Evolutionary Genetics Community in Munich

Program EvoGenMunich conference

19.-20.3.2026

Carl Friedrich von Siemens Stiftung - Südliches Schloßrondell 23, 80638 München

Thursday 19th of March

08:30 Registration
09:00 Welcome

Plenary talk: Molly Schumer

9:10 The genetic basis of adaptation: from molecular mechanism to evolution in nature
Molly Schumer, Dept. Biology, Stanford University

Talks: Genomic histories

10:20 Genomic insights into the co-evolutionary history of humans and dogs
Lachie Scarsbrook, Paleogenomics, Veterinary Medicine, LMU
10:40 A genomic history of african cattle
James Ward Animal System Genomics, Veterinary Medicine, LMU
11:00 Coffee break

Talks: Expression evolution

11:30 On the number of species required to detect stabilizing selection in gene expression evolution
Haoqing Du, Paleontology & Geobiology, Geosciences, LMU
11:50 prime-seq2 & zUMIs-prime: an end-to-end framework for scalable cross-species transcriptomics
Felix Pförtner, Human Genomics, Biology, LMU
12:10 Assessing evolution of primate atherosclerosis using iPSCs
Eva Briem; Human Genomics, Biology, LMU
12:30 Lunch & Coffee

Talks: Genomic diversity

14:00 Genomic insights into mutation load and genetic purging in cheetahs (*Acinonyx jubatus*) for applied species conservation; *Besufekad Wolde; LAFUGA, Gene Center Munich, LMU*
14:20 Genomic insights into the conservation and divergence of the avenacin biosynthetic gene cluster in oats; *Samara Correia de Lemos; Computational Plant Biology, Life Sciences, TUM*
14:40 The contribution of transposable elements of *Blumeria hordei* to cross-kingdom compatibility with cereal hosts; *Xinyi Liu; Population Genetics, Life Sciences, TUM*
15:00 Population genetics of *Blumeria hordei*
Miles Anderson; Population Genetics, School of Life Sciences, TUM

Poster Session

Hosted by the Botanical Institute at the Botanical Garden (Menzingerstr. 67, see map)

15:20 walk to botanical garden (see map)
16:00 Poster Session and snacks at the Botanical Institute (Foyer)
18:00 End

Evolutionary Genetics Community in Munich

Friday 20th of March

09:00 Welcome

Plenary talk: Matthew Hahn

09:10 A unified model for duplication, loss, introgression, and coalescence
Matthew Hahn; Departments Biology and Computer Science, Indiana University Bloomington

Talks: Genomic function

10:20 How taste system evolution shaped vertebrate diets
Qiaoyi Liang; Evolution of Sensory and Physiological Systems, MPI-BI, MPG

10:40 Thermal stress responses of a sponge holobiont: Linking tissue phenotypes with microbial genomic potential; *Anshika Singh; Paleontology & Geobiology, Geosciences, LMU*

11:00 Coffee break

Talks: Epigenetic evolution

11:30 Technical repeatability of DNA methylation in two wild avian species
Ioanna Garefalaki; Evolutionary Biology, Biology, LMU

11:50 Modelling and simulating the dynamics of neighbor-dependent epigenetic changes
Dirk Metzler; Evolutionary Biology, Biology, LMU

12:10 Leveraging multimodal single-cell data of early primate development to study the evolution of regulatory elements; *Dana Lopez-Parra; Human Genomics, Biology, LMU*

12:30 Lunch & Coffee

Plenary talk: Jörg Overmann

14:00 Biodiversity beyond Inventories - from Bacteria to higher Organisms
Jörg Overmann; Director general, Bavarian State Collections (SNSB)

Talks: Genomic methods

15:10 The impact of rate variation assumptions on phylogenetic accuracy
Basanta Khakurel; Paleontology & Geobiology, Geosciences, LMU

15:30 Comprehensive detection of structural variants in diverse South-East European cattle using a pangenome framework
Maulik Upadhyay; Genomics Core Facility, Bavarian State Collections (SNSB)

15:50 GAP-MS: A proteogenomic pipeline for automated validation of eukaryotic gene models
Qussai Abbas; Bioinformatics, School of Life Sciences, TUM

16:10 Coffee break

Breakout sessions Mingle with methods

Goal is to provide another opportunity for exchange by splitting into groups with similar methods interests and/or expertise. The hosts will give a brief introduction.

16:45 Genome assembly (Andreas Hauser)
16:45 Long-read sequencing (Stefan Krebs)
16:45 (single-cell)-RNA seq (Wolfgang Enard)
16:45 (single-cell)-ATAC-seq (Ines Hellmann)

18:00 End & walk to Biergarden

18:30 Dinner at Hirschgarten (Hirschgarten 1, 80639 München, see map)

Evolutionary Genetics Community in Munich

Locations

Poster Session
Botanisches Institut, Foyer

Walk from Stiftung to Botanical garden via south entrance of botanical garden at Maria-Ward-Str. (~20min)

Conference location
Carl Friedrich von Siemens Stiftung

Walk from Stiftung to Beergarden (~15 min)

Conference Dinner
Beer Garden Königlicher Hirschgarten

Menzinger Str. 67

Südliches Schloßrondell 23

Hirschgarten 1

Talks

Bring your talk on a stick or on your laptop and you can copy your talk to the presenter laptop or plug in your own.

Posters

Please bring your poster (typically A0, portrait format; other formats will also work) to the poster session. You can hang it up there and should take it with you again after the session.

Evolutionary Genetics Community in Munich

Talk abstracts

(random order)

Genomic insights into the coevolutionary history of humans and dogs

Lachie Scarsbrook*[1]

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Abstract

Fuelled by methodological advancements and technological breakthroughs, the palaeogenomics revolution is rapidly transforming our understanding of animal domestication. Large numbers of ancient and modern nuclear genomes are now readily accessible, and new bioinformatic tools are enabling increasingly complex population genetic analyses. Here, we applied state-of-the-art palaeogenomic techniques to infer ancestry and demography in both ancient dogs and wolves. We analysed individuals from distinct geographic and cultural contexts spanning the last 20,000 years, with a specific focus on reconstructing relationships between dogs, wolves and humans. We demonstrate that the evolutionary histories of humans and dogs are inextricably linked, reflecting the long-term and integral role that dogs have played across a multitude of societies, from Palaeolithic hunter-gatherers through to post-colonial Indigenous communities. We also found frequent and often intentional gene flow between dogs and wolves in both ancient and historic contexts despite no clear evidence for admixture in contemporary populations. Altogether, our results highlight the impact of anthropogenic processes, especially migration, and shifting cultural attitudes, in shaping the diversity of present-day populations, and the pivotal role of palaeogenomics in reconstructing complex domestication histories.

*Speaker

How Taste System Evolution Shaped Vertebrate Diets

Qiaoyi Liang*[1], Hao Zhang[2], Lei Luo[2], Lifeng Tian[2], Yong Shao[2], Xiuping Zhang[3], Kaixun Cao[2], Anna Luo[2], Chengsan Wang[2], Peter Kamau[2], Dong-Dong Wu[2], Maude Baldwin†[1], and Ren Lai‡[2]

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[3]Kunming Institute of Zoology, Chinese Academy of Sciences – Kunming Institute of Zoology, Chinese Academy of Sciences, Kunming, Yunnan 650223, China

Abstract

Taste guides animal perception and dietary choices. Sourness typically triggers aversion, whereas sweet taste attracts animals to sugar-rich foods. We investigate how these sensory modalities evolved across vertebrates. Recently, we uncover molecular mechanisms underlying acid tolerance in birds as well as concordant changes between sour and sweet taste in songbirds. The coordinated evolution of these two modalities may have played a role in enabling songbirds to consume diverse fruits, perhaps facilitating the radiation of this clade. Additionally, by examining the functional evolution of the sweet receptor gene family receptor across the major lineages of vertebrates, we pinpoint the origin of sugar detection to before the appearance of flowering plants and document a previously undescribed diversity of sugar-sensing mechanisms. These findings demonstrate how taste receptor modifications may have repeatedly facilitated dietary expansion throughout vertebrate evolution.

*Speaker
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The impact of rate variation assumptions on phylogenetic accuracy

Basanta Khakurel*[1], Sebastian Höhna[1], and Alessio Capobianco[1]

[1]Ludwig Maximilians Universität München (LMU) – Richard-Wagner-Straße 10, 80333 München, Germany

Abstract

Mutations are not evenly distributed across the genome, and neither are substitutions. Phylogenetic methods rely on models of among-site rate variation (ASRV) to account for heterogeneity in substitution rates across sites. As the true biological distribution of substitution rates is unknown, current approaches assume that the underlying variation is unimodal and approximate continuous rate distributions (e.g., Gamma or Lognormal) using a finite number of discrete categories. This discretization is a critical technical step; however, the consequences of mismatches between the number of categories used for inference and the true generating process, as well as how these effects interact with the underlying level of rate heterogeneity, are not well understood.

Using simulations under varying levels of rate heterogeneity, we investigate whether mismatches between the modeled number of rate categories and the true generating process introduce systematic biases. We find that such mismatches in the number of rate categories severely bias the estimation of the rate heterogeneity shape parameter. These biases propagate to the estimates of tree length. While tree length is relatively robust under low heterogeneity, this robustness breaks down dramatically under high rate variation, leading to significant misestimation. Our results reveal that a seemingly technical modeling choice of discretization can compromise fundamental phylogenetic estimates. This has important implications for downstream evolutionary analyses that depend on accurate branch lengths and rate parameters.

*Speaker

GAP-MS: A proteogenomic pipeline for automated validation of Eukaryotic gene models

Qussai Abbas*†[1] and Dmitrij Frishman[1]

[1]Technische Universität Munchen - Technical University Munich - Université Technique de Munich (TUM) – Arcisstrasse 21, D- 80333 München, Germany

Abstract

Accurate genome annotation is fundamental to modern biology, yet distinguishing authentic protein-coding sequences from prediction artifacts remains challenging, particularly in complex plant genomes. We present GAP-MS, an automated proteogenomic pipeline that leverages mass spectrometry evidence to systematically validate the protein-level accuracy of predicted gene models. Applied across 18 major crop species, GAP-MS consistently improved prediction precision for four widely used tools, with substantial gains of up to 32%. Beyond filtering artifacts, the pipeline identified 13,171 novel peptide-supported gene models absent from current RefSeq annotations. Furthermore, GAP-MS successfully corrected structural errors by identifying independent translation initiation and termination sites via specific N- and C-terminal peptides. These results demonstrate that direct proteomic evidence provides a robust framework for resolving annotation ambiguities and defining high-confidence reference proteomes.

*Speaker
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Genomic Insights into the Conservation and Divergence of the Avenacin Biosynthetic Gene Cluster in Oats

Samara Mireza Correia De Lemos*[1] and Nadia Kamal[2]

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[2]Technische Universität München (TUM) – Alte Akademie 8, 85354 Freising, Germany

Abstract

Plants produce specialized metabolites to adapt to their environmental conditions. Some plant natural compounds are products of biosynthetic gene clusters (BGCs), which consist of physically neighbouring genes with distinct ancestral origins but now function together in coordinated metabolic pathways. Species of the genus Avena produce avenacins, antimicrobial triterpene glycosides that accumulate in root epidermal cells and protect against soil-borne pathogens. These compounds are unique to oats and absent from other cereals, making them attractive targets for engineering disease resistance in crops such as wheat. Although avenacins were first described decades ago, only recently have high-quality genome assemblies become available for multiple Avena species. As a result, the diversity and evolutionary dynamics of oat BGCs remain largely unexplored. Here, we analyzed the presence, organization, and variation of the avenacin biosynthetic gene cluster across a broad Avena pangenome comprising diploid, tetraploid and hexaploid oat lines. Using orthology inference, we identified 70 avenacin-like BGCs, including complete, partial, and variable clusters across species and ploidy levels. A total of 28 complete clusters were identified across all ploidy levels, while others show gene loss or copy number variation. In contrast, non-clustered precursor genes required for the final biosynthetic steps were conserved across all species, indicating pathway retention despite structural divergence. Overall, our results show that avenacin-like BGCs are more widespread and structurally dynamic within Avena than previously recognized, highlighting the impact of polyploidization and genome evolution on specialized metabolism and providing a genomic framework for future crop improvement efforts.

*Speaker

Genomic Insights into Mutation Load and Genetic Purging in Cheetahs (Acinonyx jubatus) for Applied Species Conservation

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[3]Ecology and Genetics Research Unit, University of Oulu, Oulu, Finland – Pentti Kaiteran katu 1 Oulu, Finland, Finland

Abstract

The rapid loss of biodiversity highlights the urgent need to assess genetic vulnerability in threatened species. The cheetah (Acinonyx jubatus, Schreber 1775) is a keystone species in many habitats but facing significant extinction risks due to human impact. These are further amplified by its very low genetic diversity. Crucially, its mutational load (the presence of potentially harmful mutations in the genome) and ability to purge deleterious mutations remain unknown. However, these genomic factors have a strong impact on the cheetah's health and ability to adapt to changing environments. Genomic tools like GERP (Genomic Evolutionary Rate Profiling) offer promising avenues for evaluating population health, but their application in cheetah conservation is unexplored. This proposal is based on a comprehensive dataset of cheetah whole-genomes from Africa and southwestern Asia, including modern and historical specimens and has the aim to investigate genetic load and its conservation implications. I plan to examine population structure and genetic diversity, including runs of homozygosity (ROH) to identify inbreeding. Additionally, I will determine the extent to which sequencing coverage influences mutation load estimates and identifies potential biases. To assess the functional impact of variants, I stratify homozygous (realized load) and heterozygous (masked load) alleles based on GERP scores. This allows me to assess temporal shifts in deleterious variation and distinguish between purging and accumulation of harmful mutations. Ultimately, my findings will establish the utility of evolutionary constraint analyses in conservation genomics, providing crucial insights for evidence-based cheetah conservation management.

*Speaker

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Population Genetics of Blumeria hordei

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Abstract

Blumeria hordei is a species of powdery mildew with economic relevance as a pathogen of Barley. After 2021, B. hordei was taxonomically reclassified. Once considered to belong to the species Blumeria graminis, it is now recognized as it's own species with a high degree of host specificity. As such, characterizing the specie's history and selective pressures may prove useful to developing new management strategies, as well as revealing potential ways in which adaptation might occur in highly host specific organisms.

*Speaker

Technical repeatability of DNA methylation in two wild avian species

Ioanna Garefalaki*[1], Sarah Mueller[2], Dirk Metzler[3], Justin Merondun[3], Sonja Lečić[4], Emmi Schlicht[5], Bart Kempenaers[5], Gilles Gasparoni[6], Rebecca J. Safran Safran[7], Drew Schield[8], Jörn Walter[9], and Jochen Wolf†[10]

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Abstract

Epigenetic mechanisms influence phenotypic plasticity and may contribute to evolutionary processes if epigenetic variation is heritable. Wild populations provide a realistic context for studying such variation. However, the increased biological and technical complexity requires not only reliable measurements, but proper bioinformatic processing to avoid spurious biological conclusions. To separate biological variation from the variance introduced from technical sources, we estimate how reliable are DNA methylation estimations across technical replicates using two wild avian species. We develop and apply a statistical framework in order to quantify and model DNA methylation repeatability. We use Reduced Representation Bisulfite Sequencing (RRBS) and introduce key analytical steps not widely used

*Speaker

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in the field, including post alignment SNP filtering, use of technical replicates and the estimation of per site repeatability metrics. Preliminary results show that repeatability varies widely across CpG sites. We found that genomic context and data quality features affect the site repeatability in different weights. We identify predictors of repeatability, which enable the classification of CpG sites into reliable and unreliable candidates for downstream interpretation. Finally, we assess how aggregation across genomic windows and functional regions may alter data structure and analytical outcomes. Our pipeline provides a statistically grounded basis for robust estimation of DNA methylation signals that are valuable for analysing epigenomic data in evolutionary studies.

Leveraging multimodal single-cell data of early primate development to study the evolution of regulatory elements

Dana Lopez-Parra*[1], Philipp Janssen[1], Jessica Jocher[1], Fiona Edenhofer[1], Antonia Kessler[1], Wolfgang Enard[1], and Ines Hellmann†[1]

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Abstract

Understanding the cis-regulatory code-how enhancers and promoters orchestrate transcriptional output-is central to decoding gene regulation, yet its principles remain elusive. While cis-regulatory elements (CREs) show poor positional conservation between species, gene expression appears remarkably conserved. This makes the comparative analysis of CRE activity and associated changes to regulatory phenotypes a powerful approach to understanding gene regulation, directly linking sequence variation to functional consequences. We describe the creation of a reference dataset for the comparative study of early primate development through the generation of 10x snMultiome data from embryoid bodies from two human and two macaque individuals.

We address the key challenges in cross-species analysis of multimodal data along a developmental trajectory: identifying comparable cell types and constructing a shared chromatin accessibility feature space. To this end we developed a semi-automated computational pipeline combining classification and marker-based cluster annotation to identify comparable cell types across primates based on the snRNA-seq data. For chromatin accessibility analyses, we will identify orthologous CREs through whole-genome alignments and apply sequence-based activity prediction to establish functional correspondence across species.
This framework will enable quantitative assessment of regulatory network conservation and divergence, directly linking CRE sequence variation to species-specific expression phenotypes and revealing the principles governing transcriptional regulation in early primate development.

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A Genomic History of African Cattle

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Abstract

Over roughly the last 7,000 years, cattle across Africa have adapted to a remarkably wide spectrum of environments, from tropical and arid landscapes to temperate zones and high-altitude regions, while also fitting into a variety of production systems and human needs. Central to their success has been their complex, mosaic-like genetic makeup. African cattle carry a blend of ancestry from multiple distinct lineages: taurine cattle, first brought from the Near East no later than the 7th to 6th millennium BCE and later supplemented by European breeds during colonialism, alongside genetically distinct indicine (zebu) lines originating in South Asia, which arrived through one or more waves of historical or prehistoric contact and migration. This mixed heritage likely served as a rich genetic reservoir for adaptation, enabling cattle to spread into and thrive across Africa's diverse ecological and cultural landscapes. Our consortium is currently analyzing close to 2,000 cattle genomes, and we will present our latest findings. Using these data, we explore questions such as when zebu cattle were introduced to different regions of Africa and how human communities harnessed and managed genetic diversity in response to shifting environmental and social pressures.

*Speaker

ASSESSING EVOLUTION OF PRIMATE ATHEROSCLEROSIS USING IPSCS

Eva Briem*[1], Alex Starr[2], Hunter Fraser[2], and Wolfgang Enard†[1]

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[2]Stanford University – Stanford, CA, United States

Abstract

Atherosclerosis is a chronic inflammatory disease characterized by lipid-driven plaque formation within the arterial wall and represents a major global health burden. Early stages of plaque development involve macrophages, which become lipid-laden foam cells upon uptake of oxidized low-density lipoprotein (oxLDL).
While the cellular and molecular mechanisms of atherogenesis have been extensively studied in mouse and humans, far less is known about how these processes differ across primate species or how they have evolved. Non-human primates (NHPs), particularly chimpanzees, are of special interest in this context due to their close evolutionary relationship to humans and reported differences in susceptibility to atherosclerotic plaque formation.

Here I present an in vitro model of foam cell formation from induced pluripotent stem cell (iPSC)-derived macrophages. Our methodology allows the differentiation of NHP iPSCs into macrophages and investigation of their uptake of oxLDL in vitro. The usage of fused human and chimp iPSCs additionally serves as basis to remove trans effects in the evolutionary comparison and acts as tool to merely study cis-regulatory changes between the species.

Gene set enrichment analysis of RNA-seq data identifies significant divergence in the cholesterol efflux pathway between the species, with chimpanzee macrophages exhibiting elevated expression of multiple efflux-associated genes upon oxLDL exposure. These results indicate evolutionary changes in the regulatory architecture of lipid handling pathways. Ongoing functional assays will determine whether these transcriptional differences translate into altered cholesterol efflux capacity.
This system provides a framework to investigate how regulatory evolution shapes human susceptibility to atherosclerosis.

*Speaker
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On the number of species required to detect stabilizing selection in gene expression evolution

Haoqing Du*[1,2], Nicolas Lichilin[3], Ana Catalan[3], and Sebastian Höhna†[1,2]

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Abstract

Differentiating between genes that evolve under neutral drift versus stabilizing selection is one of the first explorations in comparative phylogenomic studies. Neutral drift and stabilizing selection of gene expression levels across a phylogeny are modelled using a Brownian motion and an Ornstein-Uhlenbeck process, respectively. Most empirical gene expression datasets contain only a few species, raising concerns about statistical power for model selection and parameter estimation. Here, we designed a simulation study to evaluate the power to identify stabilizing selection, emphasizing the impact of the number of species, strength of selection and within-species variances. Our results show that distinguishing weak selection from neutral drift is challenging, whereas the power to detect strong stabilizing selection increases substantially with the phylogeny size. In contrast, varying levels of within-species variance have only minor effects. In conclusion, we suggest that gene expression datasets including at least 30 taxa are required for reliable inference.

*Speaker
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Thermal stress responses of a sponge holobiont: linking tissue phenotypes with microbial genomic potential

Anshika Singh*†[1] and Gert Wörheide[1]

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Abstract

Marine sponges are among the oldest extant animal phyla, originating in the Neoproterozoic era (_˜640–750 million years ago). Having survived multiple mass extinction events, they represent a remarkable evolutionary success grounded in long-term, conserved microbial symbioses. This deep evolutionary history makes sponges an excellent model for understanding how host–microbe partnerships shape resilience to environmental change. As climate change accelerates ocean warming, marine biodiversity faces increasing thermal stress. To examine how sponges and their associated microbiomes (the holobiont) respond to elevated temperatures, we performed a controlled thermal stress time-series mesocosm experiment using explants of the blue aquarium cyanosponge *Lendenfeldia chondrodes*. Temperature was gradually increased to threshold temperature 34–35 ∘C and then returned to baseline to capture both stress and recovery dynamics. We combined experimental manipulation with a Computer Vision Annotation Tool (CVAT)–based human-in-the-loop framework to generate precise, high-resolution measurements of tissue loss, regression, recovery, and growth over time. Our results show a strong temperature-dependent response: rapid tissue regression at peak thermal stress followed by partial to substantial recovery after return to ambient conditions, demonstrating pronounced phenotypic plasticity at the holobiont level. Previous microbial analyses of *L. chondrodes* under short-term heat stress similarly reveal restructuring of the core microbiome, including shifts in cyanobacterial symbionts. Given the evolutionary stability and metabolic importance of sponge–cyanobacteria associations, particularly *Synechococcus spongiarum*, these findings suggest that specific symbiont lineages play a central role in maintaining host performance under thermal stress.

*Speaker

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prime-seq2 and zUMIs-prime: an end-to-end framework for scalable cross-species transcriptomics

Felix Pförtner*[1], Eva Briem[2], Daniel Richter[3], Wolfgang Enard[4], and Ines Hellmann[5]

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Abstract

Comparative transcriptomics is increasingly important to evolutionary biology, but cross-species RNA-seq studies are often limited by scalability and data analysis. Costs limit sample numbers and replicates, constraining statistical power and, in turn, the biological insight achievable within a given budget. To make large, well-powered cross-species studies more affordable, we introduce an improved bulk RNA-seq protocol and a dedicated analysis workflow.

prime-seq2 is an optimized, UMI-based 3' early-barcoding bulk RNA-seq protocol that reduces per-sample cost while maintaining sensitive and specific expression quantification. 3' UMI-based protocols are especially suitable for cross-species experiments as they directly provide digital transcript counts. By systematically addressing protocol steps that drive read loss and technical variability, prime-seq2 increases the fraction of usable exonic+intronic UMIs by 60% while maintaining library complexity and technical variance. In practice, this reduces sequencing costs and, combined with low library costs and scalable multiplexing, enables large, well-controlled experimental setups across species.

To translate experimental standardization into computational comparability, we developed zUMIs-prime, a user-friendly processing workflow for UMI-based bulk RNA-seq data. zUMIs-prime automates mapping and UMI-aware counting with STARsolo and generates standardized QC summaries to diagnose potential artifacts. Downstream, modular, user-guided steps for filtering, visualization, differential expression testing, and power simulations support reproducible analyses and study design.

Together, prime-seq2 and zUMIs-prime make large, balanced cross-species transcriptomic designs more feasible, with standardized processing that strengthens reproducibility and interpretation.

*Speaker

The contribution of transposable elements of Blumeria hordei to cross kingdom compatibility with cereal host

Xinyi Liu*[1], Marion Müller[2], Luzie Wingen[3], Aurélien Tellier†[4], and Ralph Hückelhoven‡[5]

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[5]Chair of Phytopathology, TUM – Emil-Ramann-Str-2 85354 Freising, Germany

Abstract

Filamentous plant pathogenic fungi often have large genome sizes within the kingdom of fungi, due to the proliferation of transposable elements (TEs). *Blumeria hordei*, the causal agent of the powdery mildew disease on barley, is a filamentous obligate biotrophic fungus with a high TE proportion of 75%. We used B. hordei as a model to study the impact of TEs on genome evolution and virulence. In *B. hordei*, the effector ROPIP1 is encoded on the first open reading frame (ORF) of a TE, Eg-R1. In addition, Eg-R1 insertions into genes might have given rise to chimeric open reading frames containing the ROPIP1 peptide. More evidence should be obtained to understand the contribution of TEs in creating, disrupting, or cis-regulating effector genes as well as the putative function of TE-derived ORFs (TE-derived effector candidates(TEDECs)). The goal of this study is to identify novel peptides formed and regulated by TEs. Both short- and long-read RNA sequencing were conducted, and by combining the full-length transcript information with our manually curated TE annotation, we detected extensive co-transcription of TEs and genes. In particular, non-autonomous short interspersed nuclear elements (SINEs), such as Eg-R1, are enriched in the flanking regions of expressed genes. We also identified TE insertions within gene ORFs, potentially giving rise to novel chimeric genes. Next, we aim to evidence the existence of these predicted TE-derived peptides using deep proteomic data. Our study will provide insights into the mechanisms by which TEs impact genes and the genome structure of *B. hordei*.

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Comprehensive Detection of Structural Variants in Diverse South-East European Cattle Using a Pangenome Framework

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Abstract

Most studies investigating structural variation (SV) in livestock have relied on aligning short reads to a single linear cattle reference genome, which limits the accurate and comprehensive detection of genomic variation. Recent advances demonstrate that pangenome-based approaches can mitigate ascertainment bias and enable the discovery of novel lineage- and breed-specific sequences. However, most of these efforts have focused on widely studied commercial breeds such as Holstein-Friesian and Jersey cattle. In this study, we address this gap by generating genomic resources for underrepresented South-East European cattle breeds. Using a combination of Illumina short-read and Oxford Nanopore Technologies (ONT) long-read sequencing, we sequenced 230 individuals from 15 genetically diverse breeds to medium and high coverage (up to _˜70×). High-coverage samples were assembled de novo using hifiasm-ont, followed by scaffolding with the ARS-UCD1.2 cattle reference genome as a backbone. We then constructed a cattle pangenome using minigraph-cactus, incorporating both newly generated assemblies and publicly available cattle genomes. Structural variants were identified and genotyped across individuals using paired-end sequencing data. In addition, publicly available short-read data from zebu cattle were aligned to the constructed

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pangenome to enable comparative analyses. The resulting SVs and SNPs were analyzed using population genomic approaches to investigate patterns of genetic diversity, introgression, and selection across breeds. This work provides a comprehensive framework for studying genomic variation in diverse cattle populations and highlights the value of pangenome approaches in uncovering previously undetected genetic diversity.

Modelling and simulating the dynamics of neighbor-dependent epigentic changes

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Abstract

We model the dynamics of epigenetic changes (such as DNA methylation) with two kinds of correlations: first, a local change can depend on the state of neighboring loci and, second, whole regions can be affected by simultaneous changes of contained loci and of the stationary destribution of the states in that region. Our R package MethEvolSIM allows to simulate this process along genealocical trees. Thus, simulation-based inference methods like Approximate Bayesian Computation can be applied to fit the model to data and to infer which type of correlations apply. We discuss the challenges and our current approaches in to extend the models and simulation algorithms to ancestral recombination graphs.

*Speaker

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Evolutionary Genetics Community in Munich

Poster abstracts

(random order)

Using ancient DNA to track the phenotypic history of dogs

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Abstract

Dogs have been domesticated for over 20,000 years through a process that involves strong directional selection. Yet many of the highly derived phenotypes that define modern breeds are widely attributed to positive selection, as well as relaxation of selective constraints, acting primarily within the last ~150 years of intensive breed formation. In fact, although positive selection is presumed to be an important aspect of domestication, we do not yet understand the degree to which it shaped dog biology during the vast majority of their evolutionary history. The genetic architecture of many traits differentiating dog breeds is simple, often underlied by single SNPs or indels. Here, we take advantage of this simple genetic architecture to track the occurrence and frequency of variants underlying known traits in genome-wide data from more than 800 ancient canids spanning ~100,000 years and more than 2,000 modern individuals, ultimately inferring shifts in selective pressure. This approach enables us to quantify the extent to which both purifying and positive selection acted on variants underlying traits that define dog breeds today, across a wide range of archaeological contexts throughout Eurasia and North America, and to address fundamental questions about the nature of selection during the domestication history of dogs.

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Distribution and thermal tolerance of two wood ant species and their hybrids in Southern Bavaria.

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Abstract

Thermal tolerance, the ability to withstand temperature changes, is a crucial trait in assessing species' vulnerability to climate change. European mound-building Formica wood ants, forest keystone species and ecosystem engineers, provide a suitable model for studying thermal limits and the potential role of hybridization in adaptation to a changing climate. While extensive hybridisation has been observed in Southern Finland, the extent of hybridisation in Southern Bavaria remains mostly unexplored. In this study, we aim to fill this geographical knowledge gap by assessing the species distribution along the hybrid zone and determining the hybrid ancestry using whole-genome sequencing. Further, we focus on thermal tolerance of two species, F. aquilonia and F. polyctena, and their hybrids. To compare their thermal limits, we test whether elevation and/or species identity predict their thermal tolerance using heat knockdown test (HKT) and chill coma recovery test (CCRT). I will present our results in comparison to findings from Southern Finland, highlighting the importance of geographical context in shaping the outcomes of hybridization.

*Speaker

Modelling the molecular basis of human speech evolution

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Abstract

Heterozygous loss-of-function mutations in the transcription factor FOXP2 lead to speech and language disorder. Two human-specific amino acid substitutions (T302N and N324S) occurred in the conserved FOXP2 protein after the human-chimpanzee split, suggesting a role of FOXP2 in the evolution of speech. Mouse models (Foxp2hum) with these human-specific substitutions showed enhanced synaptic plasticity in the form of stronger long-term depression (LTD) in the medium spiny neurons (MSN) of the striatum, decreased tissue dopamine levels, enhanced performance during certain learning tasks, and altered gene expression of striatal neuronal pathways during learning. To understand the molecular basis of speech development and evolution, we use homology-directed CRISPR-cas9 genome editing to create the two amino acid substitutions, which generates a "chimpanized" version of FOXP2 in human iPSC cell line. Additionally, we generate mouse iPSCs from Foxp2hum and WT mice. We will differentiate these cells into MSNs and subsequently perform RNA-seq to investigate to what extent human and mouse *in vitro* MSNs can recapitulate the differential expression found in the striatum of Foxp2hum mouse model.

*Speaker

Evolutionary Trade-offs in the Gastric Niche: Integrated H. pylori Molecular Profiles Predict Survival in Gastric Cancer

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Abstract

Background: *Helicobacter pylori* contributes to gastric carcinogenesis through virulence activity and rising antimicrobial resistance (AMR). How these features integrate into coordinated bacterial "states" within the tumor microenvironment-and how such states influence survival-remains unclear.
Methods: We analyzed 158 gastric cancer tissues with quantitative Polymerase Chain Reaction (PCR)-positive *H. pylori*. Twenty-one molecular features (AMR mutations and virulence gene expression) were quantified. Unsupervised k-means and TwoStep clustering defined bacterial profiles. Prognostic relevance was assessed using Kaplan–Meier estimates and multivariable Cox regression adjusting for age, sex, and tumor, node, metastasis (TNM) stage.

Results: Two molecular states emerged.

"Competent Colonizer" (80.4%)-higher *cagA* and *vacA* expression (both $p < 0.001$), greater histological detectability (91.3% vs. 45.2%, $p < 0.001$), and more *rdxA* mutations ($p < 0.001$).

"Resistant Inflammatory" (19.6%)-enriched for clarithromycin-associated 23S rRNA mutations ($p = 0.011$), elevated *iceA* expression ($p = 0.001$), and reduced *cagA/vacA* (both $p < 0.001$). This profile was associated with whole-stomach involvement ($p = 0.042$) and atypical histology ($p = 0.047$).

*Speaker

The "Resistant Inflammatory" profile was independently associated with a **63% lower hazard of death** (HR = 0.37, 95% CI 0.16–0.85; p = 0.019). Model discrimination was strong (concordance = 0.739). Sensitivity analyses (age-restricted, stage-only, numeric coding) produced consistent effect sizes (HR range 0.34–0.55).

Conclusion: These findings reveal an evolutionary trade-off in the gastric tumor niche, where antibiotic-selected resistance mutations co-occur with reduced oncogenic virulence. Integrated molecular profiling provides a systems-level framework for microbe-informed risk stratification in gastric cancer.

Hybrid Capture based Metagenomic Next-generation Sequencing Workflow

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Abstract

Metagenomic next-generation sequencing (mNGS) enables unbiased detection of viral pathogens, but its diagnostic utility is often limited by low sensitivity, incomplete genome recovery, and inflexible bioinformatic workflows. Hybrid capture–based enrichment improves sensitivity by selectively enriching viral nucleic acids, while long-read sequencing enhances genome reconstruction and subtype-level resolution. However, few pipelines are optimized for combining hybrid capture with long-read data.

We present a hybrid capture mNGS workflow coupled with a reference-guided bioinformatic pipeline developed for Nanopore sequencing. Viral nucleic acids are enriched using the Twist Comprehensive Viral Research Panel, comprising over one million probes targeting conserved regions across more than 3,000 viral species. The workflow integrates a curated viral reference database with a mapping-based strategy to enable accurate pathogen detection, coverage assessment, and consensus genome generation for downstream mutation and drug-resistance analyses.

Long-read sequencing supports contiguous genome coverage across complex regions and facilitates assembly-informed consensus calling, even in samples with heterogeneous viral populations. Beyond diagnostics, the pipeline enables evolutionary genetic analyses, including studies of host–virus interactions, within-host diversity, and viral adaptation. It has been applied to approximately 250 clinical and environmental samples and supported genome-resolved investigations of SARS-CoV-2 evolution and diversification during the COVID-19 pandemic. The workflow further demonstrated robust performance in an international viral mNGS external quality assessment (EQA).

Ongoing development focuses on improving analytical precision and scalability, supporting hybrid capture mNGS as a flexible framework for viral diagnostics, evolutionary research, and genomic surveillance.

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Genome-to-Genome inference of GxGxE interactions for climate-resilient pathogen resistance in barley

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Abstract

Breeding for disease resistance in barley is complicated by genotype-by-genotype-by-environment interactions, where resistance outcomes depend jointly on host and pathogen genotypes and local climatic conditions. Classical GWAS approaches treat pathogen diversity and environmental variation as noise, limiting identification of resistance loci that remain effective across pathogen populations and changing environments.
The BarleyCOPA project addresses this gap by developing the first Genome-to-Genome (GtoG) association framework for crop breeding, focusing on spring barley and two economically damaging fungal pathogens in Germany: Fusarium graminearum, the causal agent of Fusarium Head Blight, and Ramularia collo-cygni, responsible for Ramularia Leaf Spot. Both diseases have increased in prevalence since the 1980s and currently rely on chemical management, with consequences for soil biodiversity and agricultural sustainability.

The GtoG framework integrates three modules: a forward-in-time population genomics simulation modelling pathogen diversity across field locations, an epidemiological model estimating disease encounter rates per barley variety and field, and an Approximate Bayesian Computation scheme testing all pairwise barley x pathogen SNP/CNV associations against interaction matrices. The experimental design involves 200 spring barley lines grown across five German field locations over four years, with over 1,000 isolates per pathogen sequenced from three locations across two seasons.
Current progress includes SNP array genotyping of hundred barley cultivars to identify the most genetically divergent lines for long-read sequencing and high-quality reference genome assembly. In parallel, a co-infection epidemiological model is under development, and the GtoG framework is being extended to accommodate diploid host data and dominance effects within interaction matrices.

*Speaker

Identify how coinfections influence the genetic diversity of pathogen populations

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Abstract

Coinfection by multiple pathogen strains within a single host is commonly observed, yet the genetic mechanisms underlying such coexistence remain unclear.
In particular, it is unknown whether coinfection results from shared genetic determinants, such as common genes or specific SNP variants facilitating joint invasion (coexistence), or whether it arises independently of genetic similarity. More generally, we want to reveal the genetic determinants of coinfection between strains of the same pathogen species. Coinfecting strains may display distinct patterns of SNP variation, reflecting different epidemiological and evolutionary outcomes: i) transient coexistence when a single strain dominates the competition, ii) stable coexistence due to balanced strain frequencies, or iii) asymmetric stable coexistence due to trade-offs. Here, we combine an epidemio-genetic model with Bayesian inference (Approximate Bayesian Computation) applied to pathogen SNP data from the wheat–Zymoseptoria tritici pathosystem to identify genetic signatures associated with coinfection and to infer candidate loci involved in multistrain coexistence. We aim to find loci involved in infectivity on resistant host plants, loci responsible for advantage in competition, and loci determining trade-offs between infectivity and competitive ability. A GWAS analysis is performed to cross-validate the results obtained.

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Investigating RNA dynamics in ferruginous environments

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Abstract

How life emerged on Earth is one of the most important, yet difficult questions to answer. While there is a growing consensus that self-replicating RNA molecules were an important precursor to the first cells, it is not well understood how the hypothetical 'RNA world' could have survived in the geological conditions of the Hadean era. While the location of the emergence of life is still being discussed, it is widely accepted that a large ferruginous ocean with deep-sea hydrothermal activity existed at that time. Until now, few studies have investigated RNA dynamics in deep-sea environments and ferruginous chemical gardens of the Hadean era. Through experimentation, we aim to explore potential compatibilities between these two major hypotheses. In this study, we examine the stability of RNA in ferruginous conditions and in the presence of iron oxyhydroxides, to simulate the Hadean deep-sea. Our experimental data indicates that ferruginous conditions increase RNA degradation in a size-dependent manner. Furthermore, we have identified that the β-iron oxyhydroxide Akaganeite can adsorb RNA molecules. In addition to the upconcentrating effect the mineral prolongs the half-life of bound RNA molecules.

*Speaker

Signals in the Dark: Genome-Wide Insights into Species Boundaries and Population Structure of European Luciola Fireflies

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Abstract

Fireflies of the genus Luciola (Lampyridae) are flashing bioluminescent beetles primarily distributed across Asia, with several species extending into southern Europe. Despite being among the most charismatic insects in the European fauna, their diversity and evolutionary history remain poorly understood. Across Europe, three species are currently recognized (L. italica, L. lusitanica, and L. novaki), though molecular evidence suggests L. lusitanica may represent an unresolved complex of distinct lineages. Here, we present a population genomic study of European Luciola based on genome-wide SNP data from nine populations spanning all three recognized species. Using phylogenomic inference, population structure analyses, and multiple species delimitation approaches, we aim to clarify species boundaries within the genus and characterize population-level diversity, structure, and gene flow across Europe.

*Speaker

Quaternary Evolution of the Bavarian Flora: Genetic and Metabolomic Landscape of Gypsophila repens

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Abstract

Climate and land-use change are major drivers of biodiversity loss, imposing rapid environmental fluctuations and increasing stress on ecosystems. The response of alpine species to environmental change is of particular interest, as they often exhibit specialized adaptations to high-altitude conditions. By examining species occurring along elevational gradients, we aim to test whether observed trait variation reflects adaptive genetic differentiation or phenotypic plasticity.
Gypsophila repens L. (Caryophyllaceae) is an alpine plant species that typically grows on calcareous screes at higher altitudes in the northern Alps. The species also occurs along alpine rivers and in lowland regions of Bavaria, where its populations have declined markedly in recent decades.

By integrating botanical collections, field surveys, and common-garden experiments with cutting-edge genomic and metabolomic approaches, we aim to (i) reconstruct the Quaternary biogeographic and demographic history of this species, (ii) test whether contemporary populations of *G. repens* have adapted to lowland and highland conditions, and (iii) elucidate how river dynamics have influenced the species' adaptive potential.

We place a particular emphasis on secondary metabolites, assessing whether metabolite diversity represents an adaptive response to contrasting environments or environmentally induced variation. Integrating genomic and metabolomic data enables the identification of genetic mechanisms underlying metabolite production and their evolutionary significance.
This research provides a comprehensive framework for understanding how historical and contemporary environmental change shapes plant evolutionary trajectories, functional diversity, and conservation vulnerability in alpine ecosystems.

*Speaker

Unveiling the spatial relationships of gene expression with TAMED FISH

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Abstract

Trancriptor Assisted Multiplexed Expression Detection FISH (TAMED FISH) is a cost-efficient and easy-to-use spatial transcriptomics pipeline. It combines a full wetlab protocol utilizing multiplexed hybridization chain reaction RNA fluorescence in situ hybridization, which requires no specialized equipment, with a powerful automated analysis.
This enables a user-friendly workflow that can be used by any lab without any prior image analysis knowledge. The analysis includes automated image registration for iterative multiplexing, as well as a 2D and 3D analysis pipeline that utilizes powerful machine learning algorithms to provide the user with a single-nucleus, single-transcript-resolution dataframe of the input image. The novel transcript detection model matches the field standard in accuracy but exceeds it in the information output. The pipeline can not only handle massive images but also run on standard hardware by using a tiling algorithm to process images in small portions, saving computational resources. TAMED FISH has been successfully used with different kinds of brain tissue across multiple species, demonstrating its robustness. It is a powerful yet easy-to-use approach to answering biological questions in a spatial context.

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Microbially Mediated Formation and Long-Term Preservation of Biogenic Greigite in Baltic Sea Sub-seafloor Sediment

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Abstract

Biogenic magnetic minerals, particularly magnetite (FeO) and greigite (FeS), can record Earth's magnetic field and local environmental conditions at the time of formation, making them important palaeomagnetic and palaeoenvironmental proxies. However, active microbial communities and redox-driven diagenesis can also form or transform magnetic minerals after burial, potentially overprinting older signals. This study investigates the formation and preservation of biogenic greigite in Baltic Sea subseafloor sediments, with a focus on distinguishing primary magnetic signals from microbial overprints. We apply a multidisciplinary approach that combines magnetic measurements with molecular analyses to link magnetic mineral signatures to active microbial communities. Magnetic data identify five distinct greigite-rich horizons in the LL19 sediment core (north-central Baltic Proper), with signatures consistent with both biologically induced mineralisation (BIM) and biologically controlled mineralisation (BCM). Molecular and geochemical proxies (PCR, ATP, TN/TOC) from 120 samples across 0–5.5 m indicate active microbial communities throughout the core, with elevated biomass/activity in greigite-enriched layers. In addition, 16S rRNA gene sequencing shows that different microbial groups are associated with biologically induced versus biologically controlled mineralisation, supporting distinct microbial pathways of greigite formation. Together, these results highlight a strong microbial influence on greigite formation and demonstrate the value of integrating magnetic and molecular methods to improve the interpretation of sedimentary palaeomagnetic records.

*Speaker

Improving cross-species comparability of human and cynomolgus macaque iPSCs

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Abstract

Cross-species comparisons are central to evolutionary developmental biology because they enable the identification of conserved and divergent gene regulatory mechanisms. Such analyses require orthologous cell types, which are often inaccessible in primates due to ethical and practical limitations. Induced pluripotent stem cells (iPSCs) provide a scalable *in vitro* system to generate these cell types and thus offer new opportunities to study the evolution of molecular phenotypes. The cynomolgus macaque, a well-established non-human primate model for early development, is particularly informative due to its phylogenetic distance from humans. However, limited sample numbers and variability among iPSC lines currently restrict cross-species comparability.

The defining feature of any iPSC line is pluripotency, its ability to differentiate into all three germ layers. Yet, although human iPSC lines typically express canonical pluripotency markers and exhibit characteristic colony morphology, they often differ substantially in their differentiation potential. This variability is influenced by technical factors such as the cell type of origin, reprogramming method, and culture conditions, and may exacerbate species differences. Incomplete resetting of the epigenetic state is thought to be a major contributor. To address these challenges, we generated a panel of human and cynomolgus macaque iPSC lines from fibroblasts and urine-derived stem cells. Through comprehensive characterization of clonal lines, systematic comparison of culture conditions, and increased biological replication, we aim to identify conditions that maximize similarity in gene expression profiles between species and thereby enhance the power of cross-species comparisons.

*Speaker

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How does regucalcin1 influence visual mating preferences in Heliconius butterflies?

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Abstract

Visual preference can shape mate choice and sexual selection, yet little is known about its genetic basis and how molecular variation shapes behaviour. In *Heliconius* butterflies, *regucalcin1* has been implicated as a major-effect gene influencing male preference for red patterns. *Regucalcin1* is expressed across the visual pathway from eye to brain, raising the question: where does *regucalcin1* act to generate variation in visual mate preference? In this project, I will test whether preference evolution is mediated by changes in the visual periphery. First, I will compare the visual periphery across species with different preference phenotypes and ecology: *H. cydno* males prefer white females, whereas *H. timareta* and *H. melpomene* prefer red females. Although *H. timareta* shares its preference and pattern with *H. melpomene*, it is more closely related to *H. cydno* and similar in habitat. I will map red filtering pigments across the retinal mosaic, and test whether differences predict functional differences using modified optomotor assays for visual acuity across different light environments and colour sensitivity. I will then test *regucalcin1* function using CRISPR-Cas9 by assessing whether *regucalcin1* knockouts of *H. melpomene* differ in retinal mosaic or visual performance. Finally, I will investigate whether *regucalcin1* contributes to visual preference evolution more broadly across *Heliconius* by testing for differential expression between species pairs beyond the *melpomene-cydno-timareta* clade that diverged _˜12 million years ago. This work will reveal whether *regucalcin1* shifts mate preference via peripheral sensory tuning and clarify how a large-effect preference gene contributes to reproductive isolation and speciation in *Heliconius*.

*Speaker

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Speciation genomics of eye size variation in Heliconius butterflies

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Abstract

Vision is a key sensory modality in Heliconius butterflies and may influence population divergence as eyes play a key role in mate choice. However, the morphology across much of the genus has not yet been characterized and the genetic basis is unknown. Previous studies have characterized differences in eye morphology between H. cydno chioneus and H. melpomene rosina in Panama, as well as their hybrids, and showed that H. cydno has larger eyes than H. melpomene, with hybrids exhibiting a more H. melpomene-like eye phenotype. Furthermore, it was shown that eye size is an adaptive trait based on the niche occupied by each species. In the first project of my PhD, I will build on this work by further characterizing eye morphology both within and between species, including more broadly across the melpomene-cydno-silvaniform clade . In particular, intraspecific variation will also be used to test for evidence of character displacement by comparing samples from Panama, Colombia and French Guiana, where H. melpomene occurs at all three sites, H. cydno occurs in Panama and Colombia, and H. timareta occurs in Colombia. To begin to investigate the genetic basis of eye morphology, I will use quantitative trait locus (QTL) mapping between H. cydno cydno and H. melpomene martinae. This will allow us to test whether genetic variation underlying interspecific differences in eye morphology are associated with barrier loci.

*Speaker

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Harnessing a Nearly Complete Herbarium Collection to Unravel the Evolutionary Radiation of Astragalus

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Abstract

Astragalus, with over 3,100 species, is the largest genus of flowering plants and represents an outstanding example of recent, rapid evolutionary radiation, particularly across the arid regions of the Northern Hemisphere. Despite its remarkable diversity, the evolutionary processes underlying this mega-diversification remain poorly understood, largely due to limited taxon sampling and unresolved phylogenetic relationships.

To address this, we are constructing a robust phylogenomic framework for *Astragalus* using a custom-designed bait set targeting 686 orthologous genes (819 exons) tailored to the Astragalean clade. This approach provides high-resolution inference across both deep and shallow phylogenetic splits, including ecologically and morphologically divergent taxa. Our sampling focuses on Old World centers of diversity and draws extensively from the Botanical State Collection Munich (BSM-SNSB), leveraging approximately 22,000 herbarium specimens, including material up to 115 years old and collections from politically inaccessible regions such as Afghanistan and Iran.

We further integrated publicly available genomic resources-including genome skimming, transcriptomes, and prior target enrichment datasets-to generate the most comprehensive phylogeny of Old World *Astragalus* to date. While largely congruent with previous studies, our results reveal substantial gene tree discordance, cytonuclear conflict, and signals of reticulate evolution, highlighting a complex evolutionary history. By combining museomics, phylogenomics, and machine learning–assisted specimen digitization, this project advances our understanding of the ecological, morphological, and biogeographic drivers of diversification in this hyperdiverse lineage.

*Speaker

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Evolutionary Dynamics of Sex-Biased Gene Expression in Sexually Dimorphic Fireflies

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Abstract

Sexual dimorphism arises from differential selection pressures, often resolved molecularly through **sex-biased gene (SBG)** expression. Fireflies (Lampyridae), with a ~150-million-year history, exhibit extraordinary dimorphic diversity-from monomorphic species to those with flightless, neotenic females-yet the evolutionary forces (selection vs. drift) shaping their gene expression remain largely unexplored.
Utilizing a newly consolidated phylogenomic backbone and RNA-seq from 17 globally distributed species, this study investigates **how stabilizing selection, directional selection, and genetic drift drive SBG expression across the firefly tree of life.** Our pipeline involved generating and reannotating reference genomes, followed by alignment via STAR and SALMON. Differential expression was computed using DESeq2 (p-adjusted < 0.05; $|\log2FC| > 1.5$), with phylogenetic comparative methods in R used to quantify the evolutionary forces shaping transcriptomic divergence.

Preliminary results indicate tissue-specific and lineage-specific evolution. We observed more SBG in heads than bodies. In bodies, male-biased genes predominated, while heads showed a female-biased trend. Notably, the subfamily **Lamprohizinae** exhibited higher SBG counts in heads than other lineages. These patterns suggest divergent selective pressures on dimorphic traits like bioluminescence and flight.
By integrating comparative genomics and SBG expression in fireflies, we show that SBG expression is lineage-specific, influenced by a combination of stabilizing, directional selection, genetic drift and life history traits of each firefly species. These findings deepen our understanding of how sex-specific selection and regulatory evolution contribute to the emergence of morphological and behavioral dimorphism, with broader implications for evolutionary biology. Ongoing sampling will expand our taxonomic coverage and further refine these evolutionary inferences.

*Speaker

Shaping Immunity: Genetic Diversity as a Key Resource for Crop Protection

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Abstract

Plant immunity is shaped by a rich but largely untapped reservoir of genetic diversity distributed across wild germplasm and related species. With the advent of long-read sequencing and pan-genomic approaches, it is now possible to survey immune-related loci at population and genus scale, revealing layers of defence complexity invisible to single-reference analyses. Using barley pan-genome resources spanning 76 wild and domesticated accessions, we identify expanded clusters of immune receptor genes in wild barley (*Hordeum vulgare* ssp. *spontaneum*) relative to cultivated lines. These include canonical NLR (nucleotide-binding leucine-rich repeat) families as well as genes involved in reactive oxygen species signalling, cell-wall modification, and transcriptional regulation many residing in structurally variable, copy-number-variable regions such as the *Mla* powdery mildew resistance locus. Extending this framework to the *Solanum* genus-wide pan-genome, we uncover lineage-specific expansions in receptor-like kinase and NLR families across wild and domesticated species, with distinct evolutionary trajectories reflecting ecological pressures and domestication-driven bottlenecks.

Beyond canonical resistance genes, we survey biosynthetic gene clusters (BGCs) encoding specialised immune metabolites across *Solanum* species, including the withanolide BGC conserved across Solanaceae, demonstrating how pan-genomic analyses can illuminate the metabolic dimension of plant innate immunity.
Together, our analyses position wild germplasm as a critical source of immune-gene diversity and provide candidate loci for cloning, association mapping, and deployment in resistance breeding programmes.

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Spatial population genetics of the alpine riparian plant Myricaria using herbariomics with the Angiosperms353 target-capture baits set

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Abstract

Herbaria are a vast source of untapped genetic material that can be harnessed through **NGS target-enrichment**, especially when collecting fresh specimens on extensive geographical scales is unfeasible. Sampling over 90 herbarium specimens across its wide Eurasian range, we use the alpine riparian plant genus *Myricaria* to illustrate how **herbariomics** with the **Angiosperms353 bait set** can be used for spatial population genetics. It is challenging to collect these plants for specific studies due to their habitat in mountainous regions such as the Himalayas. We show that herbariomics is an attractive alternative to other methods like microsatellite genotyping that require fresh samples. Recently developed **bioinformatics tools** such as **conStruct** (continuous structure) can aid understanding population structures over a continuous geographical area, while **EEMS** (Estimating Effective Migration Surfaces) uses "**isolation by resistance**" to identify and visualise areas of high and low gene flow. Analyses with conStruct show that genetic differentiation among *Myricaria germanica* is continuous along its geographic range from Europe to Asia. Conversely, there are two discrete non-mixing groups of *Myricaria* in Siberia and the Altai, supporting the hypothesis that there are two distinct species in this region: *Myricaria germanica* and *Myricaria longifolia*. Here, we show that in conjunction with phylogenomics (presented in a separate study), spatial population genetics on target-captured loci **facilitates species delimitation**. Meanwhile, EEMS analyses suggest that high mountain regions (such as the Eastern Sayan Mountains) constitute **barriers to gene flow** in *Myricaria* populations, while river basins (such as the Yenisey River valley) function as **corridors**.

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Population genomics of the snowy plover reveals limited population structure in presence of high gene flow

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Abstract

The genomes of contemporary species can reveal the evolutionary and ecological forces that shape genetic diversity, population connectivity and demographic history. The snowy plover (*Anarhynchus nivosus*) is a small shorebird that inhabits coastal areas and inland salt lakes of the American continents. Because of its unusual mating and care system that includes polygamy and flexible brood care, snowy plovers have been the subject of many evolutionary studies. Despite its wide distribution and high dispersal abilities, snowy plovers face numerous threats, which have resulted in population declines across its distribution. As a result, many population segments are threatened and protected.

Here, we used whole genome sequencing to assess genetic variation, population differentiation, and evolutionary history of the snowy plover. We assembled the first de novo reference genome for the species and performed whole genome re-sequencing data from 125 plovers collected at 17 locations across their range. Our sampling comprises locations representing all three known genetic lineages: *nivosus*, *tenuirostris* and *occidentalis.*

PCA and Admixture analysis show a clear differentiation among lineages mirroring previous population genetic analyses. Within the *nivosus* lineage, we found that samples from the northern coast of the Gulf of Mexico clustering, whereas for the rest of the distribution we did not detect any meaningful population structure. A reconstruction of the population demography suggests a decrease in effective population size since the Last Glacial Period. In addition, we calculated the resistance to dispersal under future climate scenarios. These results will help to inform conservation management in this vulnerable shorebird.

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Firefly genomics and transcriptomics

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Abstract

Our first research focus is to understand the evolution of extreme sexual dimorphism in fireflies. Such dimorphism includes female wing loss and eye reduction, as well as the loss of light organs in males. These traits have evolved repeatedly and independently across the firefly phylogeny. To investigate the genomic architecture underlying these traits, we analyze whole genomes and transcriptomes from 25 firefly species. Using Brownian Motion and Ornstein–Uhlenbeck models, we test the evolutionary forces shaping gene expression and identify convergent expression shifts associated with sex-biased gene expression. Despite the popularity of fireflies due to their bioluminescence, their colonization history, adaptive processes, and species delimitation remain poorly understood. As a second research focus, we therefore sampled the three major European firefly genera across eight European countries to investigate, in a comparative framework, their demographic histories, divergence times, migration rates, and signatures of positive selection. Our initial analyses reveal evidence of incipient speciation, the presence of cryptic species, and the identification of previously undescribed firefly species.

*Speaker