

Abstracts from the EvoGenMunich kick-off meeting October 2023

Baldwin lab: Maude Baldwin and Meng-Ching Ko

Evolution of sensory and physiological systems.

Sensory systems are critical for an organism's survival and display remarkable diversity--as different species inhabit different environments and occupy diverse niches, sensory systems rapidly evolve to detect the cues relevant for a particular species. Examining these changes in a comparative context yields insight into the evolution of the nervous system and animal behavior, and into broad questions about basic evolutionary processes such as the extent of convergence, the role of epistasis and contingency, and how novel protein functions arise. As the link between genotype and phenotype is very direct--changes in receptor properties can translate into direct shifts in behavior--sensory receptors provide unique windows into underlying evolutionary mechanisms and allow us to examine the evolution of a behavioral trait across large groups of species. Moreover, examining sensory shifts in the context of additional changes in an organism's physiology, for instance with comparative genomic analyses of convergent sensory and physiological traits, can yield important insights into the relative timing of different traits, allowing us to reconstruct the series of events by which complex integrated phenotypes arise. We will highlight current projects as well as new directions in our work examining the evolution of sensory and physiological diversity in vertebrates.

Becker lab: Claude Becker and Niklas Schandry, LMU Munich

The genetic basis of plant-organismic interactions.

Plants are exposed to and engage with their living environment in a multitude of ways and have evolved intricate strategies to defend themselves and to interact with the organismic communities in their vicinity. My lab studies the genetic and epigenetic components that shape such plant-organismic interactions. In particular, we are interested in the role of plant-derived specialized metabolites and their role in modulation the interaction of plants and microorganisms.

In the first part of the presentation, Claude Becker will illustrate our research using two examples from ongoing studies: First, many Solanaceae produce withanolides, defense compounds that display an enormous variability across the family. We have identified a potential biosynthetic gene cluster that underwent a duplication and sub-functionalisation via epigenetic mechanisms, resulting in two adjacent clusters that are responsible for tissue-specific biosynthesis of different withanolide variants. Our data show that this cluster originated basally in the Solanaceae family and underwent independent lineage-specific

duplications. In the second example, I will show how the modulation of the root-associated microbiome by plant-derived compounds feeds back on plant growth, and how we can use the genetic diversity in *Arabidopsis thaliana* to uncover the genetic basis of the feedback reaction in the plant.

In the second part of the presentation, Niklas Schandry will present his recent work on the mutability of plant-associated bacteria when these are exposed to plant-derived compounds.

Enard lab:

Evolution of Molecular Circuitries.

We are interested in the molecular basis of human evolution and study it using a comparative molecular approach. We investigate brain size evolution, the evolution of speech and the evolution of regulatory networks in primate induced pluripotent stem cells (iPSCs) and their derivatives. Methodologically, we focus heavily on generating and characterizing primate iPSCs and on (single-cell) RNA-seq technologies during early development. We work very closely with the group of Ines Hellmann on the computational aspects of these questions.

Hellmann Group: InesHellmann, ZaneKliesmete, AnitaTermeg

Computational Genomics: Evolution of Gene Expression.

With the advent of sequencing technologies it became clear that the apparently large phenotypic differences between us humans and our close primate relatives must to a large extent be due to regulatory changes. We want to investigate how those regulatory changes and gene regulation per se are encoded in large mammalian genomes. To this end, we take a comparative genomics approach which focuses on closely related primate species. We develop and evaluate methods that enable quantitative comparisons of (single cell) omics data across species. We then find innovative ways to integrate such data to obtain insights about the regulatory code and how it evolves. Two exemplary projects are the investigation of the effects of pleiotropy on regulatory evolution and a method for cross-species comparison of gene regulatory networks.

Höhna lab:

The Höhna lab is working on theoretical and empirical aspects of phylogenetic models of evolution, with a time perspective ranging from thousands of years to deep geological time. On shorter time scales, we infer population trees using genomic data and models that

account for standing genetic variation (polymorphic states). On longer time scales, we use traditional substitution models to infer both gene trees and species trees, learning about shared histories of species. The ultimate goal is to learn about evolutionary patterns and processes over long time scales. Examples include inferring diversification rates in deep time, patterns in phenotypic evolution (e.g. adaptation), and biogeographic history. A central theme in our lab is computational development and implementation of evolutionary models in efficient and easy-to-use softwares. Most analyses are incorporated in the RevBayes software, a flexible and modern successor to the popular MrBayes program used for Bayesian inference of phylogenetic trees. Since RevBayes is modular and allows the user to mix and match different models as necessary, this enables us to combine evidence and models across what has historically been separate fields of research. We show that combining evidence from several disciplines, such as integrating genomic extant data with morphological fossil data, can have a profound impact on evolutionary inference, indicating that there is great but largely untapped potential in cross-disciplinary investigations.

The Kadereit Work Group at LMU:

The Kadereit Work Group at the Chair of Systematics, Biodiversity, and Evolution of Plants of Ludwig Maximilian-Universität München is led by Prof. Dr. Gudrun Kadereit. We focus on Angiosperm phylogenetics, systematics, and biogeography. We have worked in families like Amaranthaceae, Melastomataceae, Crassulaceae, Aizoaceae, Zygophyllaceae, among others. We are also interested in the evolution of C₄ photosynthesis and Crassulacean Acid Metabolism (CAM). We will briefly overview the group's member (postdocs) research interests. Research interests vary from the evolutionary history of Australian arid flora, the dynamics and effects of the Sunda-Sahul floristic exchange, biodiversity and evolution of Afrotropical plants, the evolution of Crassulacean Acid Metabolism (CAM) and related traits, to finally, the evolution of C₄ gene regulation. We will also show the results of a research project focusing on the possible role of hybridization in the evolution of photosynthetic pathways in *Flaveria* (Asteraceae), the prime model of C₄ photosynthesis evolution.

LAFUGA genomics:

Is a collaborative research platform providing access to sequencing technologies for researchers in the Munich area. We have long-standing experience in the generation and analysis of short-read and long-read sequencing data and we provide optimized solutions for a large variety of research questions, dealing with all kinds of samples. We both work service-oriented, providing fast and easy access to our sequencing technologies and research-oriented by helping in experimental design, selection of protocols and method

optimisation and development. In my talk I give an overview of available technologies, own research projects and our capacities for future collaborations.

Clemens Küpper: Research Group Behavioural Genetics and Evolutionary Ecology, MPI for Biological Intelligence Seewiesen

Genetics of reproductive strategies.

Intraspecific variation plays a key role in determining the adaptive potential of species and populations. Sexual selection influences a substantial proportion of intraspecific variation as it affects males and females differently. Our group investigates the ecological and evolutionary mechanisms that shape and maintain intraspecific variation in reproductive strategies. We study causes and consequences of variation in reproductive behaviours with a focus on shorebirds (plovers, sandpipers and allies). This group of birds shows an unusual intraspecific diversity in mating strategies, dispersal rates and sex ratios that are thought to have evolved as a response to differences in sexual selection. We study whether and how variation in population sizes and gene flow is linked to mating systems. Variation in mating systems is thought to have consequences for genetic diversity harbored by autosomes and sex chromosomes. This line of our research uses population genetic analyses to determine genetic diversity of sex chromosomes and autosomes, characterize variation between populations and species in the context of their natural history. As many shorebird populations are declining and require conservation management, these studies help to clear up systematics and focus conservation efforts. Another line of our research aims to characterize the genetic features and maintenance of a prominent genetic and behavioural polymorphism in ruffs *Calidris pugnax*. In this iconic ecological model of sexual selection, an autosomal inversion polymorphism with a limited number of genes encodes different male reproductive tactics that show near discrete differences in reproductive physiology, aggression and courtship. Here, we use transcriptomic studies to characterize variation in gene expression and study candidate genes that are linked to discrete phenotypes. In combination, our studies shed light on the role of reproductive strategies in shaping key population genetic metrics and genomic features.

Plant (pan-) genomics @ Helmholtz Munich: Manuel Spannagl, Nadia Kamal and Klaus Mayer

High-quality and multi-dimensional genomic data have become essential resources to understand evolutionary and biological processes in plants and identify genes and regulatory networks underlying important agronomic traits. Recent years brought breakthroughs in assembly and analysis of even the largest and most complex plant

genomes, such as bread wheat, barley and oat. Reference quality genome assemblies have been generated for barley in 2017 (Mascher et al, Nature), for wheat in 2018 (IWGSC, Science) and for oat in 2022 (Kamalet al., Nature). The high repeat content, extensive transposon activity, large genome sizes and polyploidy have complicated the assembly and analysis of these and other cereal genomes for a long time.

While single reference genomes have now become a standard for most staple crops, multi-genome comparisons are needed to address important questions in plant biology, evolution and breeding. These include the identification of structural variations, domestication of crop plants, identification of regulatory elements and networks as well as access to the core and accessory gene complements of a species. Therefore, pan-genome projects are underway for wheat, barley, oat and many other plants. The intermediate results of these efforts were recently published in Nature (Walkowiak et al, Jayakodi et al, Nature 2020). These projects aim for an integrated analysis of dozens of high-quality genome assemblies representing the natural diversity of the sampled species. The PGSB group at Helmholtz Munich pioneered the analysis of complex plant genomes and pan-genomes, which resulted in the identification of novel genes underlying specific traits such as disease resistances and provided new insights into the evolution of some of our most important staple food crops.

Merrill lab:

Our lab is primarily interested in understanding how ‘speciation behaviours’ are generated during development, and across evolutionary time. To give a sense of the questions and techniques we use, I will give an overview of a major project on the genetics of visual preference in *Heliconius* butterflies. In particular, I will show data on how male preferences for red patterns segregate with a genomic region of increased admixture between red-preferring *Heliconius* butterfly species, indicating that adaptive introgression has contributed to the parallel evolution of visually-guided behaviours in these butterflies. Differences in neural expression of *regucalcin1*, which perfectly coincides with this introgressed region, is associated with visual preference variation, and disruption of *regucalcin1* with *CRISPR/Cas9* alters courtship towards red females, proving a direct link between a gene and behaviour. This work demonstrates how hybridisation may be important for behavioural evolution, and how variation in visually-guided behaviour is encoded at the genetic level. Finally, I will briefly describe some complimentary ongoing work on sensory adaptations in these butterflies.

Dirk Metzler: *Models and inference methods in evolutionary (epi-)genetics*

We model evolutionary processes and develop data analysis methods based on these models. Applications include the evolution of defense traits, dynamics of hybrid zones induced by epistasis on mating cue loci, and population demography inference methods. Further, we develop models for DNA methylation and demethylation dynamics in which we allow that CpG sites belonging to the same CpG island can be affected by simultaneous changes and then follow a new equilibrium distribution in their methylation dynamics. We choose a similar approach for DNA substitution models in phylogenetics, accounting for changes in G–C content.

Julia Tovar Verba: *Conservation genomics of economically valuable species*

We are working with fish genomics, focusing on using both reduced-representation and whole genome sequencing to investigate population structure and demographic history of tropical marine species. Current project focuses on a Brazilian sardine, in which it was identified two independent lineages along the distribution, with independent demographic histories.

Marion Müller: *Host specificity and virulence factors in the cereal powdery mildew pathosystems*

Species from the grass powdery mildew pathogen genus *Blumeria* infect wild grass and cereal crop plants with high but varying degree of host-specificity. The evolutionary history of the *Blumeria* species complex is highly dynamic and involves several host-jumps and hybridization events. However, the fungal and plant genes that determine infection success of individual *Blumeria* lineages on their respective hosts are still unknown and hence the understanding of the evolution of host-specificity remains incomplete. Therefore, our goal is to identify and study host and pathogen genetic factors that determine the interaction outcome and drive co-evolutionary dynamics between *Blumeria* lineages and their corresponding hosts. To do so, we use pathogen and host genomics coupled with crossing, phenotypic association studies and gene function analysis. In another line of research, we study the role of transposable elements (TE) in the evolution of *Blumeria hordei* (*Bh*). In this collaboration between the Tellier and Hüchelhoven group we combine multi-omics approaches with functional analysis and population genetics to determine the impact of transposable elements on genome organization and virulence factors in *Bh*. Specifically, we aim at identifying novel TE-derived candidate effectors that might act as virulence factors for *Bh* on its host barley. In parallel, population genetic analysis will allow us to determine the type and strength of selection occurring at these new effector loci as well as on TE-loci

in general. Together, these results will provide novel insights in mechanisms of TE-driven evolution of virulence functions and genome structure in *B. graminis*.

Parsch/Grath lab: *Evolutionary and Functional Genomics – Of Flies and Men*

In general, we are interested in understanding the molecular basis of adaptation and gene regulation. We study the evolution of genes, gene expression and genomes using various model systems. Current projects focus on variation in gene expression between populations and sexes, population genetic and functional analysis of gene regulatory elements, as well as adaptation to biotic and abiotic stresses.

Research in the Parsch lab can be divided into two major areas: (1) evolutionary and population genetics, and (2) evolution and expression of sex chromosomes. We study DNA sequence and gene expression variation within and between populations of the vinegar fly *Drosophila melanogaster*. We use both genome-wide and candidate-gene studies to better understand the role of gene regulatory changes in adaptation. Similar to humans, *Drosophila* flies have chromosomal sex determination, with males having one X and one Y chromosome and females having two X chromosomes. We study the mechanisms underlying the sex- and tissue-specific regulation of the single X chromosome in males, which is upregulated in the soma, but downregulated in the germline.

In the Grath lab, we are generally interested in understanding how the single genome of an organism can encode for its different entities, e.g. tissues, organs or individual cells. Many of these differences are caused by differences in gene regulation. Gene regulation is a complex interplay of various genetic and epigenetic molecular mechanisms such as genome-wide expression, chromatin accessibility or methylation levels. Next generation sequencing technologies have allowed us to identify genes and gene networks that contribute to the formation of an organism's various entities. Interestingly, the individual contribution of different mechanisms on gene expression regulation can vary between species. DNA methylation, for example, alters gene expression in all kingdoms of life, albeit methylation levels can vary widely. With both experimental and bioinformatic approaches we study the evolution of gene expression and gene function using various systems. Current projects focus on variation in gene expression between different phenotypes and sexes in different insects, as well as the computational and functional analysis of mechanisms that affect gene regulation, for example in human cancers.

Wolf lab: Jochen B. W. Wolf, Sarah A. Mueller, Justin Merondun.

Speciation and adaptation are the major drivers of biodiversity including (epi)genetic, phenotypic and ecological variation. In our research, we explore the evolutionary processes

at work with a focus on (epi)genetic and phenotypic variation and its interaction with the environment. We use a number of model systems ranging from fission yeast to birds and mammals. Here, we present two examples, a case study in #1 swallows and #2 cuckoos. #1: We use the swallow system to gain insight into the source of naturally segregating variation in chromatin modifications (5mC methylation). Leveraging the power of hybrid zones has potential to decompose the contribution of cis-genetic variation and environmental factors. #2: In the cuckoo system, we unravel the genetic basis of a female-limited polymorphism, where males are monochromatic grey and females exhibit either grey or rufous plumage. We show that sex-specific dimorphism in trait variation can be resolved by genetic variation residing on the sex-limited chromosome and be maintained across species boundaries by mechanisms such as balancing selection.