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Vienna Doctoral School of  
Ecology and Evolution

# Ecology & Evolution VDSEE Symposium 2025

21 February 2025

University of Vienna, Biology Building, Hörsaal 1



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# Welcome to the VDSEE Symposium 2025

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We are delighted to welcome all participants and speakers to the 2nd Vienna Doctoral School of Ecology and Evolution (VDSEE) Symposium. We hope that this day will be an exciting journey through ecological and evolutionary research.

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 happy to welcome our keynote speakers, Annika Guse (LMU Munich) and Hassan Salem (MPI Tübingen), and our Scientific Advisory Board member Nicolas Gompel (University of Bonn). Thank you for joining us and contributing to our Symposium.

We would like to thank the organizing committee—Marilena Heitger, Paul Knabl, Emily Pigott and Silvia Bulgheresi 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, Shimadzu, Starlab, LabConsulting, Szabo-Scandic, Avantor 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](mailto:docschool.vdsee@univie.ac.at).

## Useful information

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### 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 Symposium location 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 \(+43-1-4277-50028\)](tel:+431427750028) or contact the Portier right behind the main entrance.

# Programme

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## Welcome

08:30-09:00 Registration

09:00-09:10 Welcome address and remarks

## Keynote 1

Chair: Paul Knabl

09:10-10:00 Annika Guse

*10:00-10:10 Short break*

## Session 1

Chair: Marilena Heitger

10:10-10:30

**Julian Bibermaier** - Evolution and morphology of phylactolaemate bryozoans

10:30-10:50

**Sanjay Narayanaswamy** - Self-organization of an Organizer in cnidarian gastruloids

*10:50-11:05 COFFEE BREAK*

## Session 2

Chair: Steffen Waldherr

11:05-11:25

**Elisa Montrucchio** - Cellular Redox Status and Carbohydrate Metabolism in the Old Oilseed Crop *Camelina* under Drought and Waterlogging Stress

11:25-11:45

**Hayk Palabikyan** - CO<sub>2</sub> recycling into bioplastics by *Archaea*

11:45-12:05

**Daniel Saavedra** - Multifunctionally diverse alkaline phosphatases of *Alteromonas* drive the phosphorus cycle in the ocean

12:05-12:25

**Dmytro Spriahailo** - Comparative genomic analysis of antibiotic resistance genes in marine bacteria from anthropogenically influenced and pristine northern waters

12:25 – 12:35

Poster pitches round 1 (odd numbers)

*12:35 – 13:45*

*LUNCH BREAK and Poster session group 1 (odd numbers)*

## Keynote 2

Chair: Emily Pigott

13:45-14:35 Hassan Salem

*14:35-14:45 Short break*

## Session 3

Chair: Silvia Bulgheresi

14:45-15:05

**Emily Pigott** - Palaeoproteomic analyses of bone fragments from Palaeolithic Crimea reveals three new hominins

15:05-15:25

**Konstantina Cheshmedzhieva** - First genetic insights into ancient population history in the Highlands of Papua New Guinea

15:25-15:45

**Michelle Hämmerle** - The Last Journey: Genomic Insights Into Three 500-Year-Old Inca Mummies

15:45-16:05

**Arne Bielke** - Untamed Genomes: Genetic Insights into the Kaimanawa Feral Horse Population

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

**Pablo Aycart Lazo** - Landscape effects on bat conservation in Amazonian agricultural areas under land-use change

17:20-17:40

**Ekin Kaplan** - Assessing the trajectories of local plant community change: a literature review

17:40-18:00

**Krystof Chytry** - Will alpine plants make it into the next century?

*18:00-18:10 Short break and grab a beer*

18:10-18:20

Poster and talk awards, closing remarks

*18:30 – 21:30 Dinner and party*

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# Keynote Lecture 1

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## Annika Guse

(Ludwig-Maximilian University Munich, Germany)

### **Adaptation to the environment through symbiosis - a model system's approach**

Symbiotic interactions between organisms occur in all domains of life. A prime example is the symbiosis between corals and eukaryotic, photosynthetic dinoflagellates. However, key aspects about coral symbiosis establishment, maintenance, its evolution and ecosystem functions are still largely unknown. Here, I will present our advances in developing *Aiptasia*, a marine sea anemone, as a tractable model to dissect fundamental aspects of symbiosis establishment at the mechanistic level. I will give an overview over our current understanding of the mechanisms underlying symbiont uptake via phagocytosis, how the symbionts escape the hosts' defensive strategies to persist intracellularly, and how symbionts integrate into host cell metabolism and our future directions. Our symbiosis research provides fundamental insight into how two very distinct cells coordinate their cellular functions to adapt to nutrient-poor environments and drive the productivity and biodiversity of the ecosystem.

To uncover the molecular mechanisms of coral symbiosis, Annika Guse uses the sea anemone *Aiptasia* as a model and combines cell biology, biochemistry and -omics with organismal biology and coral-reef fieldwork. Annika has an unconventional track record: before starting her symbiosis research program, she received her PhD for work on cell division in *C. elegans* and mammalian cells with Michael Glotzer at the IMP in Vienna and she did a Postdoc at Stanford University with Aaron Straight using *Xenopus* egg extracts to dissect the function of centromeric chromatin. During her academic education, Annika has also carried out environmental work in Ecuador, Mexico and Egypt and continues to regularly lead coral reef fieldwork in Okinawa Japan for comparative experiments and thus integrating her laboratory finding into the broader ecological and evolutionary context. To support her novel approach to symbiosis, Annika was awarded an Emmy Noether Grant, an ERC Consolidator grant, and selected into the EMBO Young Investigator Network. Recently, she has been appointed Chair for the department of Quantitative Organismic Networks at the LMU in Munich. Annika is dedicated to inter- and transdisciplinary approaches in research, teaching and outreach. She co-founded the arts & science initiative *!vamos, symbiosis!* and the Center for Life Science and Society within the Faculty of Biology at the LMU.

# Keynote Lecture 2

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## Hassan Salem

(MPI for Biology, Tübingen, Germany)

### **Adaptation through symbiosis**

Symbiosis binds organisms from all domains of life. These interactions evolved frequently in animals and exhibit remarkable functional diversity. Where numerous animal traits are encoded by beneficial microbes, as a research group, we study the role of symbiosis in facilitating adaptation. By dissecting how partnerships are regulated and propagated across generations, we also describe the mechanisms ensuring specificity between microbe and host. Using leaf beetles as an experimental study system, I will outline (i) the molecular, developmental, and behavioural features ensuring symbiont maintenance and transmission, (ii) the beneficial roles microbes fulfil towards host nutrition and defence, (iii) the context dependency governing these interactions, and, finally, (iv) the adaptations that must arise to offset symbiont loss following 60 million years of co-dependence. Throughout this talk, I will highlight how timing the acquisition of a beneficial symbiont relative to the evolutionary history of its host can shed light on the adaptive impact of a partnership. This theme is further contextualized relative to our work on mutualism breakdown and the metabolic consequences of going it alone.

Hassan Salem carried out his undergraduate studies in Biology at Earlham College, Indiana, USA, followed by a Ph.D. at the Max Planck Institute (MPI) for Chemical Ecology in Jena, Germany. With support from the Alexander von Humboldt Foundation and Smithsonian Institution, he conducted his postdoctoral training at Emory University in Georgia, USA, with Nicole Gerardo, followed by a research stay at the Institute for Advanced Study in Berlin. Since 2020, he has led the Max Planck Research Group on Mutualisms at the MPI for Biology in Tübingen, Germany. He was selected as an EMBO Young Investigator in 2023.

## Julian Bibermaier

### Evolution and morphology of phylactolaemate bryozoans

Julian Bibermaier<sup>1</sup>, Ahmed Saadi<sup>1</sup>, Thomas Schwaha<sup>1</sup>

<sup>1</sup>Department of Evolutionary Biology, University of Vienna

#### Abstract

Bryozoans are a phylum of colonial, suspension feeding lophotrochozoans that occur in marine and fresh-water habitats. Colonies are formed by individual zooids which include a protective body wall (cystid) that houses the retractile polypide with a ciliated tentacle crown (lophophore) and most of the organs. Phylactolaemata are considered the earliest branching bryozoans and constitute the sister group to all other bryozoans, hence they are crucial for ancestral state reconstruction. Phylactolaemates are exclusively limnetic, have non-calcified cystids and comprise only about 100 species in 6-7 families. The morphology of those 'fresh-water bryozoans' has been of interest from early days of bryozoan research onwards, but focused on a few species, mostly of the family Plumatellidae and involved phylogenetic considerations far different from today. Recently, a transcriptome-based phylogeny of phylactolaemates was erected, that provides a molecular backbone for further analysis. This study aims to fill gaps in our knowledge of phylactolaemate morphology by using confocal microscopy, histology and section-based 3D-reconstruction. So far, the project could provide first modern data on the neuro/myoanatomy of lophopodids, one of the earliest branching phylactolaemates of which data were scarce. Also, the re-investigation of the species Plumatella frusticosa, whose phylogenetic position has always been ambiguously discussed, lead to the erection of a new phylactolaemate family. Eventually, all generated data will provide a useful character matrix that will assist in the reconstruction of the ancestral state of phylactolaemate bryozoans.

## Sanjay Narayanaswamy

### Self-organization of an Organizer in cnidarian gastruloids

Sanjay Narayanaswamy<sup>1</sup>, Franziska Haas<sup>1</sup>, Emmanuel Haillot<sup>1</sup>, Elly Tanaka<sup>2</sup>, Ulrich Technau<sup>1</sup>

<sup>1</sup>University of Vienna, Department of Neuroscience and Developmental Biology, Vienna, Austria;

<sup>2</sup>Institute of Molecular Biotechnology of the Austrian Academy of Sciences (IMBA), Vienna BioCenter, Dr. Bohr-Gasse 3, 1030 Vienna, Austria

Nematostella embryos show an early axis and germ layer specification, which leads to invagination of the SnailA+ inner layer (here called mesoderm) and formation of the FoxA+ pharynx (endoderm) by the former blastopore lip. However, axis and germ layer formation can also occur through alternative developmental trajectories, such as by self-organization in aggregates of embryonic cells. Using a standardized system of self-organizing Nematostella gastruloids that reproducibly form a single body axis, we sought to understand the morphogenetic properties of the germ layers and to elucidate the underlying molecular mechanisms. We show that dissociated single SnailA+ mesodermal cells individually translocate first to the periphery of the gastruloids. Then, these mesodermal cells group in larger clusters, which eventually ingress collectively in a specific time window. Interestingly, through a Notch signaling-dependent loss of germ layer identity segregation, FoxA+ endodermal cells acquire an endomesodermal fate, gathering around the mesodermal clusters to later form a primary pole, giving rise to the future pharynx of the developing polyp. Our results highlight distinct morphogenetic behaviors of mesodermal and endodermal cells and the hitherto unknown role of Notch signaling in germ layer boundary formation in self-organizing gastruloids.

## Elisa Montrucchio

### Cellular Redox Status and Carbohydrate Metabolism in the Old Oilseed Crop *Camelina* under Drought and Waterlogging Stress

Elisa Montrucchio<sup>1,2</sup>, Claudia Jonak<sup>2</sup>

<sup>1</sup>Vienna Doctoral School of Ecology and Evolution Department, University of Vienna;

<sup>2</sup>Center of Health and Bioresources, AIT Austrian Institute of Technology

Extreme weather events such as prologued droughts or heavy precipitations are becoming more frequent due to climate change, threatening the global food security. Therefore, there is a pressing need to develop robust crops and sustainable farming methods. *Camelina sativa*, a Brassicaceae oilseed crop with high-quality seeds, is valued for its adaptability to a variety of climatic conditions and represents a viable option for sustainable oilseed production in the face of climate change [1]. *Camelina* is a versatile, but underutilized crop with different cultivars and landraces originating from diverse climatic and geographical zones, differing in their breeding history and degree of stress tolerance.

This study investigates cellular redox status and carbohydrate metabolism in *Camelina* plants grown under drought and waterlogging conditions. These metabolic pathways are crucial for plant survival under stress and for efficient energy reallocation. Previous research in our group has demonstrated that profiling carbohydrate enzyme activities in response to salt stress allows the identification of specific activity signatures associated with differences in yield stability [2]. This study investigates the dynamic changes in cellular redox status and activity pattern of key carbohydrate enzymes in response to limiting and excess water. The knowledge gained can contribute to developing improved *Camelina* varieties with enhanced climate change resilience and provide valuable insights into plant stress response mechanisms that could be applied to other crops.

[1] Zanetti, F., Alberghini, B., Marjanović Jeromela, A., Grahovac, N., Rajković, D., Kiprovski, B., & Monti, A. (2021). *Camelina*, an ancient oilseed crop actively contributing to the rural renaissance in Europe. A review. *Agronomy for Sustainable Development*, 41(1), 2. <https://doi.org/10.1007/s13593-020-00663-y>.

[2] Stasnik, P., Vollmann, J., Großkinsky, D., & Jonak, C. (2024). Leaf carbohydrate metabolic enzyme activities are associated with salt tolerance and yield stability in the climate-resilient crop *Camelina sativa*. *Plant Stress*, 14, 100629. <https://doi.org/10.1016/j.stress.2024.100629>.

## Hayk Palabikyan

### CO<sub>2</sub> recycling into bioplastics by Archaea

Hayk Palabikyan and Simon K.-M. R. Rittmann

Archaea Physiology & Biotechnology Group, Department of Functional and Evolutionary Ecology, University of Vienna

The sustainable developmental goals of the United Nations aim at addressing some of the greatest threats to humanity, such as the contamination of the global ecosystem with carbon dioxide (CO<sub>2</sub>) and hazardous petrochemical plastics. Among other industries, the global biotechnology sector is delivering essential nutrition, medical products and materials, the production of which is however associated with destructive practices, high energy consumption and immense carbon footprints. The negative impact of large-scale bioprocesses is linked to the metabolisms of the dominant heterotrophic bacterial and eucaryotic cell factories, utilized for the biosynthesis of essential products. In contrast, undiscovered metabolic potential of archaeal organisms can deliver an urgently needed transformation towards sustainable biotechnological advances. The core of this project is dedicated to CO<sub>2</sub> recycling into bioplastic polymers – polyhydroxyalkanoates (PHAs). A novel pathway for biosynthesis of PHA of the ammonia oxidizing archaeon *Nitrososphaera viennensis* is being characterized by its heterologous reconstruction in the hydrogenotrophic methanogenic archaeon *Methanococcus maripaludis*. The synthetic biology approach improves gene expression by testing distinct promoters and ribosomal binding sites, whereas bioprocess engineering concentrates on scaling up of cultivation and optimization of media composition for balanced carbon and electron fluxes. A comprehensive methodological toolbox is being developed for microscopy screenings and analytical quantitative and qualitative measurements of archaeal PHAs.



## Daniel Saavedra

### Multifunctionally diverse alkaline phosphatases of *Alteromonas* drive the phosphorus cycle in the ocean

Daniel E. M. Saavedra<sup>1</sup>, José M. González<sup>2</sup>, Katharina Klaushofer<sup>1</sup>, Leila Afjehi-Sadat<sup>3</sup>, Wayne M. Patrick<sup>4</sup>, Federico Baltar<sup>5,1</sup>

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<sup>2</sup> Department of Microbiology, University of La Laguna, La Laguna, Spain

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Phosphorus is a critically limiting nutrient in marine ecosystems, with alkaline phosphatases (APases) playing a crucial role in liberating phosphate from organic compounds. Despite the fundamental role of APases in the phosphorus cycle, several critical questions about marine APases remain unresolved, limiting a comprehensive understanding of their contribution to oceanic phosphorus cycling. These questions include: Which APase family is predominantly utilized by marine microbes? Which microbial taxa are the primary contributors to APase activity in the ocean? And do all APase families contribute equally to the cell-free (dissolved) enzymatic pool? While APases have

traditionally been considered isoenzymes with specific roles, our recent research has revealed the multifunctionality of PhoA, a specific APase family. However, whether this multifunctionality is exclusive to PhoA or prevalent across all marine APase families remains unknown. To address these critical gaps, here we combined the production of recombinant proteins, enzymatic kinetic assays, proteomics of a key marine bacterium, and bioinformatic quantification of global ocean metaproteomic and gene expression of the main APase families (PhoA, PhoD, PhoX, PafA). Our metagenomic and metaproteomic analyses identified PhoA as the dominant APase in the ocean, with *Alteromonas* emerging as a key player in the expression and production, particularly in the mesopelagic layer. Through metaproteomics, we found that two APase families, PhoA and PhoX, are preferentially secreted as dissolved exoenzymes, thereby expanding the relevance of these proteins in the 'APase paradox'. Enzymatic assays with purified recombinant APases from *Alteromonas mediterranea* revealed multifunctional activities across all APases families, with substrate affinities indicating distinct ecological roles. Proteomic analysis under phosphorus limitation revealed specific regulation mechanisms for APases in *Alteromonas mediterranea*. Collectively, our findings not only identify the dominant APases and their associated microbial taxa but also underscore the ecological significance of multifunctional APases in the global ocean.

## Dmytro Spriahailo

### Comparative genomic analysis of antibiotic resistance genes in marine bacteria from anthropogenically influenced and pristine northern waters

Dmytro Spriahailo<sup>1</sup>, A. Adenaya<sup>2</sup>, T. Reinthaler<sup>1</sup>, T. Brinkhoff<sup>2</sup>

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<sup>2</sup> Institute for Chemistry and Biology of the Marine Environment (ICBM), Carl von Ossietzky University of Oldenburg, Germany

The rising occurrence of microbial antibiotic resistance genes (ARGs) in the natural environments poses a significant threat to ecosystem health and human welfare. Anthropogenic activities, particularly related to farming and wastewater treatment plants have boosted the spread of ARGs in the coastal waters, yet their prevalence and distribution within marine microorganisms remain underexplored. This study investigates the occurrence of ARGs in marine bacteria from anthropogenically influenced surface waters of the North and Baltic seas and the pristine waters of West Greenland.

Samples were collected with a sea-surface microlayer sampling catamaran and with conventional Niskin bottles attached to a CTD rosette. The extracted DNA was sequenced using Illumina NGS to obtain a set of metagenomically assembled genomes that were clustered into 580 genomic operational taxonomic units (gOTUs). The identified ARGs were analyzed using both established alignment search tools as well as novel deep learning-based algorithms.

Results revealed that over 85% of the analyzed gOTUs contain at least one multidrug resistance gene. Resistances to vancomycin, phenicol, and beta-lactam were widespread, even in the samples from West Greenland. Some specific ARGs like *tolC*, associated with multidrug efflux pumps, and *bcr* which encodes bicyclomycin resistance, were found across all sampling sites. Only a small number of identified gOTUs contained virulence factors. This suggests that ARGs in marine bacteria generally do not pose a direct threat to human health, however, they may serve as an expanding reservoir of ARGs with unknown repercussions on the human society.



## Emily Pigott

### Palaeoproteomic analyses of bone fragments from Palaeolithic Crimea reveals three new hominins

Emily Pigott<sup>1,2</sup>, Konstantina Cheshmedzhieva<sup>1,2</sup>, Laura van der Sluis<sup>1,2</sup>, Manasij Pal Chowdhury<sup>1,2</sup>, Maddalena Gianni<sup>1,2</sup>, Emese Végh<sup>1,2</sup>, Thorsten Uthmeier<sup>3</sup>, Victor Chabai<sup>4</sup>, Marylène Patou-Mathis<sup>5</sup>, Gerhard W. Weber<sup>1,2</sup>, Ron Pinhasi<sup>1,2</sup>, Martin Kuhlwilms<sup>1,2</sup>, Katerina Douka<sup>1,2</sup>, Thomas Higham<sup>1,2</sup>

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<sup>3</sup> Institut für Ur- und Frühgeschichte, FAU Erlangen-Nürnberg, Kochstr. 4/18, D-91054 Erlangen, Germany.

<sup>4</sup> Institute of Archaeology, National Ukrainian Academy of Science, Volodymyr Ivasiuk av. 12, 04210 Kyiv, Ukraine.

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#### Abstract

The Crimean Peninsula contains several important Palaeolithic sites, including Kabazi II, Kabazi V, Siuren I, Starosel'e, and Chokurcha I. This region has been considered a potential Neanderthal refugium prior to their replacement by *Homo sapiens*. This hypothesis is primarily drawn from lithic technological analysis and radiocarbon dating. At all sites have a considerable number of fragmented, unidentifiable bones (<2-3 cm in size), which were assumed to belong to animals.

In this study, we use collagen peptide

fingerprinting, Zooarchaeology by Mass Spectrometry (ZooMS) to identify morphologically unidentifiable bones to genus/species level, and screen for potential presence of human remains, which are extremely rare in the Palaeolithic.

We analysed 628 bone fragments using ZooMS and found that 82.3% had sufficient collagen preservation for taxonomic identification. Our results suggest that Palaeolithic humans were mostly hunting horses (*Equidae*) at the sites of Kabazi II, Kabazi V and Starosel'e. Other sites yielded evidence for deer, mammoth, and a range of other large ungulates, revealing information on aspects of the palaeoenvironment, climate, and subsistence patterns.

Importantly, three bone fragments yielded collagen fingerprints matching Hominidae; two from Starosel'e, and one from Siuren. We have radiocarbon dated the two hominin bones from Starosel'e, revealing them to be 44–46,000 and 42–44,000 years old. This is close to the transition period between the disappearance of Neanderthals and early dispersal of *Homo sapiens*. We obtained ancient DNA from the younger hominin bone, with very low endogenous content (<0.1%). We are currently in the preliminary stages of analysing the capture data from the mitochondrial genome.

The results show that ZooMS is a powerful tool for identifying previously unidentified faunal remains, which can help reconstruct the paleoenvironment, and potentially new hominin remains that can be directly radiocarbon dated, genetically sequenced and analysed for dietary isotopes.

## Konstantina Cheshmedzhieva

### First genetic insights into ancient population history in the Highlands of Papua New Guinea

Konstantina Cheshmedzhieva<sup>1</sup>, Annette Oertle<sup>1</sup>, Atsushi Uemine<sup>2</sup>, Glenn Summerhayes<sup>3</sup>, Martin Kuhlwilms<sup>1</sup> & Katerina Douka<sup>1</sup>

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<sup>3</sup> Archaeology Matai Whaipara Takata, School of Social Sciences Te Puna Papori, University of Otago, PO Box 56, Dunedin, 9054, New Zealand

Despite the immense progress in tracking the human evolutionary journey across the globe through the study of ancient genetic data, recovery and analyses of ancient DNA from the tropics remains an extremely challenging task.

Here, we present the first ancient DNA data from human bones from Papua New Guinea, identified initially using palaeoproteomics (ZooMS) and directly dated by <sup>14</sup>C radiocarbon analysis. The human remains were discovered in three archeological sites in the Eastern Highlands of Papua New Guinea (Kiowa, Yuku and Tsak Pumakos B) and date to between 8,000 and 1,000 years ago. Typical damage patterns and fragment length distributions characterise the DNA data as ancient, and its genetic affinity is compared to present-day Papuan individuals from the Simons Genome Diversity Project.

By comparing changes in allele frequencies over time and in comparison to present-day populations, we aim at improving our understanding of the population history in this understudied part of the world, and elucidate the impact of known (and potentially unknown) events that shaped the genetic landscape of local populations, including the significant impact of the Lapita cultural expansion about 3300 years ago.

## Michelle Hämmerle

### The Last Journey: Genomic Insights into Three 500-Year-Old Inca Mummies

Michelle Hämmerle<sup>1,2</sup>, Meriam Guellil<sup>1,2</sup>, Dagmara Socha<sup>3</sup>, Olivia Cheronet<sup>1,2</sup>, Alejandro Llanos-Lizcano<sup>1</sup>, Susanna Sawyer<sup>1,2</sup>, Mario Bernaski<sup>4</sup>, Gabriela Recagno<sup>4</sup>, Johan Reinhard<sup>5</sup>, Martin Kuhlwilm<sup>1,2</sup>, Pere Gelabert<sup>1,2</sup>, Ron Pinhasi<sup>1,2</sup>

<sup>1</sup> University of Vienna

<sup>2</sup> Human Evolution and Archaeological Sciences (HEAS)

<sup>3</sup> Center for Andean Studies, University of Warsaw

<sup>4</sup> Museo de Arqueología de Alta Montaña (MAAM)

<sup>5</sup> National Geographic Society

Most paleogenomics research relies on osteological material, limiting the study of pathogens and microbiomes in ancient societies. Recent methodological advancements have addressed this limitation by sequencing coprolites and other sources of endogenous microbial communities. However, such sources are still scarce, preventing direct comparisons with the host genome and the host's living conditions. An exceptional case for studying both are the “Children of Llullaillaco”. These three 500-year-old Inca mummies were discovered in 1999 on the Llullaillaco volcano in Argentina, and are among the best-preserved mummies ever found. Their exceptional preservation can be attributed to a combination of freezing temperatures, mild humidity, and an anaerobic environment. The Inca sacrificed them as part of the “*Capacocha*” ritual, likely to enforce social control and gain socioeconomic benefits. In collaboration with the Museo de Arqueología de Alta Montaña in Salta, Argentina, and under strict supervision from the curators, we performed non-invasive sampling on the mummies, which was done by swabbing relevant body parts with cotton swabs. Through extensive sequencing of 27 samples of skin, anal, and buccal tissue, we have recovered 5.1-fold, 14.3-fold, and 25.3-fold nuclear genomes from each of the children, respectively. We have used these to infer their affinities to native American populations and narrowed their geographical origin to the southern part of Lake Titicaca on the border of Bolivia and Chile. Our non-invasive sampling approach has also enabled us to detect commensal and pathogenic microbial species. We have recovered *Bartonella quintana* reads from two individuals, yielding one high-coverage genome from one of the children, which, to the best of our knowledge, is the first ancient genome of this bacterium, and we could identify the presence of *Human gammaherpesvirus 4* (HHV4) sequences. The metagenomic composition from one of the anal samples is most similar to rural gut microbiomes from present-day individuals. We performed de novo assembly to further enhance our knowledge of ancient gut microbial diversity, obtaining 227 metagenomic assembled genomes (MAGs).

## Arne Bielke

### Untamed Genomes: Genetic Insights into the Kaimanawa Feral Horse Population

Arne Bielke<sup>1</sup>, Siavash Salek Ardestani<sup>2</sup>, Elmira Mohandesan<sup>1,2</sup>

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Domesticated horses (*Equus ferus caballus*) have influenced human history through their roles in mobility, agriculture, and warfare. Due to intensive breeding and closed studbooks modern domestic horse genomes exhibit increased inbreeding and a 16% decline in genetic diversity, over the past two centuries. With no wild ancestors remaining [1], feral populations, like New Zealand's Kaimanawa horses, offer vital genomic resources for future breeding programs. Introduced by European settlers in 1815 [2], the Kaimanawa Horse population is now the fourth-largest feral horse population in the world. Despite historical declines due to unregulated hunting, farming, and forestry, protective legislation now maintains the population at ~300 individuals annually.

The well-documented demographic history of the Kaimanawa population makes it a valuable natural laboratory to investigate the effects of founder events and conservation strategies on genetic diversity and inbreeding. Preliminary data revealed that 53% of individuals within the sampled population have second-degree or closer relatives ( $\pi\text{-hat} \geq 0.25$ ). Using 80K GGP Equine SNP arrays, we generated

the first comprehensive genomic dataset containing 144 feral Kaimanawa Horses. Our analyses revealed high levels of inbreeding ( $F_{is} = 0.065$ ) and genetic divergence from other domestic breeds, with the former result confirming earlier findings. Admixture analyses corroborated the high divergence, confirmed genetic contributions from Thoroughbred, Arabian, and British pony breeds, and identified at least two subpopulations within the Kaimanawa population. Furthermore, genome-wide nucleotide diversity analyses pinpointed specific genomic regions that may be under selection, offering deeper insights into evolutionary forces that may shape this feral population. These findings highlight the complex interplay of demographic forces and provide a valuable genomic perspective on feral Kaimanawa Horses.

This study establishes a scientific foundation for future conservation management, aiming to preserve the genomic resources represented by this feral horse population while contributing to the broader understanding of feral horse populations worldwide.

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## Pablo Aycart-Lazo

### Landscape effects on bat conservation in Amazonian agricultural areas under land-use change

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Bats play an essential role in tropical agricultural areas due to the ecosystem services they provide, such as phytophagous arthropod suppression [1]. Understanding how bat assemblages respond to landscape characteristics is essential for designing multifunctional landscapes supporting high levels of biodiversity and enhancing ecosystem services provision. We sampled phyllostomids and aerial insectivorous bats (AIB) in cacao agroforests to analyze how the taxonomic, functional and phylogenetic dimensions of the bat community responded

to landscape composition and configuration in two contrasting agricultural regions in the Peruvian Amazon. In addition, we estimated how bat diversity might vary under different future landscape composition scenarios. Phyllostomid abundance increased towards fragmented landscapes due to higher abundances of generalist species. Landscape tree cover and edge density filtered bat species based on their functional traits differently in the intensive and non-intensive agricultural regions. Moreover, edge density and landscape tree cover had positive effects on the phylogenetic diversity of AIBs in the intensive and non-intensive region, respectively. Model projections to possible future landscape composition scenarios indicate that bat diversity in tropical agricultural areas can be enhanced by increasing landscape tree cover and reducing fragmentation. However, our results indicate that landscape effects on bats can vary depending on the regional characteristics of the agricultural area, highlighting the importance of adjusting landscape design to the regional context to ensure the conservation of bat ecosystem services and genetic diversity.

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## Ekin Kaplan

### Assessing the trajectories of local plant community change: a literature review

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#### Aim

Understanding local scale biodiversity change is essential to identifying drivers of change across regions and habitats worldwide and draw generalizations. Here, we conducted a comprehensive literature review of studies on local-scale plant community change using re-surveyed plots. We focus on changes in species richness and diversity to disentangle regional and habitat-specific variations in these changes and identify the primary drivers associated with them.

#### Location

Global

#### Time Period

1827-2022

#### Taxon

Plants

#### Methods

A systematic literature review was conducted to identify literature on plant community

change. Relevant studies were extracted from Web of Science and Scopus. We applied three inclusion criteria for studies: (i) plots of plant communities, (ii) a minimum of two temporally separate assessments of plant communities, and (iii) inclusion of diversity analyses. Studies meeting all criteria were reviewed. Review papers and meta-analyses were excluded.

#### Results

Of 4,983 potentially relevant papers, 865 met the inclusion criteria. Overall, 594 studies were based on permanent plots; most studies were from Europe (469) and North America (206); 39.4 % of studies focused on forests, 27.2 % on grasslands, and the remaining on diverse habitats. For drivers, ongoing land-use was the most prevalent (283), followed by climate change (193), with some studies considering multiple drivers. Increases in species richness (52% of studies) and composition (50%) were predominantly reported, but with substantial variation across habitats and drivers of change.

#### Conclusions

Our review reveals substantial context-specific variation in local plant species richness and composition changes over time. These findings highlight the importance of considering regional and habitat-specific context, as well as disentangling the different drivers studied. Caution is needed when inferring trajectories of global local-scale plant diversity changes. Our results emphasize the need for continued research to address gaps, particularly in underrepresented regions, to better understand global plant biodiversity dynamics and inform conservation efforts.

## Kryštof Chytrý

### Will alpine plants make it into the next century?

*Biodiversity Dynamics and Conservation, University of Vienna.*

In mountains, elevation-dependent temperature controls where plant species can grow. However, the climate is recently changing and so are the elevational limits of alpine plants. To track their niches they, metaphorically, need to climb mountain slopes to still higher elevations, ultimately facing risk of a mountain-top-extinction, likely to be soon very common. Such catastrophic scenarios have recently been challenged as they overlook the role of microclimate heterogeneity, which is so typical for high mountains. The alternative scenario suggests that microclimate can compromise for the upward shifts as species will be able to survive in microrefugia, irrespective of their elevational preferences. Although appealing, this assumption has yet not been tested. For a good reason as it would be extremely demanding to obtain data to test it. And that's exactly what we tried to do.

In 2021, we have established a fine-scale monitoring scheme on one mountain in the Austrian Alps, in order to model species distributions and how they are likely to change over the coming 80 years. We particularly focused on microclimate which we measured with 900 soil temperature loggers. During the work on my PhD I used this dataset to (1) build fine-scale temperature maps on 1 m<sup>2</sup> resolution, (2) based on hourly temperature measurements derived a huge array of descriptors to test which of them are important for alpine plants, (3) tested which factors control for distribution of microrefugia in current landscape and (4) asked if fine-scale topography is indeed as important for species distributions of alpine plants as assumed by many.

Most of the questions delivered results that surprised not only me but also many of my colleagues. Over time, these results started to make sense, even though not within the framework of the conventional narrative. And that makes them even more interesting.

## Poster Presentations

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## Poster 1

### SUMO chains as degradation signals: Determining the fate of a substrate tied-up with sumoylation and ubiquitination

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Covalent addition of the small ubiquitin-related modifier (SUMO) protein to substrates has profound implications for regulating plant stress responses. In some cases, SUMO proteins themselves can be modified by additional SUMO molecules, forming SUMO chains on substrates that are further modified by addition of a ubiquitin chain, leading to degradation by the proteasome. Tagging the substrate in this manner may serve, for instance, to disassemble protein complexes. We are focusing on such cases, where SUMO is incorporated into its substrates in the form of a chain, not as a single moiety.

We have previously characterized mutants in plant SUMO E4 ligases (PIAL1 and 2) that promote SUMO chain formation [1]. *pial1/2* mutants are viable, but display a number of deficiencies when confronted with stressful conditions. We are currently analysing mutants defective in subsequent ubiquitin attachment. In particular, we are generating mutants in the SUMO-targeted ubiquitin ligase family of Arabidopsis (STUbL1 to 6). SUMO-targeted ubiquitin ligases (STUbLs) bind to SUMO chains, followed by recruitment of a ubiquitin chain to initiate proteasome-mediated degradation. Some mutant combinations display physiological anomaly, suggesting important functions for this enzyme family which we also would like to reveal. All these mutants serve as tools to investigate the biological and physiological function of SUMO chains, and to interrogate for substrates of SUMO chain-dependent protein degradation pathway.

Using proteomics and other methods to identify proteins with increased abundance in pathway mutants, we identified potential substrates of the SUMO chain-dependent protein degradation pathway [2, 3]. In particular, we study 14-3-3 proteins (phosphorylation mark readers), to investigate their regulation by SUMO chains.

[1] Tomanov et al., Plant Cell 2014, 26, 4547-4560.

[2] Nukarinen et al., Plant J. 2017, 91, 505-517.

[3] Tomanov et al., Biochemical J. 2018, 475, 61-74.

## Poster 2

### Using Ancient Crop DNA to Investigate Socio-Political Change

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Here we present a research project to push the boundaries of ancient DNA methodology to reveal the temporal dimension of maize evolution and adaptation, using a novel application in socio-political change. The proposed project will use the fossil record to explore the agency of early subsistence farmers under the influence of an expansive state. There is a gap in knowledge regarding when and in what form maize arrived in South Peru. Direct radiocarbon dating of archeological maize specimens places its arrival in North Peru shortly after domestication in Mexico. The next confirmed date is from North Chile, near Moquegua, 4000 years later. To understand what early traits were selected, ancient DNA for maize fossils spanning 2000 years will be compared with a diverse, representative modern maize DNA panel. Specifically, this project asks how colonization of Moquegua Valley in south Peru by people of the Tiwanaku state changed the maize genomic landscape. Agency by colony inhabitants will be interrogated through trait selection before, during, and after Tiwanaku colonization.

## Poster 3

### *Salinibacter ruber* Proteomic Response to Broad Salinity Variations

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*Salinibacter ruber* is an extremely halophilic bacterium with a salt-in strategy that inhabits environments with salinities ranging from 15% to 35%, such as solar salterns, where it is a key member of its microbial community. To explore the proteomic responses that enable *Sal. ruber* to adapt to salinity shifts, strains M8 and M31<sup>T</sup> were grown in rich media at 25% salinity and incubated with media at 15 %, 20 %, 25 %, 30 % or 35 % for 4 days. Proteins were digested with trypsin, peptide masses calculated with a Q Exactive mass spectrometer (Thermo Scientific) and results analysed with MaxQuant and Perseus.

In M8, 1873 proteins were detected from a predicted proteome of 3247 proteins, with 951 showing statistically significant changes across salinities. In M31<sup>T</sup>, 1503 proteins were detected from 2812 predicted proteins, with 456 proteins exhibiting statistically significant changes. Proteins involved in cellular transport, protein synthesis, DNA repair, and transcription showed statistically significant changes among salinities, some being strain-specific. Also, significant changes were detected in certain glycosyltransferases, mostly in *Sal. ruber* M8, which increased

their abundance significantly at extreme salinities (15 % and 30 %), as previously reported in field dilution experiments performed on natural communities from salterns. Additionally, comparative analysis between 20 and 30 % salinity revealed that over 150 proteins were overexpressed in both strains at 20%, while M8 repressed twice as many proteins as M31<sup>T</sup> at 20 %. These findings correlate with the observed growth differences between strains, with M8 replicating faster than M31<sup>T</sup> at 15 % salinity.

In summary, our results evidence a complex proteomic response to salinity fluctuations in *Sal. ruber*. Ongoing growth experiments aim to elucidate the impact of proteomic shifts on cellular fitness, contributing to a deeper understanding of their adaptation mechanism.

## Poster 4

### Ninety years of alien plant species accumulation across regional and local scales in central European fields

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## Abstract

Alien species are increasingly prevalent worldwide, leading to economic and biodiversity losses. We examine how the spread of non-crop alien plant species (i.e., archaeophytes and neophytes) has evolved in arable fields across ten countries in central Europe from 1930 to 2019. Specifically, we analyzed how regional and local trajectories of alien plant species have changed over the last ninety years. We used a dataset of 21,747 vegetation plots from the AgriWeedClim database and applied generalized linear mixed-effect models. We analyzed the percentage of plots containing neophytes to characterize regional scale dynamics, as well as the proportional number and relative abundance of alien species per plot, offering insights into the local scale dynamics of alien species spread in arable fields. The dynamics of species populations in the study area revealed significant contrasts between neophytes and archaeophytes over time. The percentage of plots containing neophytes strongly increased from 34.2% in 1930 to 70.1% in 2019. The proportion of neophytes, in plots nearly doubled from 5.5% in 1930 to 10.2%

in 2019. The relative abundance, meaning their biomass relative to the total biomass of all species in the plot, of neophytes followed a similar upward trend, increasing from 4.1% to 9.9%. This highlights not only the spatial spread of neophytes in arable vegetation but also their increasing cover on the local scale. Archaeophyte species displayed a different trajectory. Their proportion exhibited only a modest increase from 23.2% to 25.3% over the ninety-year period, while their relative abundance slightly decreased from 21.2% to 19.5%. A sensitivity analysis of our data further revealed that the temporal increase in the percentage of plots containing neophytes is mainly driven by a few common species, such as *Veronica persica* and *Erigeron annuus*, which had a high number of records during the study period. We anticipate an increasing occurrence of neophytes in local communities in the future, which may contribute to the homogenization of regional arable plant communities.



## Poster 5

### Palaeoparasitological studies of vertebrate coprolites with emphasis on endoparasites of Archelosauria

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Parasites and their hosts have always been engaged in dynamic co-evolutionary patterns, characterized by continuous adaptation and counter-adaptation. While many endoparasites can be detected in the faeces of modern vertebrates, fossil coprolites have the potential to provide valuable insights into parasite-host interactions in deep time. Over the past decades, the field of palaeoparasitology has gained increasing importance, with the successful identification of helminth eggs in coprolites dating back to the Permian. These findings have opened new avenues for understanding host-parasite relationships and palaeoenvironments across vast geological timescales. However, as only isolated discoveries have been made across various vertebrate taxa, this research area holds immense potential for groundbreaking discoveries.

The presented project investigates the temporal and taxonomic distribution of fossil endoparasites in coprolites of Archelosauria, a vertebrate clade that has existed since the Triassic, dominated Mesozoic ecosystems, and still persists today. Using coproscopy methods, chemical decomposition, thin-section analysis, and advanced techniques such as SEM-EDX and micro-CT scans, helminth eggs will be identified and classified from coprolites. A particular focus will be placed on the comparative analysis of modern and fossil samples to draw conclusions about food webs, ecological niches, and evolutionary developments. The results aim to expand our understanding of the taxonomic and temporal distribution of palaeoendoparasites, while also refining and improving methodologies for examining fossil coprolites and their producers.

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## Poster 6

### Abstract:

### The role of Wnt/ $\beta$ -catenin pathway in patterning the inner layer of a sea anemone embryo

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Wnt/ $\beta$ -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/ $\beta$ -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  $\beta$ -catenin-negative domain prior to gastrulation. However, during larval stages several Wnt genes start to be expressed in the mesoderm. 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 will include pharmacological modulation of the cWnt pathway, transcription factor screening, and genetic knockouts using CRISPR-Cas9. This PhD project will contribute to our understanding of axial patterning across the animal kingdom.



## Poster 7

### Genome size and rDNA evolution of chili peppers (*Capsicum*, Solanaceae)

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Genus *Capsicum* belongs to the nightshade family and comprises about 40 exclusively diploid species. Several species are cultivated worldwide and their fruits are used as a vegetables and spices. Chromosome numbers, genome sizes and positions of 5S and 35S rDNA were established for 23 wild and cultivated *Capsicum* species. Two base chromosome numbers were observed:  $x = 12$  and 13 correlating with major phylogenetic clades. Genome size measurements showed nearly 5-fold genus-wide variation, of the 1C values ranging from 1.66 pg in *C. lanceolatum* to 7.79 pg in *C. flexuosum*. Mapping of housekeeping rRNA genes revealed different patterns of evolution of 5S and 35SrDNAs. Localization and number of 5S rDNA loci were highly conserved in all taxa but one, with only one interstitial locus on (sub)metacentric chromosome pair. Only in *C. tovarii* 5S rDNA probe mapped to large subtelomeric regions of all chromosomes, suggesting the presence of 5S rDNA-derived satellite DNA. In contrast both the number and localization of 35S rDNA loci were very variable, ranging from one in most of the basal species of Andean clade ( $x = 13$ ) to 16 in species of crown clades, including cultivated species. The number of major signals, largely representing active 35S rDNA loci ranged from 1 to 3. Numerous minor loci present in some species have likely represented 35SrDNA-derived novel satellite DNAs. Reconstruction of the evolution of genome sizes and rDNA loci clearly showed that the ancestral genome sizes of the genus were very small and species diversification was largely accompanied by genome size increases and a few secondary reductions. 35S rDNA loci number has also increased in the course of evolution from 1 in most basal lineages to 3 in the crown groups which also includes cultivated taxa. The data also provide valuable chromosomal markers for identification of otherwise rather uniform chromosomes.

## Poster 8

### BMP signaling is active in the non-centralized nervous system of Cnidaria

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BMP signaling is responsible for the second body axis patterning in Bilateria and in the bilaterally symmetric members of the bilaterian sister clade Cnidaria – corals and sea anemones. However, medusozoan cnidarians (jellyfish, hydroids) are radially symmetric, and yet their genomes contain BMP signaling components. This evolutionary conservation suggests that BMP signaling must have other functions not related to axial patterning, which keeps BMP signaling components in Cnidaria under selective pressure.

To find out what these functions might be, we generated a detailed whole-body atlas of BMP activity in the adult polyp of the sea anemone *Nematostella*. We uncovered an unexpected diversity of BMP signaling domains, which are prominent in the head region, as well as across the reproductive and the neuro-muscular parts of the gastrodermis. We combined pharmacological attenuation of BMP activity with tissue-specific RNA-Seq and found that BMP signaling mostly controls developmental regulators, including many neuronal genes. Using different transgenic reporter lines, we discovered BMP signaling partially overlaps with neuronal populations, including *soxB2(+)* progenitors and *elav(+)*/*nanos1(+)* descendants. Strikingly, another

neuronal population expressing *prdm14d* never displayed active BMP signaling, suggesting BMP signaling marks only specific neural subpopulations. In accordance, analysis of two medusozoan species, the true jellyfish *Aurelia* and the box jellyfish *Tripedalia*, revealed similarly broad and diverse BMP activity, also in parts of the nervous system.

Our findings provide new insights into pro-neural roles of BMP signaling in Anthozoa and Medusozoa that possibly represents an ancestral animal trait, predating the cnidarian-bilaterian divergence.

## Poster 9

### Fluorescent Proteins in Corals: Caring for Your Photosymbionts

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Corals thrive in nutrient-poor environments by relying on light. My PhD research explored their ability to manipulate light using fluorescent proteins (FPs). I studied three *Madracis* species—*M. pharensis*, *M. decactis*, and *M. senaria*—collected from Snake Bay, Curaçao, in September 2022. Samples were taken from shallow (~5 m) and deep (~20

m) depths and from colony orientations receiving direct (top) or indirect (side) light. FP distribution differed among species. Gastrodermal GFPs were mostly diffuse, while granular GFPs were mainly epidermal. *M. pharensis* and *M. decactis* exhibited predominantly diffuse GFPs in both layers, whereas *M. senaria* had more epidermal granules and diffuse gastrodermal GFPs. Granules were more frequent in shallow samples (50% of images) than in deep samples (20%). A key finding was the GFP-symbiont colocalization difference in *M. senaria*. Deep samples with less light had a higher colocalization index, suggesting reduced light enhances GFP-symbiont colocalization. The study uncovered distinct FP strategies among *Madracis* species. *M. pharensis* and *M. decactis*, closely related species, responded more linearly to light, emphasizing an acclimatization-based approach. In contrast, *M. senaria* demonstrated a more nurturing strategy, influenced not only by light but also by FP colocalization with the symbiont layer. These findings reveal how corals optimize light use, highlighting their evolutionary strategies for survival in diverse environments.

## Poster 10

### Habitat complexity, sexual behaviour and brain properties in wild brown trout (*Salmo trutta*)

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Fish brain exhibit high plasticity in response to environmental pressures. The relative sizes of brain regions, rather than overall brain size, can change in response to selection pressure on specific cognitive skills, such as those related to sexual behaviour or habitat complexity (i.e., mosaic theory of brain evolution)<sup>[1]</sup>. Brain size and the sizes of its regions is widely used as proxies for cognitive skills, but the accuracy of this metric is highly debated, as animal cognition also depends on other structural properties of the brain<sup>[2]</sup>.

The isotropic fractionator technique (IF) allows for precisely estimation of the number of neurons in the whole brain and its respective regions<sup>[3]</sup>. For example, in laboratory lines of guppies artificially selected for overall brain size, IF revealed a negative scaling relationship between neuron density and brain size<sup>[4]</sup>. However, this relationship has never been tested in non-model species from natural habitats, where neuronal proliferation is influenced by environmental context.

In this study, we used brown trout *Salmo trutta* as a study species and we tested the correlation between the size of brain and its regions and their neuronal numbers. We then compared these metrics them across individuals of different sexes, habitats, and populations of origin to understand the role of selection pressures in shaping

the brain properties in the wild. Trout were collected from two pairs of natural streams: granite and groundwater, the latter having higher habitat complexity due to limestone dissolution, creating niches, textures, and varied substrates<sup>[5]</sup>.

We expected a negative scaling between the mass of brain and its regions and their neuronal densities. Additionally, we expected that brain regions involved in sexual behaviour, such as telencephalon, will differ between males and females. Finally, we posited that trout from groundwater streams would have higher neuronal density in brain regions associated with navigation in complex habitats, such as cerebellum and telencephalon.

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## Poster 11

### Disentangling the genetic basis of brain circuit lateralization in *Drosophila*

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The human brain exhibits directed morphological lateralization, which is thought to be important for cognitive functions. Modern large-scale imaging and genome-wide association studies support a causal link by discovering overlapping genetic variants associated with altered brain asymmetry and complex traits such as schizophrenia or autism. Like many psychiatric disorders, human brain asymmetry is rarely affected by single gene functions and exhibits wide variation between individuals, suggesting a complex interplay between genetic programs and environmental signals.

The asymmetric body (AB) is a distinct lateralized circuit module within the highly bilaterally symmetric wiring architecture of the *Drosophila* central brain, critical for memory formation and decision making. To study how genetic-developmental programs control circuit lateralization, we performed a histological characterization of neural asymmetry in a collection of highly inbred and sequenced fly lines for a genome-wide association study (GWAS). Consistent with a trait controlled by multiple genetic components, each line has a defined level of brain circuit lateralization.

Accordingly, GWAS revealed 64 genetic variants associated with brain asymmetry

including, transcription factors, cell adhesion molecules and cytoskeleton binding proteins, similar to studies in humans. While a targeted knockdown of individual candidate genes revealed little effects, changes in the level of brain lateralization can be induced by combined gene reduction, as exemplified by the two cell adhesion molecules of Fasclin2 and Connectin. Interestingly, these effects are sensitive to the environmental temperature within a defined developmental window. These results demonstrate the usefulness of an integrated approach of quantitative and molecular genetics, to gain insights into the genetic architecture of neuronal asymmetry.

## Poster 12

### Diversity, Distribution and Genomic Adaptations of Arctic Ammonia Oxidizing Archaea

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The vast amount of organic matter stored in arctic soils is at risk of becoming available to the soil microorganisms' decomposing activity, due to the ongoing rise in temperatures associated to climate change. Nitrogen is a major limiting nutrient in arctic soils, as its availability is generally scarce<sup>1,2,3</sup>. Thus, the study of the N cycle becomes essential to understand the nutrient fluxes and to predict the shifts in the ecosystem dynamics in a permafrost climate change feedback scenario<sup>4,5,6</sup>. Ammonia oxidizing archaea (AOA) are known to perform the first step in nitrification and they were found to be the dominant group of nitrifying organisms in arctic soils<sup>8,9</sup>. Their activity is especially

relevant as it results in the emissions of the potent greenhouse gas N<sub>2</sub>O<sup>7</sup>. Earlier meta-studies have also revealed that AOA display distinct ecophysiological and patterns reflecting their phylogenetic relationships, enabling their classification in distinct clades with different functional properties<sup>10</sup>. Our earlier investigations in arctic regions have shown that few specific clades of AOA are active in arctic soils<sup>8,9</sup>. Here, we explore the diversity and distribution of the main AOA clades in five different locations spread along the whole circumpolar Arctic region, based on a 16S rRNA gene amplicon sequencing analysis. We have identified that a few distinct subclades from the NS-Gamma and NS-Zeta AOA clades comprise the AOA community across the circumpolar region. In order to understand the functional capabilities of the arctic AOA clades, we have previously enriched and present here the pure culture and closed genome of the first AOA cultivated representative from arctic soils, *Ca. Nitrosocosmicus arcticus*, belonging to the NS-Zeta clade. Comparative genomic analysis between *Ca. N. arcticus* and other genomes and metagenome assembled genomes from terrestrial and arctic AOA clades were performed, in order to identify possible psychrophilic and other functional adaptations of the two AOA arctic clades. In here, we present preliminary findings from this analysis.

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## Poster 13

### Expression of anterior-posterior patterning genes in the chaetognath *Spadella cephaloptera*

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The evolutionary origins and body plan diversification within bilaterians hinge on our understanding of conserved developmental gene networks across diverse taxa. While significant advances have been made in elucidating the anterior-posterior (AP) axis patterning in central nervous system (CNS) development across well-studied bilaterian lineages, our understanding of the conservation of AP-patterning gene expression in underexplored protostomes with a phylogenetically informative position remains limited. Chaetognaths (arrow worms), a group of marine invertebrates closely related to Gnathifera, likely occupy an early-diverging branch of the spiralian lineage. Their phylogenetic position offers potentially valuable evolutionary insights on whether the AP patterning of their CNS reflects conserved bilaterian mechanisms or reveals distinct lineage-specific adaptations. Here, we explore the expression domains of AP patterning genes in *Spadella cephaloptera* using fluorescence whole-mount in situ hybridization. In *Spadella* hatchlings, anterior-patterning genes (*Sce-otx*, *Sce-six3/6*, and *Sce-nk2.1*) are expressed anteriorly, including the cerebral ganglion, while the Hox genes, which include hitherto undescribed central (*Sce-Med6*) and posterior class (*Sce-postC* and *Sce-postD*) Hox genes, display the canonical staggered pattern along the ventral nerve

center (VNC). The posteriorly expressed Hox genes are also active in patterning the hindgut and post-anal tail. Overall, our results reveal that these genes exhibit spatially organized expression in the developing nervous system, resembling the conserved AP expression profile observed in other bilaterians, including annelids, molluscs, insects, and vertebrates. These findings challenge previous assumptions of significant divergence in chaetognath development, revealing that the core bilaterian AP patterning mechanisms may have been retained in this lineage despite its distinct evolutionary trajectory.

## Poster 14

### Cooption of fibroblast activation in the origin of endometrial decidualization, a process crucial for the evolution of mammalian pregnancy

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Implantation is a key innovation of placental mammalian pregnancy. It coincides with the origin of a novel maternal cell type, the decidual stromal fibroblast<sup>1,2,7</sup>. Under the influence of progesterone and prostaglandin E2 during pregnancy, these cells undergo a process known as decidualization<sup>3</sup>. Resulting decidual tissue is necessary for successful implantation and pregnancy<sup>5,6</sup>. The process of

decidualization is highly similar to fibroblast activation- a response of fibroblasts to tissue perturbations, such as injury<sup>4,9</sup>. Fibroblast activation entails transformation of the fibroblast to a myofibroblast, which leads to wound healing. Persistent fibroblast activation is a cause of excessive scarring (fibrosis)<sup>10</sup>. In contrast, decidualization initially follows fibroblast activation, however it does not result either in wound healing nor in scarring, but in a distinct cell type - the decidual stromal cell<sup>8,9</sup>. Our hypothesis is that decidualization coopted and modified fibroblast activation, by changing its later steps to accommodate implantation and embryo support. The aim of this project is to understand how this modification evolved. In this poster, I will present preliminary results of a literature review and meta-analysis on fibroblast activation. This analysis will help us establish the shared and divergent mechanisms between fibroblast activation in different tissue contexts and endometrial decidualization. Apart from the specific questions to do with describing modifications, this project addresses a fundamental evolutionary question: How do new cell types arise?

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## Poster 15

### Genome-scale metabolic model reconstruction of *Paraburkholderia dioscoreae* MSB3

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*Paraburkholderia dioscoreae* MSB3<sup>T</sup> is a novel species with potential agricultural impact, isolated from leaf acumens of the 'air potato yam' *Dioscorea bulbifera*. *P. dioscoreae*'s genome encodes a relevant combination of features mediating beneficial plant-associated lifestyle and it exhibits significant growth promotion when applied to agriculturally important plants such as tomato. Here we constructed iPR1691, the first genome-scale metabolic model for *P. dioscoreae* MSB3, which includes 1687 reactions, 1487 metabolites, and 1691 genes. From an available annotation of MSB3's genome, a draft model was constructed using an automated approach followed by automatic gap-filling on KBASE, and was manually curated using constraint-based modeling.

*P. dioscoreae* MSB3 can grow on 1-aminocyclopropane-1-carboxylic acid (ACC), and ethylene precursor on plants, as a carbon and nitrogen source. Based on the reactions and genes present in the model, and on various pathways available on MetaCyc, a pathway for ACC usage was constructed. Flux Balance Analysis (FBA) was successfully performed to test the growth of *P. dioscoreae* on different substrats like glucose, succinate, and ACC, and diverse conditions on carbon, oxygen, and nitrogen availability were simulated. The model was evaluated through

Metabolic Model test (MEMOTE) and against proteomic data.

Metabolic models are great tools to gain deeper knowledge and understanding on the metabolism of different organisms. This model provides a representation of the growth of MSB3 on ACC which later could be used to join this model to one of a plant and thus simulate the plant-bacteria interactions. This way, there would be an approach to represent the growth promoting property of *P. dioscraeae* MSB3.

## Poster 16

### Ghost admixture in present-day African genomes

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Admixture has played a critical role in shaping the genetic diversity among human populations. Exploring the genomes of diverse and deeply divergent present-day human populations such as the Khoe-San populations of Southern Africa and Central African rainforest hunter-gatherers (RHG) is

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 source genomes from archaic populations are available.

Using methods that do not require the reference archaic genomes, we analyzed 25 high-coverage genomes from five different Khoe-San populations and a set of genomes from different RHG populations, in the context of African genomic diversity. We explored two models of early human population structure: the reticulation of multiple stems migrating between early human populations, and archaic hominin admixture from deep ghost lineages. We found that a model with introgression from an unknown source population into the ancestors of Khoe-San populations better explains patterns of outliers in terms of private polymorphisms than the weakly structured stem model. We identified genomic segments that represent putative fragments of ghost introgression in the Khoe-San individuals.

## Poster 17

### Synchrotron-Based Analysis of Heavy Metals in Moss Tissues

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The accumulation and distribution of heavy metals within plant tissues are processes of great interest for phytoremediation and environmental biomonitoring [1].

Synchrotron radiation techniques, particularly X-ray imaging and diffraction, allow high-resolution analysis of metal localization. This advanced approach enhances our understanding of metal uptake and retention in mosses, providing insights about their mechanisms for managing metal stress [2].

In this poster, we present some results of an advanced analysis conducted using the NanoMAX synchrotron (MAX IV; Lund, Sweden), an X-ray beamline for imaging and diffraction studies at the nanoscale. The aim was to localize and quantify the presence of copper and iron, alone and in combination, in the tissues of two moss species: *Physcomitrium patens* and *Pohlia drummondii*. The results highlight significant differences in metal accumulation and distribution between the two species.

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## Poster 18

### Shape-Types of Postcanine Dentinal Tooth Crowns and Their Relationship to Dental Tissue Volumes, Sex, and Geographical Origin in Modern Humans

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Previous studies on 3D dental morphology demonstrated that modern human postcanine dentinal tooth crowns vary between tall and narrow and short and broad (Teplanova, 2015; Krenn et al., 2017; Krenn, 2015; Buchegger 2015, Halász, 2019; Šimková, 2020). These findings are based on detailed virtual analyses of third and fourth premolars, first and second molars, as well as deciduous second molars, using geometric morphometrics. By integrating 3D shape measurements and additional linear and volumetric measurements, in this study we explored the relationship between shape-types and dental tissue volumes, including total cubic content, dentinal volume, and pulp volume.

Our findings indicate that tall/narrow-shaped teeth exhibit 30-60% percent larger pulp cavities, while low/broad-shaped teeth feature smaller pulps. However, the overall dentine volume of the crown remains on average consistent across both Shape-Types, suggesting a relatively constant amount of dentine, regardless of dental shape. This implies that tall/narrow or low/broad dental shapes develop from similar quantities of dentine.

Moreover, our results show Shape-Types to be rather consistent within an individual's dentition, with 87% of cases displaying only one shape-type across the entire postcanine dentition. Sex-related differences were observed in premolar Shape-Type expression, with females being 33% more likely to exhibit tall/narrow-shaped premolars compared to males. Additionally, we identified a 'north-to-south' trend, associating tall/narrow-shaped dentinal crowns predominantly (20-55% more frequently) with northern populations, while short/broad-shaped

crowns were 25% to 55% more common in southern populations. Our results suggest that, in addition to genetic factors, spatial and functional constraints might play a significant role in determining dental morphology (Saini et al., 2022; Fan et al., 2019; Sharma et al., 2016; Sikka & Jain, 2016; Radmer & Johnson, 2009; Reyes-Centeno et al., 2017).

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