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

Miles Anderson, Technical University Munich
How do plants adapt for climate change and novel habitats? Insights from a wild tomato species

Abstract: As climate change becomes more inevitable and threatens to disturb both natural ecosystems and agricultural production, the question of how plants adapt to climate change and colonization of new and more extreme environments will only become more important. Using the wild tomato species Solanum chilense as a case study, it is shown what methods can be used to identify traits of importance and their genetic basis. The life history traits of a species are also demonstrated to affect the adaptive potential of species of interest. In the case of Solanum chilense, the presence of seed banking as a bet-hedging strategy causes the preservation of genetic diversity within populations, increases the effective population size, and as a result of the increased population recombination rate, improves the power of selective sweep detection methods. Whole genome and target sequence capture data for Solanum chilense are used to infer a demographic history and detect signals of selection. Modeling of past climate data allows for the correlation of climate projections with the demographic history, allele frequencies, the age of selection events and distribution shifts.

Alessio Capobianco, Geo-Bio Center LMU Munich
How many characters are needed to reconstruct a phylogeny?

Abstract: Despite increased recent attention towards Bayesian phylogenetics and its applications in understanding macroevolutionary processes, it remains unclear how many discrete characters are needed to accurately estimate tree topologies in a Bayesian framework. This could be particularly relevant for morphological datasets, as they usually consist of a few dozens to a few hundreds of characters—orders of magnitude smaller than most molecular datasets.

We designed a simulation study in the software RevBayes to explore how the number of sampled discrete characters affects accuracy and precision of Bayesian phylogenetic estimates, under various setups differing in number of taxa, length of the phylogenetic tree, and number of states per character. Results suggest that hundreds of characters might be necessary to reach a satisfactory level of accuracy in topological estimates for as low as 20 tips, and thousands of characters for more than 100 tips. All other parameters being equal, multistate characters produce more accurate estimates than binary characters, and longer trees produce less accurate estimates than shorter ones.

The results of this study provide to empirical researchers a baseline expectation for the accuracy of a phylogenetic estimate, given the size and other characteristics of the dataset used to generate it. Moreover, they outline the continuous need for global research efforts geared towards the characterization and digitalization of interspecific morphological diversity in both extant and extinct taxa, with the specific aim of building larger data matrices for phylogenetic studies.

Luo Chen, Ludwig Maximilian University Munich

Comprehensive and Sustainable Utilization of Genomic Resources: Integrating Target Enrichment, Genome Skimming, RNA-Seq, and Deep Genome Skimming for Improved Phylogenetic Resolution in Sonerileae (Melastomataceae)

Abstract:The advent of new next-generation sequencing (NGS) methods has revolutionized phylogenetics, yet challenges remain in effectively utilizing data from a wide range of sources. In this study, we combine target enrichment, genome skimming, RNA-Seq, and deep genome skimming (DGS) data to reconstruct the phylogenetic relationships within Sonerileae, the second-largest tribe in the Melastomataceae. We sampled 176 accessions representing 40 of the 46 genera in Sonerileae, including newly sequenced Hyb-Seq and DGS data along with publicly available NGS data. A newly developed reference comprising 5,626 loci was employed to integrate data from different sources. Our analyses provide a well-supported, near-comprehensive phylogeny for the tribe, outperforming previous and current studies that used only the probe set as reference. This study provides an effective and sustainable approach to integrating genomic data from multiple sequencing strategies for phylogenetic analysis and contributes a more robust phylogeny and novel insights into the evolutionary history of Sonerileae.

Rosie Drinkwater, Ludwig Maximilian University Munich

Impacts of habitat fragmentation and human-mediated translocations in a global biodiversity hotspot

Abstract: Anthropogenic disturbances, including habitat fragmentation and the introduction of invasive species, constitute primary drivers of tropical extinctions, notably within Wallacea, a biodiversity hotspot of Eastern Indonesia. While many of these disturbances are contemporary, some predate historical records, extending into prehistoric periods. Establishing the temporal dynamics of anthropogenic impacts on species is crucial for effective conservation strategies. Ancient DNA analysis offers a powerful tool to elucidate the timing of these impacts, revealing patterns of genomic erosion and gene flow across temporal scales. Here we used a combination of over 200 newly sequenced ancient, historical and modern genomes from multiple ungulate species to assess how pre-historic translocations of species and habitat fragmentation are affecting local biodiversity across Wallacea. Using museum and archaeological genomes from Sus species (pigs and related species), we identify long-lasting effects of prehistoric livestock translocations (i.e. gene flow) on the genomic makeup of local species. This underscores the long-term consequences of human-mediated introductions of pigs on island ecosystems within the Wallacean archipelago. Furthermore, combining genomic analyses with habitat suitability modelling, we show that recent deforestation is leading to large-scale genomic erosion of ungulate populations, such as anoa (bovid) and babirusa (suid), on larger islands, which experience greater resource exploitation compared to smaller islands in the archipelago. Collectively, our results provide a comprehensive picture of the timing and impact of diverse anthropogenic disturbances acting on endemic ungulate species.

Mathieu Gardere, Technical University Munich

Biogeography and diversification of Campanula (Campanulaceae) and Conyza (Asteraceae) in North Equatorial Africa: a "Green Sahara" legacy?

Abstract: In North Equatorial Africa (NEA), plant biodiversity is unevenly distributed, mainly on the periphery of the Sahara. This distribution results from a long and complex biogeographic history linked to Saharan paleoclimatic fluctuations. However, this desert has not always been a biogeographic barrier. Since the Miocene (7–6 Ma), NEA experienced numerous climate fluctuations, characterized by periodic changes between arid and humid phases. These humid and pluvial phases, called "Green Sahara", led to intracontinental floristic movements through biological migration corridors. To deepen our understanding of the biogeographic history of the NEA, we focus here on two asterid lineages: Holarctic Campanula (Campanulaceae) and Paleotropical Conyza (Asteraceae). Our study aims to characterize their evolutionary trajectories in response to paleoclimatic fluctuations and to identify the ecological and geographical factors that favored their dispersal and diversification. For both lineages, our phylogenies reveal similar diversification patterns. The most diverse clades, composed of perennial woody species on oceanic islands or high mountains, are sister to widespreadannual herbs of lowland and/or desert habitats. Long-distance dispersal of tiny wingless seeds (Campanula) and achenes with pappus (Conyza) via anemochory is not sufficient to explain the complexity of the present-day distribution. The biological and ecological characteristics of the ancestral lineages could have played a crucial role in the colonization of NEA. Annual herbs (ubiquitous with short life cycles) could have dispersed through corridors of the "Green Sahara". Once established in mountainous and island refuges, the lineages evolved into woody perennial forms, thus adapting to the new local conditions.

Chyi Yin Gwee, Ludwig Maximilian University Munich
Ancient Crow DNA Reveals Phenotypic Genes Underpinning a Stable Hybrid Zone

Abstract: Advances in ancient DNA (aDNA) technology have revolutionized our ability to extract and analyze highly degraded genetic material, offering direct snapshots of past evolutionary processes. Using modern and aDNA spanning up to 20,000 years, we investigated the evolutionary dynamics of the European hybrid zone between the carrion crow (Corvus corone corone) and the hooded crow (C. corone cornix), distributed across Eurasia. Despite stark differences in plumage—the carrion crow's all-black feathers and the hooded crow's grey-and-black pattern—these populations are genetically almost identical, with key differences localized to a single locus on chromosome 18 spanning approximately 2.5 million base pairs. While plumage color differentiates the two forms, our analyses reveal high levels of introgression in putatively neutral genomic regions. Through aDNA analysis, we provide direct evidence that this morphological hybrid zone has remained stable for at least 5,000 years. Moreover, we identified genes on chromosome 18 that underpin plumage variation and facilitate assortative mating, shedding light on the genetic mechanisms and evolutionary forces maintaining this hybrid zone. Our study demonstrates the power of aDNA in resolving genetic changes over time, enabling the identification of key genes despite the challenges posed by high linkage disequilibrium within this region.

Andreas Hauser, Ludwig Maximilian University Munich

A Telomere to Telomere haplotype resolved genome of the Auckland Island Pig for Xenograft bioengineering

Abstract: The Auckland Island Pig is the basis of our approach to produce Xenograft pig hearts for human use. To make our bioengineering approach more precise and verifiable, we were interested in a high resolution assembly of our cell lines that are the basis for the modifications. Here we present a Telomere to Telomere haplotype resolved genome of the Auckland Island Pig, that enables a more precise bioengineering approach. The highly controlled offspring population might also be interesting from an evolutionary point of view.

Antonia Keßler, Ludwig Maximilian University Munich, Anthropology and Human Genomics

Primate induced pluripotent stem cells for cross species comparison

Abstract: Cross-species comparisons are crucial for understanding evolution and human biology. As molecular phenotypes are highly cell-type specific, for comparative studies, orthologous cell type across species are needed. However, due to ethical and practical constraints, access to these cell types is often limited. Somatic cell reprogramming into induced pluripotent stem cells (iPSCs) has revolutionized cross-species studies, enabling the generation of otherwise inaccessible cell types from multiple species. To study evolution on a molecular level, we generate and culture iPSCs from different primate species in vitro. So far, we have generated and validated iPSCs across seven primate species - human, gorilla, orang-utan, baboon, cynomolgus, rhesus and vervet. However, for non-human primates, only few iPSC lines per species have been generated. As molecular and cellular phenotypes in iPSCs are sensitive to technical factors like cell type of origin, reprogramming method and culture conditions, we aim to quantify the influence of these technical factors across individuals and species. With improved reprogramming, culture conditions and larger biological replicates we seek to enhance the power of species comparisons. By expanding this resource to more individuals and species in a standardised manner, our work will further extend the zoo of available cell lines and improve iPSC-based cross-species comparisons.

Meng-Ching Ko, Max Planck Institute for Biological Intelligence, Germany

Genomic insights into shared adaptations for sugar consumption in diverse avian lineages

Abstract: Dietary specialization requires coordinated adaptations across multiple physiological systems, yet the genomic basis for such adaptations remains poorly understood. Here, we investigate the molecular underpinnings of high-sugar diets across four independently evolved nectar and fruit-consuming bird lineages: hummingbirds, parrots, honeyeaters, and sunbirds. Through comprehensive genomic analyses, including whole-genome sequencing of nine species, transcriptome profiling of five metabolically relevant tissues, and examination of both protein-coding genes and regulatory elements, we identified evident patterns of repeated molecular evolution associated with sugar consumption. Our comparative framework, incorporating closely related non-sugar-consuming outgroups, allowed us to distinguish diet-specific adaptations from lineage-specific traits. Statistical analyses revealed a higher

degree of shared genomic changes across sugar-consuming birds compared to their non-sugar-consuming relatives, with changes affecting both protein-coding and regulatory regions. These shared adaptations primarily involve carbohydrate metabolism pathways and, intriguingly, cardiovascular functions. Particularly noteworthy is MLXIPL (encoding ChREBP), which shows positive selection signals in all four sugar-consuming clades. Functional validation demonstrated increased transcriptional activity of hummingbird MLXIPL compared to its swift counterpart, supporting the adaptive significance of these genomic modifications. Our findings further reveal that accelerated conserved non-exonic elements in sugar-consuming birds are enriched for genomic loci associated with Type 2 Diabetes in humans, suggesting these birds have evolved mechanisms to manage metabolic challenges that would be detrimental to mammals. This study highlights how integrative genomic approaches can reveal the molecular basis of complex physiological adaptations to specialized diets.

Vanda Marosi, Helmholtz Zentrum Munich
Barley pan-transcriptome comparative correlation network analysis reveals ortholog divergence.
Abstract: Barley is a globally important cereal crop, ranking fourth in crop production worldwide. It is known for its resilience and adaptability. As a diploid species with a relatively small genome, it serves as a valuable model organism for Triticeae research. Advances in sequencing technologies have facilitated the development of high-quality barley reference genomes and pan-genomes, providing a solid foundation for detailed functional and transcriptomic studies. However, gene co-expression studies in barley have so far been limited to individual varieties, failing to leverage the potential of pan-transcriptomic and cross-variety approaches. We developed a barley pan-transcriptome to identify core genes based on their presence in twenty inbred genotypes. We have investigated the functional divergence of core genes in barley by systematically comparing the transcriptomes of these varieties. Twenty co-expression networks were constructed based on the 13,561 core, single-copy genes and based on 296 RNA sequencing samples across five distinct tissues (root, embryo, seedling, shoot, developing inflorescence, and caryopsis). Analysis of the co-expression networks revealed six major communities, each associated with specific tissues and biological processes. A subset of 1,371 orthologous groups (10% of single-copy genes) exhibited conserved co-expression, residing within a single community across all 20 genotypes. In contrast, the majority (12,190, 90%) were distributed across two or more communities, indicating substantial functional differentiation of biological processes among the barley cultivars. Our results highlight the presence of both conserved and diverged co-expression patterns among core genes in barley, revealing the transcriptional complexity underlying genotype-dependent functional differentiation.

Lucas Miller - Technical University Munich
Caucasian Origin, frequent long-distance dispersal, and recent diversification of the navelworts (Umbilicus, Crassulaceae)

Abstract:Umbilicus is a genus of Crassulaceae with a distribution in Eurasia, Africa, and Macaronesia. The genus includes 16 accepted species, the identification is oftentimes difficult, due to high intraspecific variation. So far, the only genetic analyses that include Umbilicus have been at the family level. Here, we sequenced six plastid regions plus the nuclear ribosomal ITS region of 202 specimens covering the entire distribution range and all accepted species. Using molecular dating and BioGeoBEARS we estimated a stem age of 16.4 (9.5–25.9) Million years and inferred the Caucasus as the geographic origin. The first diverging clades include species with yellow or white, open flowers. These lineages are restricted to the eastern range of the genus. The third clade includes species with greenish, tubular flowers and diverged 5 (2.5–8.2) Ma. Within this clade we inferred repeated LDD events, including the colonization of Angola, India, and Macaronesia. The genetic analysis revealed widespread homoplasy in morphological characters and further comprehensive sampling is necessary to test species boundaries. Our data supports up to 70 lineages, which would result in an average diversification rate compared to other Crassulaceae genera. Compared to the first diverging lineages, the tubular flowers of the third lineage, which can heavily deviate in shape and size, suggest specialization and shifts in pollinator. This could have led to rapid reproductive isolation, but even though pollinators likely played a key role in the evolution of the genus, pollinator data remains very poor and field observations are necessary to test this hypothesis.

Daniel Mills, Ludwig Maximilian University Munich
The Rise of Algae promoted eukaryote predation in the Neoproterozoic benthos
Abstract: The proliferation of marine algae in the Neoproterozoic Era (1000-539 million years ago) is thought to have stimulated the ecology of predatory microbial eukaryotes. To test this proposal, we introduced algal particulate matter (APM) to marine sediments underlying a modern marine oxygen minimum zone with bottom-water oxygen concentrations approximating those of the late Neoproterozoic water column. We found that under anoxia, APM significantly stimulated microbial eukaryote gene expression, particularly genes involved in anaerobic energy metabolism and phagocytosis, and increased the relative abundance of 18S rRNA from known predatory clades. We additionally confirmed that APM promoted the reproduction of benthic foraminifera under anoxia with higher-than-expected net growth efficiencies. Overall, our findings suggest that algal biomass exported to the Neoproterozoic benthos stimulated the ecology of benthic predatory protists under anoxia, thereby creating more modern food webs by enhancing the transfer of fixed carbon and energy to eukaryotes occupying higher trophic levels, including the earliest benthic metazoans.

Bart Nieuwenhuis, Ludwig Maximilian University Munich
The Evolution and Turnover of Mating Type Alleles in Mushroom Forming Fungi
Abstract: Mating requires sexual compatibility, which in many eukaryotes is regulated by mating types, where they ensuring outcrossing and regulate the life cycle. Mating types are typically governed by negative frequency-dependent selection, favoring rare alleles, which maximize mating opportunities. In mushroom forming (basidiomycete) fungi, mating compatibility is generally controlled

by two unlinked multi-allelic loci that both must differ for mating partners to be compatible. This unique system allows for an extraordinary diversity of mating types. In the model species Schizophyllum commune, with more than 80 and 200 alleles at the two mating type loci, over 23 thousand mating types are expected. Despite this extreme polymorphism, little is known about the rise, maintenance, and turnover of these alleles over evolutionary timescales of these loci. To address this, we analyzed a global population sample of S. commune, investigating the evolutionary dynamics of mating-type alleles. Our findings reveal different evolutionary patterns for the two mating-type loci. We find ancient trans-specific polymorphism at the first locus, suggesting balancing selection, while the other, more variable locus shows repeated evolution of novel alleles, indicating high turnover. These results provide new insights into how mating types evolve in response to selection pressures and genomic constraints. Understanding the mechanisms driving mating type diversification in fungi offers broader implications for the evolution of self-incompatibility and population dynamics under negative frequency dependent selection.

Neža Pogorevc, Ludwig Maximilian University Munich, Population Genomics Group
Evolutionary dynamics of adaptive introgression and balancing selection in the genomes of wild and domestic goat species
Abstract: Introgression is increasingly recognized as a key evolutionary factor influencing the genomic composition of species. We examined the genomic footprint of introgression and balancing selection among various breeds of domestic goat (Capra hircus), their wild ancestor bezoar (C. aegagrus), and three ibex species (C. ibex, C. pyrenaica, and C. sibirica). The analysis of whole genome sequences from 167 individuals, including goat-ibex hybrids, revealed shared genetic variations between wild and domestic goats. Strong evidence pointed to adaptive introgression between ibexes and goats, primarily concentrated in 23 genomic regions. Enrichment analyses of these regions identified genes associated with olfactory and immune functions. While the detection of immune-related genes supported previous findings, further analysis indicated that some of these results might be false positives due to balancing selection. This selection process appears to have been ongoing since the divergence of the ibex and bezoar lineages, which includes the lineage of domestic goats. We conclude that Capra species may have adapted to new environments more frequently than previously believed, driven by range expansions associated with glacial cycles. Consequently, the extent of adaptive introgression and selection on immune genes likely varied with these cycles, reflecting the adaptation of Capra species to differing pathogen challenges and their need to respond effectively to these challenges with a robust immune response. These findings underscore the dynamic relationship between adaptive introgression and the selection of functionally significant genes, highlighting their critical roles in the resilience and evolutionary trajectories of Capra populations in response to changing environmental conditions.

Joëlle Van Der Sprong, Ludwig Maximilian University Munich

Next-Generation Species Discovery and Delimitation in Sponges Using Target-Captured, Genome-Wide Markers

Abstract: Discovering and delimiting species is pivotal for understanding biodiversity, which is becoming increasingly urgent given the accelerating global decline of species. Although effective for many organisms, traditional morphological taxonomy faces significant challenges in groups with high phenotypic plasticity or subtle diagnostic features. High-throughput sequencing technologies enable cost- and time-effective sequencing of multiple orthologous loci, opening new research opportunities in taxonomy and systematics. We assess the applicability of target-captured genome-wide loci combined with model-based species delimitation methods for species identification and discovery in sponges, a group with notoriously difficult species distinction. We analyse a well-characterised demosponge group from the Mediterranean (genus Tethya) to explore the applicability of different species delimitation methods. Building on these insights, we apply these approaches to taxonomically unresolved clades within the demosponge order Haplosclerida. We examine how different methods perform across datasets and assess the influence and sensitivity of parameter selection and the consistency of hypotheses across methods. Genome-wide markers have great potential to improve species discovery in taxonomically challenging groups. We demonstrate that they offer a reproducible approach that contributes to solving taxonomic uncertainties and discuss the advantages and limitations of different methodologies and their integration into species delimitation. Our results show that model-based species delimitation methods improve objectivity in taxonomic decisions by providing probabilistic species hypotheses when applied within a biologically meaningful context. Using multiple lines of evidence (e.g., morphological, ecological, and biogeographical), model-based approaches can enhance biodiversity assessments for taxonomically complex marine invertebrates, which eventually help develop better-informed conservation strategies.

Laura Villegas, University of Cologne, Institute of Zoology
Ultraconserved Elements and Machine Learning for Scalable Nematode Phylogenomics

Abstract: Nematodes are among the most diverse animal groups, inhabiting nearly all ecosystems. Over a million species of nematodes are expected to occur on earth, however only around 28.000 have been described to date. Nematode phylogenetics remains challenging due to their small size, morphological simplicity, and cryptic diversity. Traditional morphological and molecular approaches, such as single-locus markers (e.g., 18S rRNA, COI), often lack resolution, particularly at shallow evolutionary scales. Moreover, discrepancies between morphology-based classifications and molecular phylogenies underscore the need for improved genomic methods. Here, we design and test the first ultraconserved elements (UCEs) probe set for two nematode families: Panagrolaimidae and Rhabditidae. This approach captures thousands of loci without requiring whole-genome or transcriptome sequencing. Our probe set successfully retrieved 1,612 and 10,397 UCE loci for Panagrolaimidae and Rhabditidae, respectively, enabling a robust phylogenetic reconstruction. Genera classifications within Panagrolaimidae were congruent with prior phylogenies. We applied machine learning classifiers to determine the minimum loci required for genus-level classification. For Panagrolaimidae, despite extensive laboratory isolates, genomic resources are limited. We identified

~200 loci as the most informative for classification. Further testing the Panagrolaimidae-specific machine learning model on shallow Nanopore sequencing data, we found that genera classification was possible with as few as 20 UCEs. In summary, our UCE probe sets offer a scalable, cost-effective tool to enhance taxonomic resolution and evolutionary inference in nematodes. This approach has the potential to improve biodiversity assessments and deepen our understanding of this ecologically important group.

Raúl Y.Wijfjes, Ludwig Maximilian University Munich
Detecting evolutionary constraint in a panel of diverse Brassicaceae genomes
Abstract: The Brassicaceae family is a central pillar of evolutionary studies in plants, containing plant species showing a range of environmental adaptations and the model plant Arabidopsis thaliana. High-quality genome assemblies are available for many Brassicaceae, allowing us to measure evolutionary constraint, defined here as the probability of small mutations and larger structural variation being retained at a given genomic position between different species of the family relative to neutral expectations. Such information enables us to identify genomic positions likely involved in molecular function or trait evolution, that would not have been identified using intraspecific measures of constraint only. Despite its importance, our understanding of the degree of evolutionary constraint in Brassicaceae genomes is limited, as previous efforts to measure it used a small number of genomes of mostly closely related Brassicaceae. To address this, we present a panel of Brassicaceae genomes tailored to detect evolutionary constraint with high power and resolution. To maximize the phylogenetic diversity represented in the panel, we collected publicly available chromosome-level genome assemblies of a variety of Brassicaceae and complemented these with newly generated ones to cover more clades. We annotated protein-coding genes in each assembly and used conserved gene order to infer syntenic orthologs, leveraging the chromosome-level contiguity of the assemblies. Here, we show how such syntenic orthologs can be used to identify genome rearrangements and reconstruct ancestral gene order in Brassicaceae.

Alex Zemella, Max Planck Institute for Biological Intelligence, Germany
How to turn off high testosterone: genetic regulation of androgens in male mating morphs
Abstract: Alternative mating tactics can be a major agent for the evolution of intraspecific variation. Males using different tactics often show profound steroid hormone differences. These hormones shape vertebrate m Anthropology and Human Genomics ating phenotypes, but how their concentrations are genetically regulated is unclear. The ruff (Calidris pugnax) has three distinct mating morphs, determined by a supergene. During breeding season, these morphs show discrete variation in aggression, courtship, and circulating testosterone. Satellites and Faeders have low testosterone, while the common morph has high testosterone. This study explores the molecular mechanisms behind these differences, combining genomic, transcriptomic, modelling, and enzyme conversion data. We found that androgen differences among ruff morphs are due to changes in 17-beta hydroxysteroid dehydrogenase 2 (HSD17B2) sequence, expression and activity. This enzyme, encoded by HSD17B2

within the supergene, converts testosterone to androstenedione. Low-testosterone males, despite producing high testicular testosterone, overexpress derived HSD17B2 transcripts in blood and other tissues related to testosterone regulation and social behavior. Mutations increasing enzymatic activity are under positive selection. Our findings show how evolutionary changes within a single gene create and amplify endocrine variability, altering male social behaviors crucial for reproduction.