Abstracts from the poster presentations of the EvoGen Munich young scientists meeting in March 2025

Eva Briem, Ludwig Maximilian University Munich, Anthropology and Human Genomics

Assessing Evolution of Primate Atherosclerosis using iPSCs

Abstract: Atherosclerosis is a global disease characterized by a hardening of the arteries. This is caused by a plaque accumulation, primarily composed of foam cells derived from macrophages that take up oxidized low-density lipoprotein (oxLDL). To understand the disease in detail, mainly mouse models and in vitro human models are used. To bridge the evolutionary gap between mice and humans, non-human primates (NHPs) are also used as a model system for biomedical research. However, we know very little about the molecular similarities and differences among NHPs and humans in atherogenesis. In particular, it has been suggested that NHPs are less likely to form the typical plaques in response to a high-fat diet, making it especially important to elucidate common and distinct mechanisms in atherosclerosis among NHPs.

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 their uptake of oxLDL. In turn, this allows to compare the transcriptional profiles between human and NHP macrophages and foam cells to identify conserved and diverged regulatory networks of primate atherogenesis.

Jiayu Chen, Ludwig Maximilian University Munich, Group of Populations genomics

Genomic Introgression signature in the Fleckvieh population

Abstract: Fleckvieh (FV) cattle have undergone crossbreeding with Red-Holstein (RH) since the 1970s to improve traits such as milk production and udder quality. This project aims to map and analyze genomic introgression signatures in the FV population, focusing on identifying regions where RH chromosome fragments have been introduced. Using bioinformatics tools and haplotype analysis, we have identified several genomic regions with high levels of identity-by-descent (IBD) between FV and RH across multiple chromosomes. Interactive visualizations further suggest that these introgressed segments likely harbor genes influencing economically relevant traits. Future work will focus on fine-mapping these regions, functional annotation, and validating their selection across diverse FV populations.

Mitali Chitnis, Ludwig Maximilian University Munich

Magnetoreception by an anaerobic ciliate via tripartite symbiosis

Abstract: Magnetotactic bacteria (MTB) use magnetosomes as built-in compasses to navigate along geomagnetic field. Magnetosomes are composed of biomineralized magnetic iron minerals and guide MTB toward optimal redox conditions along dissolved O2gradients[1]. Magnetosensing has been well studied in MTB, but also extends to microbial eukaryotes. Indeed, certain protists exhibit magnetoreception, potentially through mechanisms like predation upon MTB, symbiosis with MTB, or the direct biomineralization of magnetosomes[2]. Here we report the discovery of a novel magnetic protist with endosymbiotic MTB and methanogens.We observed that this holobiont is responsive to magnetic fields and possesses bullet-shaped magnetosomes. 18S rRNA gene analysis revealed that the protist is a ciliate(Tropidoatractidae) and transcriptomes show that it expressed an Fe-hydrogenosomal hydrogenase gene - indicating an anaerobic lifestyle and H2 production through fermentative hydrogenosomes. Transcriptomes of the magnetic protist revealed expression of genes involved in magnetosome formation (mamA), sulfate reduction (dsrB), which are closely associated with magnetotactic sulfate-reducing bacteria (Desulfovibrionaceae). Expression of the mcrA gene involved in methanogenesis was also detected, that was derived from a group of endosymbiotic H2 oxidizing methanogenic archaea(Methanoregula). These results indicate that a bacterial endosymbiont likely produces the magnetosomes inside of the ciliate, and reduces sulfate using molecular H2 produced by hydrogenosome-like organelles of the eukaryote host. A second archaeal symbiont also uses hydrogenosomal H2 for methanogenesis. Overall, these findings expand the diversity of magnetotactic microbes to include anaerobic ciliates, suggesting that magnetotaxis in eukaryotes may be wider distributed than previously thought.

Samara Correia De Lemos, TUM School of Life Sciences Germany

Comparative Genomics Analysis of Metabolic Gene Clusters in Avena spp.

Abstract: Plant natural products are essential for pharmaceuticals and agrochemicals, with many synthesized by metabolic gene clusters (MGCs)—co-located genes with shared biochemical functions, distinct evolutionary origins, and transcriptional co-regulation. Studying homologous MGCs offers insights into plant metabolism and evolution. Oat (Avena spp.) is a nutritionally valuable crop with growing potential in sustainable agriculture. Despite the recent expansion of genomic resources for oats, their MGCs and biochemical diversity remain largely unexplored. We present a comparative genomics analysis of three Avena species: the hexaploid cultivated oat A. sativa Delfin, its diploid (A. longiglumis), and tetraploid (A. insularis) progenitors. Using PlantiSMASH, we identified 166 MGCs in A. sativa Delfin, 131 in A. insularis, and 52 in A. longiglumis. Among 236 classified MGCs, saccharides (100), terpenes (68), polyketides (43), lignans (22), and alkaloids (3) were represented, with clusters ranging from 3 to 38 genes. Comparative analysis revealed 31 MGCs in A. sativa Delfin conserved from A. insularis, five from A. longiglumis, while 16 appear unique to A. sativa. Further research is needed to determine whether these unique MGCs result from de novo evolution, parental gene diversification, or selective pressures. This study lays the foundation for discovering novel bioactive compounds and improving oat cultivars.

Vanessa Helmbrecht, Ludwig Maximilian University Munich

Simulated early Earth geochemistry fuels a hydrogen-dependent primordial metabolism

Abstract: Molecular hydrogen is the electron donor for the ancient exergonic reductive acetyl-coenzyme A pathway (acetyl-CoA pathway), which is used by hydrogenotrophic methanogenic archaea. How the presence of iron-sulfides influenced the acetyl-CoA pathway under primordial early Earth geochemistry is still poorly understood. Here, we show that the iron-sulfides mackinawite (FeS) and greigite (Fe3S4), which formed in chemical garden experiments, produce abiotic H2 in sufficient quantities to support hydrogenotrophic growth of the hyperthermophilic methanogen Methanocaldococcus jannaschii. Abiotic H2 from iron-sulfide formation promoted CO2-fixation and methanogenesis and induced overexpression of genes encoding the acetyl-CoA pathway. We demonstrate that H2 from iron-sulfide precipitation under simulated early Earth conditions fuels a H2-dependent primordial metabolism.

Zane Kliesmete, Ludwig Maximilian University Munich, Anthropology and Human Genomics
A comparative study of neural differentiation in primates
Abstract: Advances in transcriptomics and comparable cell culture conditions across species allow us to study recent evolution not only on gene sequence, but now also on gene expression level in a specific cellular context. Leveraging dynamic processes across the primate phylogeny can inform on the molecular basis of phenotypes and human disease, because conserved gene expression patterns are expected to reflect functional importance. Here, we aim to strengthen this hypothesis by investigating expression dynamics across primates. We investigated early neural differentiation in two great apes, human and gorilla and an Old World monkey, cynomolgus macaque, in multiple biological replicates across six timepoints using single cell RNA-sequencing. After aligning temporal expression trajectories, we identified a set of genes that is constantly upregulated during the cell state transition from induced pluripotent stem cells to neural precursor cells in all three species. We characterized the genes with conserved expression regulation and found that a substantial fraction is associated with relevant differentiation processes. Moreover, the monotonically upregulated genes show higher sequence conservation across primates and a higher probability of being mutation intolerant in humans than genes upregulated only in humans. This set is enriched in transcriptional regulators associated with neurodevelopmental diseases, suggesting high functional relevance for the process of neural differentiation. In summary, we show that a deeper understanding of the link between regulatory conservation and functional relevance can strengthen the confidence when addressing less commonly investigated cellular processes and help prioritizing particular dysregulated genes in the context of disease.

Qiaoyi Liang, Max Planck Institute for Biological Intelligence, Germany
Behavioral and molecular responses to sweet stimuli vary in songbirds
Abstract: Although the ancestor of modern birds is thought to have lost its ability to detect sugars in its diet,early songbirds have re-gained sugar sensing through repurposing their savory taste receptor. Thisancestral sensory trait may have enabled non-nectar-feeding songbirds to consume nectar and fruit asfuel during migration. Intriguingly, while most songbirds combine sweet sensing with the physiologicalability to digest carbohydrates, members of the Muscicapida clade (including starlings and theirrelatives) are incapable of digesting sucrose. Whether species of this sucrase-deficient clade

can alsodetect dietary sugars is currently unclear. Here, we investigated the carbohydrate preferences ofstarlings and their relatives using brief-access two-choice tests in captivity and in the wild duringmigration. We observed that, in accordance with their sucrose intolerance, starlings and some otherMuscicapida members do not display any preference for sugars. In contrast, songbirds in theSylviodea superfamily (i.e. blackcaps), which are predicted to have intact sucrase activity, displayimmediate and significant preferences to sucrose as well as hexoses. These results, together withcurrent experiments on the molecular basis of taste receptor sensitivity and sucrase activity, will shedlight into how sensory abilities may shift in relation to physiological changes during vertebrate evolution.

Sidra Muntaha, Technical University of Munich, School of Life Sciences

Phenotypic and early transcriptome differences across different populations and their hybrids in Solanum chilense.

Abstract: Adaptation to the local environment is a primary force driving morphological evolution and allopatric speciation, possibly generating genetic incompatibilities between geographically separated populations. In this study, we first compared the effect of drought under controlled climatic conditions and the physiological and morphological response of different allopatric populations of Solanum chilense. Seven accession of parental populations LA4107, LA3111, LA1963, LA4330, LA4117A, LA2932, LA2755 from different local habitats i.e. coast, central, and highland were used during the experiment. We measure the germination rate of seeds, plant growth parameters, physiological responses, and morphological characters. Our result demonstrated strong variability among and between accessions, indicating the polygenic and multiple trait nature of the tolerance of Solanum chilense to water stress and adaptation to local habitat. Second, to investigate the divergence and the genetic basis of reproductive isolation between the most southern populations (coastal and highland) of S. chilense on either side of the Atacama desert, we performed crosses between these parental populations. We successfully produced both F1 and F2 generations and indeed observed strong compatibility between the crosses. We notably observed a pronounced maternal effect in the crosses between coastal and highland populations LA4107× LA4117A. To further validate and decipher the genetic basis of this maternal incompatibility effect, we are conducting an RNA-Seq experiment focusing on early root and stem developmental stages of F1 plants. We aim to find out differentially expressed genes responsible for developmental differences between the reciprocal crosses.

Dörte Neumeister, Ludwig Maximilian University Munich

Unraveling the genetic architecture of male song and female preference in Chorthippus grasshoppers

Abstract: Speciation occurs when populations accumulate genetic differences that lead to reproductive barriers, such as incompatible mating signals, ecological interactions, or gene interactions. However, gene flow can erode these barriers through recombination. To understand the genetic basis of these traits, particularly in systems primarily driven by behavioral isolation, experimental approaches beyond the observation of natural populations are essential. Chorthippus grasshoppers, although broadly sympatric, lack recognizable ecological differentiation but exhibit strong behavioral isolation driven by male mating songs and female preferences. We conducted experimental crosses between two sympatric sister taxa, C. brunneus and C. biguttulus, to investigate male mating signals and female preferences. First, we recorded the mating traits of F2 and backcrossed individuals to characterize their variation. Next, we plan to use genetic analyses to identify the genomic regions associated with these traits, shedding light on the mechanisms of reproductive isolation. By mapping these traits to specific genomic regions, we aim to determine whether signaling-preference coevolution arises through assortative mating or is facilitated by physically linked loci. Our findings will help clarify the genetic architecture of behavioral isolation and contribute to the ongoing debate on speciation in the presence of gene flow.

Namratha Pavuluri, Technical University of Munich, School of Life Sciences

DroughtDB – a manually curated compilation of plant drought stress genes

Abstract: Drought, along with heatwaves and warm spells, poses a significant threat to global food production. Climate change is contributing to more droughts and water shortages on continents around the world. As droughts become more frequent worldwide, the risk of prolonged, multiyear events—lasting years to decades and severely impacting agriculture and food security—continues to rise. As publicly available data continues to grow, specialized databases, developed and curated by biologists are essential for organizing this information into meaningful and accessible resources. Several genes involved in drought stress response have already been characterized, and compiling them into a dedicated database will facilitate research and aid in the development of drought-resistant crop varieties. DroughtDB is a comprehensive biological database designed to centralize and promote access to information on drought-related genetic, physiological, and environmental factors. It integrates information about the initially identified gene, their functional and physiological roles, and provides detailed information about computed orthologous genes to support research on drought tolerance and adaptation across eight essential crop species. Identifying orthologs is crucial for understanding gene function across species, as they share a common ancestor and often retain similar roles. Orthology analysis would help transfer functional insights from well-studied model species to less-studied crops. By offering a curated resource, DroughtDB is a valuable tool for advancing drought-related studies, supporting crop improvement efforts, and enhancing our understanding of plant responses to water stress.

Leonhard Schaffmayer, Ludwig Maximilian University Munich

Unveiling molecular signatures of learning in the striatum of humanized foxp2 mice through spatial transcriptomics

Abstract: Foxp2 was the first gene directly linked to the human ability of vocal learning. Additionally, it was shown that Foxp2 has two unique amino acid substitutions across the human lineage. Introducing the humanized version of Foxp2 in mice facilitates altered transcriptomes in the striatum and better performance in learning-based assays compared to their wild-type counterparts. The plasticity of neuronal connections in the brain enables the process of learning. Intermediate early genes bridge neuronal activation to the adjustment of synaptic strengths by ultimately altering transcription or protein states in neurons. This enables experience-dependent neural circuit remodeling, which is necessary for plasticity and learning. Therefore, we aim to analyze the spatial expression patterns of intermediate early genes in the temporal context of learning in mice carrying the human version of Foxp2. Consequently, we developed an end-to-end image-based spatial transcriptomics workflow with single-cell resolution. It utilizes multiplexed hybridization chain reaction RNA fluorescence in situ hybridization and machine learning algorithms as well as a new powerful transcript classifier, Transcriptor, to investigate a large number of samples precisely and cost-effectively. This allows us to understand how the molecular changes in the brains of humanized Foxp2 mice result in their increased learning performances, potentially leading to crucial insights into the complexity of learning.

Anita Térmeg, Ludwig Maximilian University Munich, Anthropology and Human Genomics
Cross-species comparison of gene regulatory networks using single-cell CRISPRi screens in primate iPS cells
Abstract: Phenotypic differences between us humans and our non-human primate relatives are shaped to a large extent by regulatory changes. Therefore, to better understand primate evolution and the emergence of unique human traits, we need to investigate the underlying gene regulatory networks (GRNs) and how they were rewired across the primate tree. Genetic perturbation screens coupled with transcriptomic profiling make it possible to infer direct regulatory relationships at an unprecedented scale. Using single-cell CRISPRi screening, a high-throughput perturbation approach, we knocked down >90 transcription factors in human and cynomolgus macaque iPS cells and compared the perturbation-inferred regulatory networks across the two species. We performed this comparison on two levels. First, we investigated the large-scale effects of the perturbations by quantifying changes in stemness, cell type composition and cell survival rate. Secondly, we zoomed in to find out what are the immediate transcriptomic responses that trigger these cell fate decisions. To this end, we performed DE analyses among control cells and undifferentiated perturbed cells. We focused on identifying differentially regulated genes - genes that are significantly more up- or downregulated upon a perturbation in one species compared to the other. Using the power-corrected fraction of differentially regulated genes among all affected genes, we aim to quantify how diverged the regulon of each transcription factor is across species. This divergence metric can then be compared to other transcription factor characteristics, such as sequence conservation, evolutionary age or the extent of interactions with other transcription factors, to better understand the principles of GRN evolution.

Yi Peng Toh, Ludwig Maximilian University Munich
Evolution of the olfactory system during the radiation of Heliconiini butterflies
Abstract: Sensory system evolution plays a crucial role in shaping species' interactions with their environment, yet the extent to which olfactory system diversity reflects ecological and evolutionary

pressures at a macroevolutionary scale remains unclear. Here, we investigate the evolution of the olfactory system across the Heliconiini butterfly tribe, an ecologically diverse but closely related group. Using a comparative approach, we examined variation in antennal lobe morphology and its constituent structures, the glomeruli and antennal lobe hub, as well as olfactory receptor repertoires across species. We found that antennal lobe size variation is driven by independent shifts in glomerular and antennal lobe hub volumes, with species-specific differences occurring against a backdrop of broader phylogenetic stability. While no direct associations with ecological traits were observed, certain species showed large expansion in glomerular volume and olfactory receptor numbers, warranting further investigation into unmeasured ecological or behavioural factors. Additionally, comparisons between wild-caught and insectary-reared individuals revealed a surprising pattern of developmental plasticity, with antennal lobe hub volumes increasing and glomeruli volumes decreasing in captivity, highlighting the influence of environmental conditions on neural development. These findings suggest that olfactory evolution in Heliconiini is shaped by both evolutionary divergence and developmental plasticity, emphasizing the need to integrate phylogenetic, ecological, and developmental perspectives to fully understand sensory system adaptation.

Jingjie Wu, Technical University of Munich

Genome evolution in Rubia (Rubiaceae)

Abstract: Rubia L. is the type genus of the Rubiaceae and with c. 88 accepted species distributed throughout the temperate and tropical regions of the Old World. Due to their high Alizarin content, the roots of several species, including R. tinctorum, R. cordifolia, and R. peregrina, have been important sources for purple dye since the Bronze Age. We try to use the genus Rubia to analyze species recovery after man-made or natural bottlenecks. Here we present de novo annotation on the genomes of seven species (R. yunnanensis, R. fruticosa, R. balearica, R. occidens, R. agostinhbi, R. tinctorum and R. rechingeri). Phylogenomic analyses indicate that R. yunnanensis and European species diverged c. 15 million years ago. Comparative genomic analysis reveal expanded and positively selected genes related to biological features. This study provides genomic resources for the genus Rubiawhich will allow more detailed analyses of the genomic consequences of population decline and recovery.