Further, we found that HT dormice had a greater use of seasonal heterothermy during the winter, but meanwhile shortened telomeres faster than LT individuals across four years of life. Hence, we conclude that developmental expression of heterothermy in the garden dormouse determines the use of heterothermy and affects the somatic maintenance of individuals later in life.

Münster Evolution Meeting

O'DONNELL-LURIA, Anne

Time: 17:25 -17:40
Room: S1 (session 2)

Approaches from the Genome Aggregation Database (gnomAD) to improve rare variant interpretation

In contemporary human populations, genomic and phenotypic variation reflect patterns of evolutionary change across deep biological time. Our ability to sequence human genetic variation and measure population allele frequencies has far outpaced our ability to interpret the functional impact of genetic variants. In the diagnostic evaluation of rare disease, this poses a critical challenge as exome sequencing is employed with increasing frequency, yet half of patients still do not receive a molecular diagnosis. Large reference datasets have helped to characterize the amount of rare variation across the human genome, including from the >180,000 individuals in the Genome Aggregation Database (gnomAD). Additional datasets of structural variants, mitochondrial variants, and tandem repeat expansions further enrich the utility of the database. While only aggregate data is available from gnomAD, a recently added feature is the ability to query whether two rare variants within a gene co-occur in individuals in gnomAD and whether these variants are predicted to be on the same or different haplotypes. This approach was validated using 4,992 trios, leveraging the fact that we can uniquely phase variants using trios (father, mother, child) as a "truth" set, where it was shown that there is 92-99% accuracy for variants when they are on the same haplotype (cis) and 90-97% accuracy for variants when they are on different haplotypes (trans), depending on the population. We are expanding this approach to report aggregate biallelic variant pairs for each gene in gnomAD, such as the percentage of individuals with two loss of function variants or a loss of function and a predicted damaging missense variant. The power of reference data will continue to increase as the databases grow in size, with the generation and quality control of gnomAD v4 currently underway for release in 2023. Thus, gnomAD is a dynamic genomic resource for the evolutionary biology community and enables uncovering both broad evolutionary patterns and specific information about individual genes.

Münster Evolution Meeting

JONES, Alun Robert Claude

Time: 17:40 -17:55
Room: S1 (session 2)

Transcription factor in Blattodea

“Endless forms most beautiful” is an iconic phrase in biology describing the stunning diversity in morphology and behaviour across the tree of life. Eusocial insects, with their queen and worker caste system, exemplify this by displaying inordinate behavioural and morphological polyphenisms across species. Despite variation between castes being a defining trait of eusociality the molecular process regulating the determination of caste from a single genome are poorly understood. This study investigates the evolution of transcription factors (TFs) in 8 species of the comparatively lesser studied blattodea, which consist of solitary and gregarious cockroaches and eusocial termites. By looking at how transcription factors evolve in relation to social evolution, we hope to identify trends that are consistent with eusocial evolution. Using 70 known insect TF DNA binding domains, we identified 1692 TF containing orthogroups of these 45 had undergone significant gene family expansions or contractions in termites. We found relaxed selection in 13 genes compared to only 3 undergoing intensified selection and 8 genes under relaxed selection. None of these consist of specific TF families but the promoters of TFs showed enrichment in homeo and C2H2 zinc fingers in termites. This would indicate that within blattodea polyphenism characteristic of social evolution is driven more by changes in gene regulatory networks rather than changes in particular gene families but looking into the dynamics of the PFAM domains and gene family changes relate to one another will give a clearer insight into this.

Münster Evolution Meeting

JOVANOVIC, Vladimir M.

Time: 17:55 -18:10
Room: S1 (session 2)

Evolution of non-coding DNA in great apes – species-specific binding sites of ZEB2

Evolutionary new complex phenotypes, such as the larger human forebrain, cannot be solely attributed to protein-coding changes between humans and great apes. Understanding the molecular basis of such changes also requires an analysis of the non-coding parts of the genome and its regulatory outcome, the transcriptome. Transcription factors (TFs) play an important role in regulating transcriptional dynamics by binding to specific short non-coding sequences of the genome, called Transcription Factor Binding Sites (TFBS). Here we analyzed evolutionary changes in binding sites of one TF, ZEB2, which has been proposed to be involved in human brain evolution. We performed ChIP-Seq in EBV-transformed lymphoblastoid B-cell lines of three primate species (human, chimpanzee, and orangutan) with three biological replicates each. Surprisingly, we found that ZEB2 is not only binding to its known canonical binding E-box sequence, but also to an array of similar TFBS. Furthermore, we also discovered TFBS that differed noticeably among the studied species in regard to the nearest gene that could be regulated by ZEB2, as well as regarding binding motifs. A high share of the potential ZEB2 target genes unique to humans are involved in gene regulation, for example as chromatin regulators, or by binding to RNAs or proteins. On the other hand, the targets conserved across all three studied species were mostly connected to immune functions. Taken together, we identified conserved, as well as species-specific binding sites of ZEB2, with human specific diversification in bound sequences pointing to an increased complexity of gene regulation downstream of ZEB2 in humans.

Münster Evolution Meeting

16th MARCH, 2023

Münster Evolution Meeting

FOITZIK, Susanne

Time: 09:35 -09:50
Room: Aula (session 1)

Task-specific patterns of odorant receptor expression in worker antennae indicates a sensory filter regulating division of labour in ants

Division of labor (DOL) is a characteristic trait of insect societies, where tasks are generally performed by groups of specialized individuals. In social insects, young workers perform duties within the safety of the nest (e.g., brood care), while older ones undertake riskier tasks (e.g., foraging for food). This DOL remains dynamic, and workers may switch back and forth when colony needs require. Theoretical models propose that workers differ in their thresholds to take on certain tasks when confronted to task-related stimuli, resulting in variation in their response to such stimuli, task-specialization, and thus DOL. Such models assume that workers differ in how they respond to task-related information rather than in how they perceive such information. Here, we test the hypothesis that DOL rather stems from workers differing in their efficiency to detect task-related stimuli. We used transcriptomics to compare gene expression in the antennae and in the brain between nurses and foragers in the ant *Temnothorax longispinosus*. We found that seven times as many genes were differentially expressed between the behavioral phenotypes in the antennae compared to the brain. Moreover, nearly half of all odorant receptors genes were differentially expressed, with an overrepresentation of the 9-exon gene subfamily upregulated in the antennae of nurses. These findings indicate that nurses and foragers differ in how they perceive their olfactory environment, and task-related signals. The results of this study support the hypothesis that a sensory filter in the antennae predisposes workers to specialize in specific tasks, and may improve our understanding of DOL in insect societies.

Münster Evolution Meeting

DOBLER, Susanne

Time: 09:00 -09:30
Room: Aula

Genetic constraints and degrees of freedom in the escape from toxic cardiac glycosides - lessons from herbivores, predators and prey

Cardiac glycosides are chemical defense toxins known to fatally inhibit the essential transmembrane Na,K-ATPase throughout the animal kingdom. Nevertheless, several animals that are exposed to dietary or endogenous cardiac glycosides have evolved target-site insensitivity through substitutions in the otherwise highly conserved cardiac glycoside binding pocket of the Na,K-ATPase. Most strikingly, identical amino acid substitutions in the first extracellular loop of the enzyme evolved convergently in vertebrates and insects alike. Yet, despite a high degree of convergence, intra-molecular epistasis influences the optimal solution to achieve resistance. To understand the rules that govern these fine scale evolutionary processes we functionally tested genetically engineered proteins and crispr-cas9 genome edited flies. These experiments revealed that compensatory mutations in other parts of the protein help mitigate pleiotropic effects that pronounced resistance otherwise has an ion pumping activity and higher level phenomena.

GIROUD, Sylvain

Time: 09:35 -09:50
Room: Aula (session 1)

Lifelong effects of the use of energy-saving strategies during development in a small hibernator

Heterothermy, or torpor, allows individuals to save energy via metabolic depression associated with reduced body temperature. Social thermoregulation, or huddling, can be used in association with torpor to enable individuals to minimize energy needs while maintaining a relatively high body temperature necessary for growth. To date, little is known about the developmental flexibility of heterothermy and how it relates to its expression later in life. In this study, we assessed torpor patterns of juvenile garden dormice (*Eliomys quercinus*) subjected to four distinct conditions, i.e., housed singly or in groups of four individuals, and provided with food ad-libitum or intermittently-fasted. We further determined the expression of heterothermy at adulthood and measured telomere lengths, the end caps of chromosomes that are a good indicator of cellular ageing, over four years of life in individuals which expressed different levels of torpor during development; the highest (top third) or the lowest (bottom third), namely 'high torpor use' ('HT') and 'low torpor use' ('LT') respectively. We found that juvenile dormice use more frequent and longer torpor bouts when housed individually than in groups during fall, and that torpor use was stimulated by reduced food availability prior to hibernation. Interestingly, we found that HT dormice still displayed a higher torpor frequency and longer torpor duration compared to LT individuals one year later (as subadults) irrespective of food treatment. This significant difference in torpor use between HT and LT individuals remained visible among two years-old dormice (adults) fed ad- libitum, but disappeared when the latter were intermittently-fasted during the pre-hibernation fall. Further, we found that HT dormice had a greater use of seasonal heterothermy during the winter, but meanwhile shortened telomeres faster than LT individuals across four years of life. Hence, we conclude that developmental expression of heterothermy in the garden dormouse determines the use of heterothermy and affects the somatic maintenance of individuals later in life.

Münster Evolution Meeting

LENHART, Anna

Time: 09:50 -10:05
Room: Aula (session 1)

Survival and gene expression in an invasive ant

Most organisms face a trade-off between fecundity and longevity. Social insects seemingly overcome this trade-off, as the most fertile individuals (queens) are also the longest-lived ones. In contrast, workers do not or cannot reproduce, and live shorter lives. Yet, after queen loss, workers in many ant species become fertile, lay unfertilized, haploid eggs, and exhibit increased lifespans. In polygynous societies, workers rarely have the opportunity to reproduce. However, we demonstrated that workers of the polygynous invasive ant *Tapinoma magnum* frequently develop eggs in their ovaries. We investigated whether queen number affects fecundity and survival of large and small inside workers (nurses) and outside workers (foragers) of this polymorphic species. Moreover, we analyzed how tissue-specific transcriptomes vary between young and old queens and how workers respond to queen number. We created queenless, one-queen, and two-queen colonies and examined ovarian development, oxidative stress resistance and survival in workers over eight weeks. Workers from monogynous colonies survived best, followed by those from two-queen colonies and finally from queenless colonies. Survival differences are not due to variation in oxidative stress resistance as this did not vary between treatments. Indeed, inside workers showed an increased resistance against oxidative stress compared to outside workers. *T. magnum* workers may activate their ovaries as a response to queen number, possibly explaining variation in survival. As we have no evidence that worker-laid eggs develop, our results indicate that increased production of trophic eggs might be linked to a decrease in mortality in monogynous colonies. Ovarian development in young (< three months) and old (> one year) *T. magnum* queens did not differ, and we are currently conducting transcriptomic analyses in queens and workers to investigate how gene expression changes with age and social structure in this invasive ant species.

Münster Evolution Meeting

TUGRUL, Murat

Time: 10:05 -10:20
Room: Aula (session 1)

Evolutionary and demographic outcomes of damage dynamics in single-cell bacteria

Ageing influences evolutionary dynamics, for instance by altering the fixation probability of new mutations in a population. Despite this importance, the molecular roots of ageing and how they are linked to demographic and evolutionary outcomes are surprisingly little understood. Damage accumulation is a leading factor driving ageing dynamics in individuals and shapes the fitness components like reproduction and survival. Bacterial single cells provide unique opportunities to study ageing dynamics at the molecular, demographic and evolutionary levels. Here, we first present a modelling approach that links stochastic damage dynamics at the single-cell level to the demographic fates of the individual cell lineages and to the population dynamics in bacteria. We show for example how noise in damage accumulation changes the variation in lifespans and how it alters population growth, i.e., fitness. In parallel with our theoretical work, we conduct experimental investigations in the mother machine (microfluidic devices combined with fluorescence microscopy) to better observe molecular and demographic patterns in damage and ageing dynamics at the single-cell level over several generations. Here we consider general stress response evaluated by RpoS transcriptional activity under different nutritional conditions including starvation. RpoS is the stress-response sigma factor in *E.coli* and is considered to correlate with intracellular damage levels. We present lifespan distributions under different nutritional and stress levels and show how both mean and variance in RpoS signal increases across cell lineages before they die. Our results shed light on the underlying stochastic damage dynamics leading to observed heterogeneity in life courses with possible evolutionary consequences.

PALLARES, Luisa

Time: 10:20 -10:35
Room: Aula (session 1)

The dynamic nature of the Genotype-Phenotype map: a story about how dietary stress remodels the genetic architecture of lifespan variation in *Drosophila*

Our understanding of the genetic basis of complex traits, including fitness-related traits, is mostly based on mapping studies that identify genotype-to-phenotype associations. Due to the challenges in performing high-resolution mapping experiments, such genotype-phenotype map in usually explored in just one environment. However, evolutionary theory as well as empirical work suggest that such map is often environmentally dependent, and that such genotype-by-environment (GxE) interactions are key to understanding phenotypic variation. Here, we use a large population of outbred *Drosophila melanogaster* to identify the genetic basis of lifespan in two conditions: control and high sugar diets. We sequenced over 10,000 individual flies to track genome-wide allele frequency changes over the lifetime of six replicate populations, recording in real time the changes in the genomic composition of each population as flies aged. The high statistical power of this experimental design allowed us to draw the genotype-phenotype map for lifespan variation under control conditions, and the way such map got remodeled in response to dietary stress. Remarkably, a third of the lifespan-associated alleles appear cryptic in control diet but play an important role in high sugar conditions. Our results provide strong evidence for the pervasive nature of cryptic genetic variation and the key role that it plays in shaping phenotypic variation between individuals.

Münster Evolution Meeting

RAVI, Bharat

Time: 09:35 -09:50
Room: S1 (session 2)

Evolutionary trajectory of de novo gene emergence

New protein coding genes can emerge from genomic regions that previously did not contain any genes, via a process called de novo gene emergence. To synthesize a protein, DNA must be transcribed as well as translated. Both processes need certain DNA sequence features. Stable transcription requires promoters and a polyadenylation signal, while translation requires at least an open reading frame (ORF). We develop mathematical models based on mutation probabilities, and the assumption of neutral evolution, to find out how quickly genes emerge and are lost. We also investigate the effect of the order by which DNA features evolve, and if sequence composition is biased by mutation rate. We rationalize how genes are lost much more rapidly than they emerge, and how genes with long ORFs preferentially arise in regions that are already transcribed. Our study not only answers some fundamental questions on the topic of de novo emergence but also provides a modeling framework for future studies.

Münster Evolution Meeting

AUBEL, Margaux

Time: 09:50 -10:05
Room: S1 (session 2)

De novo proteins and their unevolved random-sequence counterparts

De novo gene emergence provides a route for new proteins to be formed from previously non-coding DNA. Proteins born in this way are considered random sequences, and typically assumed to lack defined structure. While it remains unclear how likely a *de novo* protein is to assume a soluble and stable tertiary structure, intersecting evidence from random-sequence and de novo- designed proteins suggests that native-like biophysical properties are abundant in sequence space. Taking putative de novo proteins identified in human and fly, we aim to experimentally characterise libraries of these sequences to assess their solubility and structure propensity. We compare the de novo protein sequences to a set of synthetic random proteins with no evolutionary history. Bioinformatic prediction suggests that de novo proteins may have remarkably similar distributions of biophysical properties to unevolved random sequences of a given length and amino acid composition. However, upon expression in vitro, *de novo* proteins exhibit higher solubility which is further induced by the DnaK chaperone system. We suggest that while synthetic random sequences are a useful proxy for de novo proteins in terms of structure propensity, *de novo* proteins may be better integrated in the cellular system than random expectation, given their higher solubility.

Münster Evolution Meeting

CHEN, Yao-Chung

Time: 10:05 -10:20
Room: S1 (session 2)

Unwinding the regulatory networks of KRAB zinc finger genes and transposable elements in the evolution of primate brain

Transposable elements (TEs), with their ability to change positions within a genome, have paradoxically been seen both as a dangerous and deleterious genomic phenomenon, and as the evolution's mighty driving force. The genome-safeguarding KRAB-containing zinc finger genes (KZNFs) participate in repressing TEs' expression in mammalian genomes. We hypothesized that the evolutionary arms race between KZNFs and TEs have played a role in the emergence of the primate brain, especially in the evolution of the human brain. Another hypothesis spoke of a "side" consequence of this evolution, that as the human brain has grown larger and more complex over time, it may have become more susceptible to neurodegenerative disorders, such as Alzheimer's Disease (AD). We speculated that TE-KZNF relationships have changed between primate species and in the brain of patients with neurodegenerative disorders. To test these hypotheses, we analyzed co-expression networks of KZNFs and TEs in two independent RNA-seq datasets: (1) from 33 brain regions of multiple humans, chimpanzees, bonobos and macaques, and (2) from the temporal cortex and cerebellum of control individuals and persons with AD. For an efficient way to systematically analyze the regulatory networks, we developed an R package called TEKRABber, that estimates the correlations between TEs and KZNFs across species. Focusing on the strongest correlations between TEs and KZNFs (Pearson's Correlation Coefficient larger than 0.8 or lower than -0.8, $p < 0.05$), we found more negative correlations in areas including cortices and white matters in humans than other primates. On the other hand, we detected more positive correlations in areas such as hypothalamus, thalamus, and striatum. Comparative analysis of the TE expression profiles between control and AD identified 198 upregulated TEs and 232 downregulated TEs in temporal cortex while in cerebellum 56 TEs were upregulated and 17 TEs downregulated. These findings suggested that the variations in TEs-KZNFs correlations across different brain regions could be related to their specific functions.

Münster Evolution Meeting

VAN DEN BOS, Esther

Time: 10:20 -10:35
Room: S1 (session 2)

Phenotypic robustness differs between queen and worker caste

The parallels between germline/soma differentiation in multicellular organisms and queen/ worker differentiation in social insects were first recognized a century ago (Weismann, 1893). In multicellular organisms, somatic cells have evolved a stunning phenotypic diversity and functional specialization, providing the foundation for complex body plans. Analogously, in social insects the worker caste has evolved remarkably specialized traits and phenotypes, thus allowing for the exploitation of particular ecological niches. Relaxed evolutionary constraints in workers due to indirect selection is one factor underlying the apparently faster trait evolution in this caste. We hypothesize that reduced phenotypic robustness (i.e. less stringent phenotypic canalization) in workers particularly under aberrant/stressful environmental condition could contribute to the seemingly accelerated trait evolution in this caste. Therefore, we tested whether phenotypic robustness differs between castes by quantifying morphological variation between queens and workers of the ant Cardiocondyla obscurior upon pharmacological suppression of Hsp90, a central player of the cellular canalization machinery. Our findings show that Hsp90 inhibition leads to an increased phenotypic variation in workers, but not in queens. Therefore, analogous to the germ-plasm theory, queens (germline) seem to have a higher level of protection against phenotypic variation than workers (soma) under stressful environmental conditions.

Münster Evolution Meeting

KÖNIG, Barbara

Time: 11:15 -11:45
Room: Aula

Mouse tales - Why do female house mice join forces to care for litters communally

Social interactions play a crucial role in the lives of organisms and influence varied aspects of an individual's life history, physiology and behaviour. Individuals benefit from social interactions, but at the same time compete over access to resources. A challenging situation here is that the social environment is characterised by a high degree of flexibility and intrinsic unpredictability and is thus considered a complex and fluctuating component of an individual's environment. Our research focusses on social interactions in an evolutionary framework and uses an integrative approach to understand how differences in the social environment lead to differences in social interactions that translate into fitness differences between individuals. We do so by utilising a long-term data set on a population of wild house mice (Mus musculus domesticus) and aim to investigate general principles underlying the evolution of sociality and its endocrine and neural mechanisms. I will highlight communal offspring care among female house mice to illustrate how decision making and social partner choice allow to stabilise cooperation and affect the dynamics of social groups and the entire population.

2ND Münster Evolution Meeting - 2023 schedule

March 13, 2023 (MONDAY)		
	Session 1 (Room: Aula)	**Session 2 (Room: S1)**
13.00-14:00	Registration	
14.00-14.15	Welcome	
14.15-14.45	Invited talk 1 – Meyer	
14.45-15.15	Invited talk 2 – Mazzoni	
15.15-15.20	change rooms if needed	
		SPP-RAPID ADAPTATION SYMPOSIUM
15.20-15.35	Pinedo	Metzger
15.35-15.50	Zemella	Eldon
15.50-16.20	coffee break	
16.20 -16.50	Invited talk 3 - Reich	
16.50-17.00	change rooms if needed	
17.00-17.15	Menzel	Roth
17.15-17.30	Feldmeyer	Wendling
17.30-17.45	Büllesbach	Krämer
17.45-18.00	Sun	Kusch
18:00-20:00	Welcome reception + Poster session 1	

March 14, 2023 (TUESDAY)		
	Session 1	**Session 2**
9.00-9.30	Invited talk 4 - Haug	
9.30-10.00	Invited talk 5 - Barton	
10.00-10.05	change rooms if needed	
10.05-10.20	Reinhold	Wang
10.20-10.35	Steiner	Stift
10.35-11.05	coffee break	
11.00-11.30	Invited talk 6 - Heide	
11.30-11.35	change rooms if needed	
11.35-11.50	Lee	Huylmans
11.50-12.05	Fic	Darras
12.05-13.50	lunch break	
13.50-14.00	Joachim Kurtz – Introducing MGSE	
14.00-14.30	Invited talk 7 - Wittmann	
14.30-15.00	Invited talk 8 - Kerp	
15.00-15.05	change rooms if needed	
		MGSE SYMPOSIUM
15.05-15.20	Salem	Mikhailova

Münster Evolution Meeting

2ND Münster Evolution Meeting - 2023 schedule

15.20-15.35	Myrie	Manske
15.35-16.05	coffee break	
16.05-16.20	Becks	Schmitz
16.20-16.35	Ona Bubach	Rinke
16.35-16.50	Pauli	Korsa
16.50-17.00	short break	
17.00-17.15	Erbii	Altinok
17.15-17.30	Lin	Temme
17.30-17.45	Schultner	Keizers
17.45-18.30	start of poster session 2	
18.30-19.30	**Public evening lecture by Marc Stoneking**	
19.30-21.00	poster session 2	

March 15, 2023 (WEDNESDAY)		
	Session 1	**Session 2**
9.00-9.30	Invited talk 9 - Widdig	
9.30-10.00	Invited talk 10 - Schlötterer	
10.00-10.05	change rooms if needed	
		SPP - GEvol SYMPOSIUM
10.05-10.20	Gröschel	Heckenhauer
10.20-10.35	Wohlleben	Dohmen
10.35-11.05	coffee break	
11.05-11.20	Edison	Posnien
11.20-11.35	Rajendra	Glaser-Schmitt
11.35-11.50	Schulz	Grandchamp
11.50-12.05	Menges	Czuppon
12.05-14.00	lunch break	
14.00-14.30	Invited talk 11 - Kuhlwilm	
14.30-15.00	Invited talk 12 - Uecker	
15.00-15.05	change rooms if needed	
15.05-15.20	van Elst	Lievens
15.20-15.35	Nieto Blazquez	Berrios-Caro
15.35-15.50	Kalyanamaran	Nyhoegen
15.50-16.20	coffee break	
16.20-16.50	Invited talk 13 - Enard	
16.50-17.20	Invited talk 14 - Feldhaar	
17.20-17.25	change rooms if needed	
17.25-17.40	Colgan	O'Donnell-Luria
17.40-17.55	Bast	Jones

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17.55-18.10	Foitzik	Jovanovic
TBA	social event	

March 16, 2023 (THURSDAY)		
9:00-9:30	Invited talk 15 - Dobler	
9:30-9:35	change rooms if needed	
9:35-9:50	Giroud	Ravi
9:50-10:05	Lenhart	Aubel
10:05-10:20	Tugrul	Chen
10:20-10:35	Pallares	Van den Bos
10.35-11.15	coffee break	
11.15-11.45	Invited talk 17 - König	
11.45-12.00	feedback and discussion for MEM2025	
12.00	farewell	

Invited talks (30 minutes: 20-25 min talk + 5-10 min discussion)

Contributed talks (15 minutes: 10-12 min talk + 3-5 min discussion)

Special symposia

13th March 2023: SPP-Rapid Evolutionary Adaptation symposium (SPP-1819)

14th March 2023 (afternoon session): MGSE symposium (Münster Graduate school of Evolution)

15th March 2023 (morning session): GEvol symposium (DFG SPP2349- Genomic basis of evolutionary innovations)

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