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**Vienna Doctoral School of
Ecology and Evolution**

Symposium

27 February 2026

Art & Science Pre-Event Music by *Strand Ohne Palme*
"Integrating art & science communication into a teaching and research program"
by Chris Martine | 26 February 2026 | 18:00 | Djerassiplatz 1, 1030 Vienna

Symposium Keynote talks by Samantha Brown und Tobias Uller
27 February 2026 | 09:00 | Djerassiplatz 1, 1030 Vienna

Register here:

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Welcome to the VDSEE Symposium 2026

We are delighted to welcome all participants and speakers to the 3rd Vienna Doctoral School of Ecology and Evolution (VDSEE) Symposium. We hope that this day will be an exciting journey through the ecological and evolutionary research taking place in our DocSchool.

The symposium was initiated with the intention of creating a platform that spotlights the research of PhD-candidates from the Doctoral School. This Symposium showcases the diverse science of the VDSEE and provides participants with the opportunity to exchange ideas and create new networks.

We are delighted to welcome our keynote speakers, Samantha Brown (National Research Center on Human Evolution, CENIEH) and Tobias Uller (Lund University), who is also a member of our Scientific Advisory Board (SAB). We are equally pleased to welcome our other SAB members, Alexandra Müllner-Riehl (University of Leipzig), Luisa Pallares (MPI Tübingen), and Carina Schlebusch (Uppsala University). Thank you all for joining us and contributing to our symposium.

We would like to thank the organizing committee Arne Bielke, Mayline Goëb, Jennifer Hennefeind, Emily Pigott and Norman Wickett who made this Symposium come to life. Furthermore, we would like to express our thanks to Doctoral Study Programme Leader, Hanna Schneeweiss, for her continuous support. Finally, we extend our appreciation to our sponsors CliniSciences, Integra, Shimadzu, and Zeiss for supporting the VDSEE Symposium!

We wish all participants an insightful event! If you would like to share your thoughts about the Symposium, please send an email to docschool.vdsee@univie.ac.at.

Useful information:

Location:

- All talks take place at "Hörsaal 1". Please enter the University Biology Building at the main entrance (Djerassiplatz 1, 1030 Wien). The lecture hall is on the ground floor, just follow the signs for the Symposium until you reach the room labeled "HS1" on the right.
- Please register at the desk in front of HS1.
- The poster sessions, coffee breaks, lunch and the sponsors' booths are in the foyer behind Hörsaal 1.
- Dinner will be served in the Mensa in UBB. It is right behind the foyer where the poster session takes place. Our vegetarian and vegan buffet is awaiting you.
- Please note that the University Biology Building closes at 22:00, therefore dinner and party end at 21:30

Wifi: Eduroam is available at the location

Contact: If you need urgent help, please call the VDSEE Executive Manager Antonia Vogel (+43-1-4277-50028) or contact the Portier right behind the main entrance.

Programme

08:30-09:00 Registration

09:00-09:10 Welcome address and remarks

Keynote 1 – Chair: Jennifer Hennenfeind

09:10-10:00 Tobias Uller

10:00-10:20 Coffee break

Session 1 - Chair: Pere Gelabert

10:20-10:40
Carla Gómez-Montes - *Chronology and subsistence strategies during the Gravettian in the Cave of Altamira (Santillana del Mar, Cantabria)*

10:40-11:00
Aigerim Rymbekova - *Ghost admixture in present-day African genomes*

11:00-11:10
Presentation of u:respect campaign

11:10-11:20 SHORT BREAK

Session 2 - Chair: Stefanie Wienkoop

11:20-11:40
Nina Kraus - *Environmental Regulation of Cardiac Development and Evolution*

11:40-12:00
Stefan Pavloski - *How do novel cell types evolve? Co-option of fibroblast activation in the origin of uterine decidualization*

12:00-12:20
Antonia Grausgruber - *Exploring differential gene expression underlying developmental arrest in a vermetid gastropod*

12:20 – 12:30
Poster pitches round 1 (odd numbers)

12:30 – 13:45
LUNCH BREAK AND POSTER SESSION GROUP 1(ODD NUMBERS)

Keynote 2 - Chair: Emily Pigott

13:45-14:35 Samantha Brown

14:35-14:45 SHORT BREAK

Session 3 - Chair: Norman Wickett

14:45-15:05 **Johannes Hausharter** - *Widespread thermophilization in Europe's mountaintop vegetation*

15:05-15:25 **Florian Brück** - *The epigenetic dimension of effects of climate change on high alpine plants*

15:25-15:45 **Thomas Buchloh** - *Chromosome Evolution Model Reveals Hidden Variation in Chromosome Number Speciation in Ferns*

15:45-16:05 **Anna-Sophie Hawranek** - *3D floral syndromes in Aquilegia (Ranunculaceae)*

16:05-16:15 Poster pitches round 2 (even numbers)

16:15-17:00 COFFEE BREAK AND POSTER SESSION GROUP 2 (EVEN NUMBERS)

Session 4 - Chair: Hanna Schneeweiss

17:00-17:20 **Anna-Chiara Barta -** *Phylogenomics supports monophyly of marsupial crustaceans: a journey to direct development*

17:20-17:40 **Iro Pierides** - *Kernel-DMD for multiome integration and control of CAM photosynthesis*

17:40-18:00 **Kim Stroben** - *Beyond Landmarks: Elastic Shape Analysis for Robust Squaliform Tooth Classification*

18:00-18:15 SHORT BREAK AND GRAB A BEER

18:15-18:30 Poster and talk awards, closing remarks

18:30 – 21:30 Dinner and party

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Keynote Lecture 1

Professor Tobias Uller

Lund University, Sweden

Philosophy of Science for Biologists

Philosophy of science is not only about grand old theories of how science works. It is about reflecting on assumptions, concepts, theories and methodologies in a structured way. By doing so, we become better equipped to identify questions that really matter and interact constructively with others to formulate answers. The goal is not become philosophers, but to become better scientists.

Tobias Uller is Professor of Evolutionary Biology at Lund University. His research investigates how organismal processes such as development, physiology, and behaviour influence evolutionary change, using an integrative approach that combines experiments, genomics, field studies, comparative methods, and mathematical modelling. In addition to empirical research on phenotypic plasticity, extra-genetic inheritance, and evolutionary diversification, he contributes to conceptual and philosophical discussions on the integration of development and evolution.

Keynote Lecture 2

Dr. Samantha Brown

National Research Center on Human Evolution (CENIEH), Burgos, Spain

Palaeoproteomics and the palaeontological record: using ZooMS to understand degradation and preservation in proteins

The advent of palaeoproteomics, the study of ancient proteins, has led to a revolution in the analysis of biomolecules in the palaeontological record. The native robusticity of proteins allows for the biomolecular analysis of bones across hundreds of thousands, if not millions of years. One of the major techniques in palaeoproteomics, ZooMS, has become an invaluable to the archaeological science toolkit; allowing for the rapid and reliable taxonomic identification of bone, teeth, feathers, fur, parchment, ivory, shell, and eggshell. ZooMS is undergoing a new wave of technological advancement, moving beyond taxonomic identification to aid in our understanding of protein preservation through deep-time. Large ZooMS studies have produced a wealth of data that can be mined using increasingly sophisticated programs, providing an invaluable record of protein degradation through time. Here, we discuss the utility of this data and the role of ZooMS in understanding damage patterns in ancient proteins. We discuss how these datasets can be used to further our understanding of both our hominin ancestors and the deep-time preservation of their remains.

Samantha received her PhD at the Max Planck Institute for Geoanthropology (formerly the Institute for the Science of Human History) in Jena, Germany, as a member of the ERC project FINDER. This project focused on the identification of human remains within the heavily fragmented bone assemblages found at Palaeolithic sites throughout Europe and Asia. Upon completing her PhD, she began working as the Junior Group Leader for Archaeo- and Palaeoproteomics at the University of Tübingen, Germany. Here, she established a new palaeoproteomics laboratory, continuing the application of ZooMS to archaeological sites through a close collaboration with the University's Zooarchaeology Department. The result of this collaboration was the establishment of new tools that aimed to bring zooarchaeological and palaeoproteomic workflows closer together. After three years at the University of Tübingen, Samantha became head of the Molecular Palaeobiology Laboratory at the National Research Center on Human Evolution (CENIEH) in Burgos, Spain.

Oral Presentations

Chronology and subsistence strategies during the Gravettian in the Cave of Altamira (Santillana del Mar, Cantabria)

Carla Gómez-Montes[1,3], Ana B. Marín-Arroyo[2], Pere Gelabert[1,3], Pilar Fatás Monforte[4]

[1] Department of Evolutionary Anthropology, University of Vienna; [2] Grupo I+D+i EvoAdapta (Evolución Humana y Adaptaciones durante la Prehistoria), Dpto. Ciencias Históricas, Universidad de Cantabria; [3] Human Evolution and Archaeological Sciences (HEAS), University of Vienna; 4 Museo y Centro Nacional de Investigación de Altamira, Cantabria, España

The Cave of Altamira, widely known as the "Palaeolithic Sistine Chapel," is renowned for its outstanding cave art; however, knowledge of the human groups that occupied the site during the Upper Paleolithic remains limited. This study aims to refine the chronology of the Gravettian occupation of Altamira and to reconstruct the subsistence strategies of its earliest Upper Paleolithic inhabitants. To achieve this, an integrated approach combining archaeozoological and taphonomic analyses with paleoproteomic methods, specifically Zooarchaeology by Mass Spectrometry (ZooMS), was applied for the study of Gravettian bioarchaeological remains curated at the Museo Nacional y Centro de Investigación de Altamira.

The results provide new insights into hunting strategies, prey transport, seasonality, and butchering practices, identifying red deer as the most represented species, followed by horse, while also clarifying the taphonomic processes involved in the formation of the assemblage. Newly obtained radiocarbon dates for level 8 place the Gravettian occupation between 27,340 and 26,000 cal BP. The application of ZooMS significantly improved taxonomic resolution for certain mammalian groups and enabled the identification of highly fragmented remains, demonstrating the complementarity of proteomic and traditional archaeozoological approaches.

This research highlights the continued scientific value of museum collections and underscores the importance of applying innovative methodologies to them. The studied materials offer substantial information on the paleoeconomic behavior of Upper Paleolithic hunter-gatherers in the Cantabrian Region. These findings confirm Altamira's high potential for advancing our understanding of early Upper Paleolithic subsistence systems and encourage future integrative studies of Solutrean and Magdalenian levels to know better their inhabitants and their ways of life.

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Ghost admixture in present-day African genomes

Aigerim Rymbekova[1,2], Gwenna Breton[3], Paul Verdu[4,5,6], Leo Speidel[7], Mattias Jakobsson[3], Carina Schlebusch[3], Martin Kuhlwilm[1,2]

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[2] Human Evolution and Archaeological Sciences (HEAS), Univeristy of Vienna, Austria;
[3] Human Evolution, Department of Organismal Biology, Uppsala University, Sweden;
[4] National Centre for Scientific Research (CNRS), Paris, France;
[5] National Museum of Natural History (MNHN), Paris, France;
[6] Paris Cite University, Paris, France;
[7] RIKEN, Japan

Admixture has played a critical role in shaping the genetic diversity among human populations. Diverse and deeply divergent present-day human populations such as the Khoe-San populations of Southern Africa and Central African rainforest hunter-gatherers (RHG) are key to understanding our evolutionary history as humans. Although several studies have previously suggested contributions from unknown deeply diverging lineages into the ancestors of different present-day African populations, there is no coherent picture due to differences in datasets, methods and frameworks considered. This problem is particularly difficult since no genomes from archaic populations in Africa are available.

Using methods that do not require genomes from a source population, we analyzed high-coverage genomes from Khoe-San and RHG populations, in the context of African genomic diversity. We found that a model with introgression from an unknown source population into the ancestors of Khoe-San populations best explains patterns of variation. Various models of early human population structure in multiple stems or stepping-stone gradients are not sufficient to explain genomic outliers. We identified such genomic fragments of ghost introgression in the Khoe-San individuals, which might influence functions related to sensory perception. Unlike in other introgression events, the X chromosome seems to carry a larger fraction of such fragments.

Nina Kraus

Environmental Regulation of Cardiac Development and Evolution

Nina Kraus[1,2], Brian Metscher[1]

[1]Department of Evolutionary Biology, University of Vienna, 1030 Vienna, Austria; [2]Konrad Lorenz Institute for Evolution and Cognition Research, 3400 Klosterneuburg, Austria

My work investigates how new environmental inputs reorganize developmental mechanisms to generate evolutionary novelty in the vertebrate heart. Rather than treating evolution as the accumulation of genetic changes alone, I focus on how developmental systems are repatterned when environmental conditions become integrated into their causal organization. In this view, the evolution of form is the evolution of the mechanisms that produce it[1,2].

I will present my theoretical framework that argues that environmentally triggered developmental responses can become stabilized within developmental mechanisms and subsequently subject to selection when environmental inputs are consistently incorporated into the developmental system, for example through shifts in developmental mode. Environmental factors such as oxygen levels or mechanical forces then do not merely modulate existing developmental programs, but consistently expand them by activating new organizational routes within the system[3,4].

Using cardiogenesis as a model, I examine how oxygen availability during development changed with major vertebrate transitions from aquatic to amniote and placental modes of development, and how these shifts are reflected in cardiac morphology across the vertebrate phylogeny. Combining comparative reasoning with experimental intervention, I show that reducing oxygen during outflow tract remodeling in chick embryos suppresses apoptosis and produces single-outlet hearts reminiscent of ancestral vertebrate morphologies. These results identify oxygen as a developmental difference-maker[5] whose historical incorporation reorganized cardiac developmental pathways and experimentally support my theoretical framework[6,7].

From this perspective, congenital malformations can be explained as secondary consequences of developmental systems that evolved to be environmentally responsive. By situating the environment within developmental mechanisms themselves, the comparative study of development offers an integrated account of evolution, development, and disease, linking phylogenetic history to present-day ontogeny and its vulnerabilities, and advancing a unified science of biological variation.

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Antonia Grausgruber

Exploring differential gene expression underlying developmental arrest in a vermetid gastropod

Antonia Grausgruber[1], Andreas Wanninger[1]

[1]Department of Evolutionary Biology, University of Vienna

Despite its curious adult appearance, early development of the caenogastropod worm snail *Thylaeodus* cf. *rugulosus* (Vermetidae) follows a conserved, gastropod-typical indirect development including trochophore and veliger larval stages. However, what appears common on a morphogenetic level, seems to be controlled by a complex brood regulation mechanism in early development. Until the late veliger stage, *Thylaeodus* develops inside of maternal brooding capsules. Several capsules are attached inside the mother's tubular shell, each containing a multitude of embryos. Out of these embryos only a small number within one capsule develops until the larval phase. Most embryos remain in a multicellular pre-blastula stage and serve as nutritive resource for their viable siblings which develop into trochophore larvae. In fact, the production of such nutritive embryos or eggs is not uncommon in marine gastropod. In *Thylaeodus rugulosus*, however, developmental arrest can also happen later in larval development. Only a maximum of three animals out of about 10 viable larvae per brooding capsule complete their development until hatching. Remaining siblings appear to get arrested in a stage that morphologically corresponds to the early veliger larva.

Our data suggests that there are two distinct time points in the early development of *Thylaeodus* at which progeny can be prevented from entering subsequent developmental stages. This could allow for additional opportunities of brood regulation. These particularities make the development of *Thylaeodus* multilayered and complex, the underlying molecular and developmental mechanisms defining this developmental arrest remain unexplored to date. The current project aims at unravelling transcriptomic differences that shape the distinction between viable and arrested animals in *Thylaeodus rugulosus*. We will apply differential gene expression analysis on stage-specific transcriptomes and investigate expression patterns in situ. This will allow for insights into the genetic toolkit that determines developmental arrest versus regular embryonic and larval development in these elusive gastropod mollusks.

Stefan Pavloski

How do novel cell types evolve? Co-option of fibroblast activation in the origin of uterine decidualization

Stefan Pavloski[1], Mihaela Pavlicev[1,2,3], Günter Wagner[1,3,4,5], Nikolaos Papadopoulos[1], Daniel Stadtmauer[6]

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A key innovation that gave rise to mammalian eutherian pregnancy is the origin of a novel cell type on the maternal side - the decidual stromal cell[1,2,7]. These cells differentiate from endometrial stromal fibroblasts under the influence of progesterone and prostaglandin E2 during pregnancy, in a process known as decidualization[3]. The resulting tissue - decidua, is necessary for successful implantation and pregnancy support[5,6]. The process of decidualization shares similarities with the process of fibroblast activation- a response of fibroblast cells to tissue perturbations, such as injury[4,9]. Fibroblast activation entails the transformation of fibroblasts to myofibroblasts, which contributes to wound healing. When activated persistently, fibroblast activation can lead to excessive scarring, i.e., fibrosis[10]. In contrast, while decidualization initially follows fibroblast activation, it does not result either in wound healing nor in scarring, but in differentiation of a distinct cell type - the decidual stromal cell[8,9]. In order to explore whether decidualization may have co-opted and later modified fibroblast activation, I am, in the first step, comparing published single-cell RNA seq data of human endometrium across stages of the menstrual cycle, and data of the human skin at different stages of wound healing. As expected, the comparison of gene expression profiles between the two processes shows that the trajectory of fibroblast activation ends at the proliferative stage of wound healing and at the secretory stage in the endometrium, where the endometrial stromal cells are differentiating to pre-decidual stromal cells in a non-pregnant (menstrual) cycle. Inflammation appears to be a striking difference between the two processes - it is a key part of the fibroblast activation trajectory in wound healing, but not in decidualization. Downregulation of genes associated with inflammation may play a role in the modification of the process of fibroblast activation during the co-option by the process of decidualization.

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Johannes Hausharter

Widespread thermophilization in Europe's mountaintop vegetation

Johannes Hausharter[1,2], Stefan Dullinger[1]

[1]Department of Botany and Biodiversity Research, Biodiversity Dynamics and Conservation Group, University of Vienna; [2]Vienna Doctoral School of Ecology and Evolution, University of Vienna

Over the past decades, considerable changes in alpine vegetation have been observed and often attributed to climate warming. Among these changes is the shift of plant community composition towards more warmth-demanding species, a process referred to as thermophilization. However, the causal link between thermophilization and warming has rarely been explicitly tested. Here we combined local long-term microclimatic temperature data with vegetation surveys in 724 permanent plots across 53 European mountain summits monitored over 21 years to evaluate a possible thermophilization trend and relate it to rates of change in ten macro- and microclimatic temperature metrics. We found both significant thermophilization of plant communities and increases in temperatures across the entire dataset, but relationships between the magnitudes of thermophilization and temperature change were weak, especially at the scale of local communities. Instead, the availability of thermophilic colonizers in the surrounding vegetation had a very strong impact on observed thermophilization rates, suggesting that the community context can obscure the expected direct link with local temperature change. We conclude that the intuitive link between temperature change and thermophilization of plant communities is far more complex and more heavily influenced by other factors than commonly assumed. Appropriately accounting for this complexity will require further, intensified monitoring efforts.

Florian Brück

The epigenetic dimension of effects of climate change on high alpine plants

Florian Brück[1], Kryštof Chytrý[1], Norbert Helm[1], Conchita Alonso[2], Claude Becker[3], Karl Hülber[1], Stefan Dullinger[1], Ovidiu Paun[1]

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Climate change strongly impacts alpine ecosystems, driving shifts in species distributions to higher elevations and demanding rapid adaptation for survival [1]. Long-term evolutionary responses may be insufficient under current rates of change. Short-term acclimation through phenotypic plasticity could therefore be critical for population persistence. Epigenetic mechanisms, particularly DNA methylation and its influence on gene regulation, are promising candidates to mediate such rapid responses, yet their role remains poorly understood outside of model organisms [2,3]. We investigated molecular responses to long-term warming in four unrelated high-alpine plant species (Luzula alpino-pilosa, Phyteuma hemisphaericum, Sibbaldia procumbens and Veronica alpina) using a multi-year in situ transplantation experiment. Plants were relocated from native high-elevation habitats to lower, warmer sites and to high-elevation control sites, generating a consistent and ecologically realistic temperature increase while allowing monitoring of survival and growth. We combined high-coverage enzymatic methylation sequencing with transcriptome profiling mapped to newly assembled reference genomes. Across investigated species, warming significantly increased global DNA methylation, driven mainly by changes in the CHH sequence context. CHH methylation strongly correlated with summer temperature and was most pronounced in transposable elements (TEs), non-transcribed regions, and putative promoter regions. Differentially methylated regions were most abundant in the CHH context and enriched in TEs, suggesting hypermethylation of transposons under heat stress to reinforce silencing and maintain genome stability. Transcriptome analyses revealed enrichment of differentially expressed genes involved in temperature, drought, light, and oxidative stress responses, confirming strong physiological reactions to warming. Integrating expression and methylation data revealed that only a subset of differentially methylated genes was also differentially expressed, but these overlaps were more frequent than expected by chance and enriched for general stress-response functions. Together, our results demonstrate consistent epigenetic responses to warming across multiple alpine species and highlight DNA methylation as a potentially important component of short-term acclimation to climate change.

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Thomas D. Buchloh

Chromosome Evolution Model Reveals Hidden Variation in Chromosome Number Speciation in Ferns

Thomas D. Buchloh[1,2], Carrie M. Tribble[3], Michael R. May[4], Norman J. Wickett[1,2]

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Change in the haploid chromosome number commonly generates reproductive isolation between diverging species. If changes to the haploid chromosome number (karyotype) most often generate new species, variation in the rate of chromosome number evolution is expected to predict variation in diversification rates. While, this correlation has been supported in some plants, we know less about how the evolution of the mode and tempo of karyotype change. Methods to address the evolution of diversification and chromosome number transition rates are computationally expensive and analyses are typically restricted to to small clades or avoided all together. We identify and describe variation in the mode and tempo of karyotype evolution (via dysploidy and polyploidy) in the Polypodiales—a species and karyotype-rich order of ferns—using an extended Chromosome Number and Hidden State-dependent Speciation and Extinction model (ChromoHiSSE). Using the fully parameterized ChromoHiSSE model we estimate rates of karyotype evolution across 962 leptosporangiate ferns of the Polypodiales. We recover two hidden modes of chromosome number evolution between which the rates of karyotype evolution differ by more than an order of magnitude. However, our stochastic mapping of these modes across fern evolution suggests lineages with high karyotype lability are less likely to persist in the long-term. These results reinforce the theory that modern fern diversity is shaped substantially by polyploid speciation but challenge the expectation that diversification rates are enhanced by karyotype-driven speciation.

Anna-Sophie Hawranek

3D floral syndromes in Aquilegia (Ranunculaceae)

Anna-Sophie Hawranek[1], Anne Le Maître[2], Maria von Balthazar[1], Gregor Traun[1], Leon Schönenberger[1], Susanne Pamperl[1], Jürg Schönenberger[1], Marion Chartier[1]

[1]Department of Botany and Biodiversity Research, University of Vienna; [2]Department of Evolutionary Biology, University of Vienna

The function of flowers in their interplay with pollinators is constrained by the three-dimensional arrangement as well as the shape and size of their floral organs. *Aquilegia* flowers are polysymmetric and their perianth comprises an inner whorl of five conspicuous petals that conceal their nectar reward in spurs. The spurs of different species differ in length and shape, likely as an adaptation to their specific pollinators. Indeed, previous studies have shown selection for spur length to ensure pollination success.

In this study, we hypothesise that not only the length of the corolla spurs but also their shape reflects pollination systems in *Aquilegia*, thus defining three-dimensional (3D) floral syndromes. To test this hypothesis, we scanned flowers of twelve *Aquilegia* species pollinated by either a single functional group of nectar-collecting pollinators (large bees, hummingbirds or hawkmoths) or by two of these functional groups together (large bees and hummingbirds or hummingbirds and hawkmoths).

By applying 3D geometric morphometrics, we study landmark- and semilandmark-sets defining the spur curvature as well as the spur opening where the pollinators insert their probing parts (proboscis or beak/tongue). A preliminary morphospace analysis showed a clear association between flower shapes and functional groups of pollinators, thus supporting our hypothesis. For example, the petal spur entrances differ in their shapes: while being laterally compressed in hawkmoth flowers, spur entrances are more or less isodiametric in bee flowers. With the advances of 3D geometric morphometrics, we expect to be able to refine the definitions of floral syndromes in *Aquilegia*, which so far largely relied on categorical data and linear measurements of floral organs.

Anna-Chiara Barta

Phylogenomics supports monophyly of marsupial crustaceans: a journey to direct development

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Peracarida (marsupial crustaceans) represent one of the most diverse and ecologically important crustacean groups, yet their evolutionary relationships have long been debated. Here, we present the most comprehensive phylogenomic analysis of Peracarida to date, incorporating the relict taxa Thermosbaenacea, Mictacea, Ingolfiellida, and Spelaeogriphacea for the first time in a phylogenomic framework. Our results robustly confirm peracarid monophyly and recover a well-supported clade uniting Mancoida (Isopoda, Tanaidaca, Cumacea), Mictacea, and Spelaeogriphacea. We propose the new taxon Panmancoida to encompass this expanded lineage defined by shared developmental and morphological traits. The inferred phylogeny further suggests that peracarid evolution involved a transition from an intermediate "pseudodirect" developmental mode to the direct development seen in most lineages. We further show that the shift to extensive brood care within the marsupium, accompanied by the loss of a free-swimming larval stage, may have accelerated rates of molecular evolution across lineages. Together, these findings provide a robust evolutionary framework for this major malacostracan lineage and highlight how key reproductive innovations reshaped the genomic and life-history trajectories of the marsupial crustaceans.

Iro Pierides

Kernel-DMD for multiome integration and control of CAM photosynthesis

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High-dimensional multiome data are increasingly used to decipher molecular mechanisms in different complex biological systems. The challenge remains on how to extract useful information that is not only significant in terms of distributions but also in terms of the underlying causal dynamics. We evaluate the performance of kernel Dynamic Mode Decomposition (kernel DMD) in its ability to integrate multiome and predict outputs of two *Clusia* species with different types of photosynthesis (C3 and CAM). In this way we are able to decompose small time series data into dynamically distinct modules (eigenmodes) and provide a rank on the most significant features that are able to shift output distributions between the two species. Our results have impact in the fields of crop science in switching to more robust modes of photosynthesis but also demonstrate the suitability of kernel DMD with control on complex biological datasets.

Kim J. Stroben

Beyond Landmarks: Elastic Shape Analysis for Robust Squaliform Tooth Classification

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Modern sharks have survived several mass extinction events throughout their evolutionary history, exhibiting a remarkable resilience against extrinsic factors. To understand the underlying mechanisms for their success, a good taxonomic resolution through time is needed. However, the fossil record of modern sharks consists predominantly of isolated teeth, directly linking knowledge about their past diversity to the use of tooth characters, such as shape, for taxonomic classification. This challenge is particularly pronounced in groups of taxa displaying highly similar tooth morphologies, such as Squaliformes.

Here, two conceptually distinct approaches to shape analysis are compared: a landmark-based eigenshape analysis (ES) and a curved-based, landmark-free elastic shape analysis method using the square-root velocity (SRV) framework. To evaluate their discriminatory power for highly similar tooth shapes, teeth from species belonging to two squaliform families, Centrophoridae and Somniosidae, were analyzed.

Although both methods successfully separate the species of the two families, the elastic shape analysis framework provides a clearer separation in morphospace and captures a higher proportion of interspecific variance. Classification results based on k-nearest-neighbor bootstrapping indicate high performance for both approaches, with SRV achieving superior classification accuracy.

These results demonstrate that outline-based elastic shape analysis is a powerful and statistically robust tool for discriminating highly similar tooth morphologies, particularly in fossil datasets where landmark information is sparse.

Poster Presentations

Using sedaDNA to Reconstruct Human-Carnivore Interactions in Late Pleistocene Iberia and Patagonia

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The reconstruction of past populations and ecosystems is fundamentally limited by the incompleteness of the archaeological record and preservation biases. Especially during the Last Glacial Maximum (LGM; ca. 29–19 kya), climatic changes affected human and animal populations; however, many aspects, such as megafauna extinction dates, species interactions and behaviour, remain unclear [1-5]. Here, sedimentary ancient DNA (sedaDNA) provides a valuable line of evidence that complements archaeological and faunal records [6]. This project investigates human–carnivore interactions in Iberia and Patagonia during the Late Pleistocene and Early Holocene by combining sedaDNA analyses with micromorphological approaches, providing high-resolution contextual information for the recovered ancient DNA.

Sediment samples are collected from well-defined stratigraphic layers in direct association with micromorphological block sampling. SedaDNA is extracted from sediments and analysed to identify key taxa (hyena, cave lion, wolf/dog, humans) and to track species presence through time. These genetic results are integrated with the (zoo-)archaeological record to evaluate patterns of cave use, such as human and carnivore (co-)occupations, and to refine extinction chronologies [7]. Direct integration of genetic signals within their microstratigraphic contexts improves the interpretation of sedaDNA data.

Five primary archaeological sites (Baño Nuevo, El Mirón, Isturitz, Llonín, and Aitzpitarte), as well as additional sites, are analysed. This project contributes to our understanding of human and animal presence across different periods, species interactions, extinction dynamics, and human population genetics. The comparison of Iberia and Patagonia offers insight into two rich but contrasting records (continuous vs. discontinuous occupations), allowing broader insights into the impact of humans on their faunal environment [8-9].

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Poster 2

Tracing Karyotype Evolution in *Capsicum* Using Chromosome-Specific Oligo-FISH Probes

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Capsicum is a monophyletic genus in the family Solanaceae comprising approximately 43 species classified into nine phylogenetic clades (Carrizo García et al., 2022). The genus originated in the South American tropics and is currently distributed from central Argentina and Brazil to the southern United States. Five species (*C. annuum, C. baccatum, C. chinense, C. frutescens* and *C. pubescens*) are domesticated and cultivated worldwide. All *Capsicum* species are diploid, with base chromosome numbers of x = 12 or x = 13 (Moscone et al., 2007). The predominance of x = 12 across *Capsicum*, has led to the hypothesis that x = 13 evolved independently in the Andean and Atlantic Forest clades (Carrizo García et al., 2022). However, the ancestral base chromosome number of *Capsicum* remains unresolved. The presence of x = 12 in *Lycianthes*, the sister genus of *Capsicum* (Särkinen et al., 2013), provides an important comparative framework to address this question.

Karyotype evolution accompanying species diversification involves chromosomal rearrangements such as translocations, inversions, duplications, and deletions, resulting in novel combinations of chromosomal segments. Identification of shared rearrangements among related taxa enables reconstruction of ancestral karyotypes. Recent advances in genome sequencing and bioinformatics have enabled the development of chromosome- and segment-specific oligonucleotide probes for fluorescence in situ hybridization (oligo-FISH), allowing detailed analysis of chromosomal rearrangements (Han et al., 2015; Šimoníková et al., 2019; Harun et al., 2023).

In this study, oligo-FISH painting using probes based on four chromosomes of *C. annuum* is applied to 1 - 2 species across all nine *Capsicum* clades and *Lycianthes* as outgroup. Comparative analysis of the distribution patterns of these chromosomal segments enables reconstruction of clade-specific ancestral karyotypes and provides insights into the ancestral karyotype of the genus *Capsicum*.

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Archaic admixture and adaptive introgression in ancient Papuan genomes

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Ancient genomic data have undeniably transformed our understanding of encounters between modern humans and archaic hominins, such as Neanderthals and Denisovans. Archaic introgression has influenced genes of functional relevance in modern humans, involved in neurodevelopment, immunity, and metabolism. While novel studies increasingly reveal variation among archaic groups across time and geography, the nature of archaic admixture in different human populations remains poorly understood.

Here, we provide new insights into Denisovan and Neanderthal gene flow and admixture proportions in low-coverage ancient genomes from Kiowa rockshelter, Papua New Guinea. We identify blocks of archaic ancestry in these ancient genomes and compare them to present-day patterns. Since such very low-coverage data has limited information, we leverage a panel of 177 modern Papuan genomes to detect high-confidence introgressed segments via state-of-the-art methods and assess their overlap with the ancient individuals. We further report an adaptive introgression scan on the modern panel, finding candidate SNPs for adaptive introgression in genes like *DLGAP1*, *BACE2*, *GPBP1* and *SLCO3A1*. Using the ancient individuals, we could trace these adapted alleles more than 8,000 years back in time.

Poster 4

Reconstructing alien plant species habitat niche breadth expansion

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Alien plant species accumulate in regional floras worldwide, yet how they spread across habitat types after introduction remains poorly understood. We analysed 835,891 vegetation plots from the European Vegetation Archive spanning nine decades across 56 European countries to quantify how residence time (the period since first regional occurrence) affects neophyte habitat associations.

Using a hurdle negative binomial model, we examined how residence time influences both the probability and magnitude of neophyte overrepresentation across 18 EUNIS habitat types, comparing each species' habitat distribution against background habitat availability within standardized spatial units [2].

Overrepresentation patterns varied markedly across habitats. Man-made and ruderal habitats exhibited the highest overrepresentation, increasing from 20% (0-20 years residence) to 44% (>200 years). Alpine grasslands and nutrient-poor habitats showed consistently low overrepresentation (<3%), functioning as invasion-resistant refugia. Species established for >200 years had 3.4-fold higher probability of occupying multiple habitats (57%) compared to recent arrivals (17%), with expected habitat counts increasing from 1.2 to 2.0 habitats across residence time categories. Habitat transition analysis revealed predictable colonization pathways, with anthropogenic habitats serving as primary entry points and mesic grasslands as common tertiary colonization sites.

These findings quantify substantial invasion debt [1]: many established neophytes have not yet reached equilibrium with available habitats. The predictable expansion from anthropogenic source habitats suggests that early detection and strategic management of ruderal vegetation could limit spread into natural areas.

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Poster 5

Spatiotemporal Variability and Drivers of Benthic Methane Production Potential in Streams

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In streams and rivers, methane (CH4) emissions and related fluxes and production in the sediment are not well understood despite their high contribution to the global CH4 budget. To unravel the magnitudes and drivers of benthic CH4 production, we measured the CH4 production potential and related sediment properties from six streams in Czechia and Austria once in all four seasons over one year. We took samples at three locations in each stream (total of 72 sediment samples) and measured the methane production potential in five replicates. First results showed that the CH4 production potential rates differed by five orders of magnitude. The mean CH4 production potential ranged from $1.34 \times 10^{-4} \pm 1.43 \times 10^{-4}$ to 15.36 ± 3.81 µg CH4 gDW-1 d-1 (mean ± SD, n = 5), varying largely within and between streams and seasons. The largest variance in CH4 production potential was explained by within stream differences, demonstrating the high heterogeneity of occurrences and production of methanogenic archaea in small streams. Further, preliminary results indicate sediment organic matter content as the more influential driver of spatial variability of benthic CH4 production potential compared to the proportion of fine sediments. This highlights the important role of organic matter as a source for methanogens for benthic methane production.

First high-quality genome assemblies of the blind cavefish *Garra longipinnis* and its surface-dwelling form.

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Striking phenotypic traits (termed troglomorphy) in cave-dwelling species, such as the loss of pigmentation and eye structures, raises the central question of whether these changes arise from relaxed selection and fixation through genetic drift or confer selective advantages in subterranean environments. To address this question, comparative genomic analyses of surface and cave-dwelling populations of the same species—such as the Omani fish *Garra longipinnis*—provide a promising system to investigate how these striking phenotypic trajectories are shaped at the genomic level through evolutionary mechanisms. In this study, we present the first de novo chromosomal-level genome assemblies and their annotations for both forms of *G. longipinnis*. By capturing key genomic components—such as the number of protein-coding genes, the transposable element landscape, mitochondrial genomes, and genome heterozygosity levels—we obtain an initial view of the genomic similarities and differences between the two forms. Additionally, the high contiguity of the surface and cave genomes (N50 = 47 Mb and 45 Mb, respectively) combined with the high completeness of single-copy orthologous genes (C: 95.7% and 96.8%, respectively) demonstrates the high quality of these genome assemblies for a non-model organism that will provide a robust foundation for future studies, into population-level selection dynamics and differential gene expression, which will enhance our understanding of the genomic basis of adaptation to cave environments.

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LC-PUFA bioconversion in *Daphnia magna* is driven by temperature, but not diet

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Organisms at the base of aquatic food webs synthesize essential nutrients, such as n-3 long-chain polyunsaturated fatty acids (LC-PUFA), which are subsequently transferred to higher trophic levels. In many freshwater systems, dominated by green algae and cyanobacteria, these primary producers synthesize the precursor α-linolenic acid (ALA; 18:3n-3), which consumers have to bioconvert to the physiologically important eicosapentaenoic acid (EPA).

Here we investigate how the bioconversion rates of *Daphnia magna* are influenced by dietary quality, and by short- and long-term exposure to different temperatures. Stable-isotope labelling with ^2H_2O was used to quantify EPA bioconversion, while fitness-related traits (size, biomass gain per day, clutch size) were measured simultaneously. Two *Daphnia magna* strains isolated from different climatic regions (a temperate and a Mediterranean lake) were cultured at 15°C, 20°C and 25°C and fed different algal diets that varied in PUFA composition but were standardized for carbon supply (0.05 mg C^{-1} ind^{-1} d^{-1}).

Daphnia fed with a mixture of non-toxic *Synechococcus* sp. exhibited reduced growth, delayed reproduction, and smaller clutch sizes compared to individuals receiving other diets. In contrast, dietary PUFA composition had no detectable effect on individual EPA bioconversion rates, which were primarily driven by temperature. Bioconversion rates were slightly higher in the strain originating from the temperate lake compared to the Mediterranean strain.

Because investment in fatty-acid bioconversion likely involves trade-offs with reproductive output, local adaptation to environmental conditions may enhance consumer fitness. Our study provides a quantitative framework for assessing LC-PUFA bioconversion in zooplankton and highlights its potential role in mediating adaptation to dietary quality and thermal regimes in freshwater ecosystems.

Genomic drivers of persimmon adaptive radiation in New Caledonia, a biodiversity hotspot

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Adaptive radiation, the rapid evolution of many species from a common ancestor, is a major source of biological diversity. While ecological opportunity is traditionally emphasized as its main driver, growing evidence suggests that changes in genome structure may also play an important role by increasing evolutionary potential. However, how such genomic processes contribute to plant diversification remains poorly understood.

The tree genus Diospyros (persimmons) provides a powerful system to address this question. New Caledonia, a global biodiversity hotspot, hosts more than 30 endemic Diospyros species that arose from a single, rapid radiation, while three other independently colonizing lineages remain species-poor. This radiated lineage occupies a wide range of environments, including extreme ultramafic soils that are nutrient-poor and rich in toxic metals. Strikingly, species in this clade have genomes roughly twice as large as those of non-radiating relatives, despite no change in chromosome number, suggesting major shifts in genome architecture.

To investigate the role of genome dynamics in this radiation, we combined high-quality genome assemblies, population resequencing, gene family evolution analysis, gene expression data, and ecological measurements across species adapted to contrasting soils. We find that the radiated lineage shows increased activity of transposable elements along with a higher rate of gene duplication. These changes appear to be associated with genes involved in stress tolerance, metal detoxification, and root development, and are associated with environment-specific gene expression patterns.

Our results suggest that genome expansion and copy number variation may have enhanced the capacity of this lineage to adapt to diverse and challenging environments. More broadly, this study highlights how changes in genome architecture can promote diversification and help drive adaptive radiation in plants.

The role of the Wnt/β-catenin pathway in patterning the inner cell layer of a sea anemone embryo

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Wnt/β-catenin signaling is responsible for the main body axis patterning in Bilateria and in their evolutionary sister group Cnidaria. However, in the model sea anemone *Nematostella*, the involvement of Wnt/β-catenin signaling has only been documented in the ectodermal and endodermal patterning, while it is still unclear whether it has a role in mesodermal patterning as well. In *Nematostella*, mesoderm is specified in the nuclear β-catenin-negative domain prior to gastrulation. However, several Wnt genes start to be expressed in the mesoderm during larval stages. Like the endo- and ectodermal Wnt-s, whose role in the axial patterning is well-documented, mesodermal Wnt-s are also expressed in staggered domains. Using advanced molecular approaches, my project aims **to identify and characterize mesodermally expressed Wnt genes and their downstream targets, elucidating their roles in oral-aboral patterning of the mesoderm.** Functional analyses include pharmacological modulation of the cWnt pathway, transcription factor screening, and genetic knockouts using CRISPR-Cas9.

Poster 10

Genomic Insights of the Migratory Divide: Investigating Population Structure in the Red-necked Phalarope

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Red-necked phalaropes (Phalaropus lobatus) are polyandrous shorebirds with a circumpolar breeding range. Recent research has shown that two geographically close breeding populations show highly distinct migration routes and wintering areas: Icelandic phalaropes migrate ca. 10,000 km over the sea to the tropical eastern Pacific Ocean, whilst phalaropes breeding in Fennoscandia and Russia migrate ca. 6,000 km — largely over land — to the Arabian Sea. Here we test whether this migratory divide reflects population structure through PCA, STRUCTURE, and Fst-based analysis of whole-genome-sequencing data.

Keywords: *Population structure, Migration, Shorebirds, Genomics*

Poster 11

Sparking explosive radiations: a comparative genomic study in subgenus Tillandsia

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Adaptive radiations generate enormous biodiversity, yet the mechanisms driving them remain poorly understood. While ecological opportunity and selection on standing variation or point mutations play important roles, they cannot fully explain why some lineages diversify explosively, but others remain depauperate. Structural genomic variation (SV) has recently been suggested as a potential catalyst of diversification, but its role in plant radiations remains largely unexplored. *Tillandsia* subgenus *Tillandsia* (Bromeliaceae) exhibits both radiated and non-radiated lineages, providing an ideal comparative system to investigate the genomic, demographic, and ecological drivers of adaptive radiations. We use this system to test if a dynamic genomic landscape, shaped by demographic shifts, has promoted phenotypic diversification in the radiated clade of subgenus Tillandsia. To this aim, I will first assemble high-quality genomes and pangenomes across radiated and non-radiated clades to characterize SVs, including transposable element dynamics and gene family evolution (duplications and losses), and compare these between clades to identify genomic signatures of rapid diversification. To place these patterns in their demographic context, I will reconstruct demographic histories (population sizes, bottlenecks, expansions) and map recombination landscapes to assess how these factors interact with SV. Morphological, ecological, and environmental trait data will be integrated with genomic variation to identify candidate adaptive loci using PhyloGWAS, genotype-environment associations, trait evolution modelling, and selection scans. By combining short- and long-read sequencing, pangenomics, demographic modelling, and phenotype-genotype-environment integration, this project will elucidate how genomic architecture, ecological adaptation, and demography interact to shape diversification. Using the unique comparative framework within *Tillandsia* subgenus *Tillandsia*, I will identify mechanisms driving explosive diversification, advancing our understanding of the evolution of plant radiations.

A Framework for Integrating Biodiversity and Nature's Contributions to People into the Climate–Conflict Nexus

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Climate change and biodiversity loss are defining, interconnected challenges of the Anthropocene that shape human well-being and security. Growing evidence links environmental change to armed conflict, yet most research has focused on climate while largely overlooking biodiversity and Nature's Contributions to People (NCPs). This poster introduces a framework that integrates biodiversity loss and NCPs into analyses of environment–climate–conflict linkages. We conducted a systematic survey of quantitative studies on this nexus and find a predominant focus on climate–conflict relationships, with limited attention to biodiversity. Our analyses show that biodiversity loss can both heighten and mitigate armed conflict risks, especially through interaction with climate change. We further demonstrate that most NCPs can be linked to conflict pathways. By foregrounding biodiversity, this framework advances understanding of conflict dynamics and highlights biodiversity's potential role in peacebuilding and conflict prevention.

Divergent Droseras - Trap leaf specialization in *Drosera rotundifolia*

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Carnivorous plants display a wide range of morphological adaptations to nutrient-poor habitats, yet specialization of traps within a single species remains poorly understood. **Drosera rotundifolia**, the round-leaved sundew, has active adhesive traps with different types of stalked glands *i.e*. central, peripheral, and highly motile snap tentacles [1,2]. We observed that tentacle type patterns in plants and populations notably differ. This study systematically examines these divergences across 22 populations from Austria, Germany, and Czech Republic, encompassing gradients in geology, hydrology, altitude, and climate.

Plant traits, leaf orientation, tentacle type distributions, and prey capture were recorded and analysed using regression and mixed-effects models incorporating environmental and plant-level predictors. Differences are highly correlated with increased geographical distance and depend on bog type, water regime, and substrate. However, tentacle patterns were best explained by different frequencies of two leaf types: prostrate basal leaves that possess abundant snap tentacles (9.0 ± 5.1 per leaf), and seemingly adapted to capturing crawling prey. This leaf type is complemented by erect leaves, exhibiting significantly less snap tentacles (3.1 ± 5.0 per leaf) and more peripheral tentacles that appear to target flying prey. Incorporating leaf dimorphism improved model fits and revealed that altitude, day length, sampling time, and water conductivity significantly influenced snap tentacle proportions. Erect leaves showed the highest probability of prey capture, while the likelihood of leaf orientation itself was shaped by environmental conditions.

These results demonstrate previously underappreciated intra-specific trap specialization in *D. rotundifolia*. Such leaf dimorphism likely enhances prey capture efficiency across heterogeneous bog microhabitats, representing an adaptive strategy. Our findings are consistent with broader patterns of environmentally driven investment in carnivory and functional diversification in sundews and other carnivorous plant lineages [3,4]. This study highlights the importance of local environmental pressures in shaping adaptive trait variation within a single carnivorous plant species.

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Poster 14

A deep learning model unveils key metabolome combination influence on biological nitrification inhibition activity

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Biological nitrification inhibition (BNI) is a key trait for climate-smart cropping, yet the metabolomic basis of high BNI remains unclear. We profiled root-exudate metabolomes from 44 wheat accessions originating from India and Austria. After defining high- and low-BNI groups, we trained an ensemble of machine-learning classifiers and introduced a Balanced Relevance Score (BRS) that quantifies each metabolite's association with BNI by combining strength, cross-method consistency, and cross-validated validity. Across conditions, BRS highlighted a compact set of candidate metabolites that robustly marked the high-BNI group. To move beyond single features, we further searched pairwise and triad combinations using non-linear interaction modelling and stability selection. Several metabolite pairs/triads reproducibly improved discrimination of high vs. low BNI over the best single-metabolite baselines, indicating synergistic effects in the exudate chemical space. Country-stratified and leave-one-country-out evaluations supported the portability of the signatures. Together, our framework—combining interpretable machine learning with the BRS metric—identifies both individual biomarkers and minimal metabolite combinations that underpin high BNI, providing actionable targets for functional follow-up and wheat breeding.

Poster 15

Palaeoproteomic analyses of bone fragments from Palaeolithic Crimea reveals two new hominins, including one being identified as a Neanderthal

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Key words: Palaeolithic Archaeology, Palaeoproteomics, Radiocarbon dating, Ancient DNA

The Crimean Peninsula contains significant Palaeolithic sites, including Kabazi II, Kabazi V, Siuren I, Starosele, and Chokurcha I. The region has been considered a potential refugia for Neanderthals before their replacement by *Homo sapiens*. This hypothesis is supported by lithic analysis and radiocarbon dating.

In this study, we used collagen peptide fingerprinting, Zooarchaeology by Mass Spectrometry (ZooMS), to identify morphologically unidentifiable bones to genus or species level and screen for potential human remains, which are rare in Palaeolithic contexts.

We analysed 628 bone fragments with ZooMS, finding that 82.3% had sufficient collagen preservation for taxonomic identification. Our results suggest Palaeolithic humans primarily hunted horses (Equidae) at Kabazi II, Kabazi V, and Starosele, while other sites revealed evidence of deer, mammoth, and other large ungulates, offering insights into the region's paleoenvironment and subsistence strategies.

Importantly, two bone fragments displayed collagen fingerprints matching Hominidae from Starosele. Radiocarbon dating of the Starosele bones revealed them to be 44–46,000 and 42–44,000 years old, close to the transition between the disappearance of Neanderthals and early dispersal of *Homo sapiens*. We obtained ancient DNA analysis from the younger bone, finding very low endogenous content (<0.1%). We sequenced a 2-fold coverage mitochondrial genome from this bone, indicating the individual belongs to the Neanderthal lineage. The mitogenome clusters with other Neanderthal mitogenomes previously generated from the Russian Altai region.

Alongside this, an analysis of the lithic corpus from both regions suggests that a wider Neanderthal dispersal, linked to the Micoquian stone tool industry, occurred after ~60,000 years ago. We assessed the palaeoclimate connection (temperature and precipitation) between these locations and identified a high habitat suitability corridor along 55°N, suggesting that the long-distance movement of Neanderthals would have been facilitated by periods of favourable climate.

Poster 16

Identifying Interactors of ESCRT-0-like Proteins in Salt-stressed Barley

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Barley (*Hordeum vulgare*) is an important and resilient cereal crop. However, salinity negatively impacts its growth and yield. The Endosomal Sorting Complex Required for Transport (ESCRT) is a protein complex involved in membrane deformation and protein sorting processes. Differential abundance of ESCRT proteins was observed during barley grain development and in salt-stressed seedlings [1, 2]. To identify interactors and regulators of barley ESCRT-0-like Tom1-like proteins (TOLs) with a putative role in salt-stress response, a pull-down protocol for GST-tagged proteins was developed. This protocol was then applied to GST-HvTOL1 and -3 with extracts of barley roots grown under salt-stress and control conditions in a dark-root phenotyping device (BIBLOX) [3]. Interactors were then identified via LC-MS/MS-based proteomics.

The analysis revealed putative interactors, and enriched protein families. For a number of these proteins, interactions are known or predicted in other organisms (e.g. proteins of the ubiquitin-proteasome pathway). Stringent filtering resulted in a list of highly likely interactors, many of which are involved in (salt-) stress response. Furthermore, kinases with putative regulatory roles were identified.

Follow-up literature research and experiments will be performed to identify and confirm interactors with potential roles in stress resilience and the regulation of the ESCRT. These results will help us further understand how the ESCRT is regulated in plants.

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Insights into Laticifer Visualization using Microtomography

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Laticifers are specialized secretory cells responsible for production and storage of latex, a complex suspension with key ecological and defensive functions in plants [1,2,3]. Understanding the distribution of laticifers throughout the plant body is crucial for elucidating their roles in plant–environment interactions; however, three-dimensional visualization of laticifer networks remains technically challenging due to their broad distribution in the tissues, highly branched morphology and heterogeneous latex content. This study provides insights into laticifer imaging using X-ray microcomputed tomography (micro-CT), focusing on contrasting strategies and imaging performance. Inflorescences of four latex-producing species of Moraceae (*Brosimum gaudichaudii* Trécul, *Castilla elastica* Cerv., *Dorstenia cayapia* Vell., and *Ficus citrifolia* Mill.) were collected, fixed in buffered formalin, dehydrated through an ethanolic series to 70%, critical point dried, and scanned under three contrasting conditions: no contrast [4], ethanolic iodine [5,6], and 1% phosphotungstic acid (PTA) [4,7]. Two microtomographs were used: Zeiss Xradia MicroXCT system and Bruker SkyScan 1174. Untreated samples exhibited strong natural contrast in lignified tissues and phenolic idioblasts, but laticifers were sporadically detectable and highly dependent on latex loss during preparation. Iodine enhanced starch-rich tissues, particularly anthers, and phenolic idioblasts, but laticifers remained largely indistinguishable. PTA at 1% improved overall soft-tissue contrast, with progressive staining over 3–14 days enhancing tissue delineation; nevertheless, most samples lacked sufficient resolution for consistent laticifer detection. Comparative analysis revealed that micro-CT system performance was a critical factor: XRadia scans provided superior laticifer visualization compared to SkyScan system, emphasizing the importance of resolution and scan duration. These results demonstrate that while contrast agents influence tissue visibility, successful micro-CT visualization of laticifers requires optimization of contrast chemistry, sample preparation, and imaging platform.

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City Invading Mosquitoes (Diptera: Culicidae) of Medical Importance

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Despite the increasing relevance of mosquitoes for public health, knowledge of their habitat use and spatial distribution remains limited, representing a critical gap highlighted by recent mosquito-borne disease outbreaks in Europe [1]. Urban environments provide a diverse array of natural and artificial breeding sites, however species-specific associations with these habitats are still poorly understood [2]. Additionally, effective mosquito detection and monitoring in heterogeneous city landscapes poses substantial challenges [3]. Approximately 25 mosquito species, including competent vectors of established and emerging pathogens, as well as three non-native mosquito species have previously been recorded in Eastern Austria [4-6]. This study provides the first city-wide assessment of mosquito assemblages and their habitat affinities focusing on immature stages.

Over two consecutive years (June–October), we conduct a systematic sampling of mosquito eggs, larvae, and adults across 30 sites distributed throughout three temperature zones within the municipality of Vienna. Here, we present the multi-facetted approach of the study as well as the preliminary results after the first year of sampling. This is a first step towards a holistic mapping of the mosquitoes, including all development stages, present within the city of Vienna and towards a sustainable and functioning risk management. Further, this study shows the different species composition between adult, larvae and egg sampling and underlines the importance of including all life stages to successfully study mosquito presence and take measurements to minimize the risk for diseases outbreaks.

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The influence of resurvey plot location on observed vegetation change

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Aim: Long-term vegetation study through resurveys is essential for quantifying how biodiversity changes over time. The accuracy of resurvey data is influenced by plot location errors, arising from spatial uncertainty of the location of historical plots. Preferential location of resurvey plots potentially underestimates vegetation change, while random location may overestimate it. To address these methodological issues, we studied the difference between preferential and random relocation approaches to assess how they influence observed temporal vegetation changes, focusing on diversity patterns across two common grassland types of Central Europe: mesic grasslands and dry grasslands.

Location: Northeastern Austria and southern Czech Republic.

Methods: We compared two methods for locating vegetation plots in resurveys at 50 sites: a) resurvey plots located preferentially by the surveyor in the field, b) resurvey plots located randomly in the same habitat type within a 300 meters spatial buffer around the probable location of the historical plot. We then compared changes in species richness, composition, and Ellenberg-type Indicator Values between the two resurvey plot location methods.

Results: Across the entire dataset, species richness change was higher and the Jaccard dissimilarity index was lower in the preferentially located than in the randomly located plots, while other metrics (species richness, number of species lost and gained, species composition, top winners and losers, Ellenberg-type Indicator Values) showed no significant differences. In mesic grasslands, resurvey plot location approach affected species richness most. In contrast, in dry grasslands, it introduced uncertainty in detecting changes in composition, as seen with a significantly higher Jaccard dissimilarity index in random plots than in preferential plots.

Conclusions: Results in resurvey studies from permanent plots should be interpreted with caution, as resurvey plot location strategy may affect temporal change detection in long-term vegetation assessments.

Solving a genetic paradox: from an essential gene to a killer

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Selfish genetic elements are a ubiquitous feature of genomes. They can act both as sources of evolutionary innovation and as genetic parasites that disrupt inheritance patterns. One group of selfish genes, toxin–antidote (TA) elements, is widespread in free-living *Caenorhabditis* nematodes, where they cause extensive genetic incompatibilities, influence population dynamics, and may even drive speciation. Yet how TAs function and originate within genomes remains unknown.

To address these questions we studied the emerging model *C. tropicalis*. Using a combination of biochemistry, genetics, and evolutionary genomics, we discovered and molecularly dissected three novel TAs. Remarkably, all three evolved through recurrent gene duplication of a two-gene module: i) an essential and highly conserved enzyme, the phenylalanyl tRNA synthetase, which gave birth to toxins, and ii) a fast-evolving F-box protein that became the antidotes.

We found that the transition from essential gene to selfish toxin was enabled by an ancestral F-box protein that fortuitously recognized the tRNA synthetase and acted as a buffering agent. This pre-existing degradation interaction allowed deleterious mutations to accumulate neutrally in the toxin ancestor without immediate lethality. Subsequent duplication of this degrader–target module facilitated the repeated emergence and spread of TA elements.

Based on these findings, we propose a general evolutionary model in which regulatory modules composed of protein degraders and their targets provide fertile ground for the *de novo* evolution of selfish genetic elements. The recurrent evolution of TA systems in nematodes may thus be an inevitable consequence of the massive expansion and diversification of F-box proteins, which – much like the immune system – recognize rapidly evolving substrates and may both enable and constrain genomic conflict.

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