Ecology & Evolution VDSEE Symposium 2024

16 February 2024
University of Vienna, Biology Building, Hörsaal 1

Vienna
Doctoral
Schools

Welcome to the VDSEE Symposium 2024!

We are delighted to welcome all participants and speakers to the first 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 external guests, Bianca Vienni-Baptista (ETH Zurich), Gianluca Corno (National Research Council of Italy – Water Research Institute (CNR-IRSA)), and Peter Iwaniewicz (science communicator, columnist at falter.at). Thank you for joining us and contributing to our Symposium.

We would like to thank the organizing committee—Marilena Heitger, Daniel Martinovic Saavedra, Christian Griebler, and Harald Wilfing, who made this Symposium come to life. Furthermore, we would like to express our thanks to DSPL Hanna Schneeweiss for her support. Finally, we extend our appreciation to our sponsors CliniSciences, Integra Biosciences, IST Innuscreen, and Shimadzu 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

Talks

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.

Registration

Please register at the desk in front of HS1.

Poster/coffee breaks/sponsors

The poster sessions, coffee breaks and the sponsors' booths are in the foyer behind Hörsaal 1.

Dinner

Dinner will be served in the UBB-mensa until 20:00. It is right behind the foyer where the poster session takes place. Our buffet with lots of vegetarian and vegan options is awaiting you.

→ Please note that the Symposium location closes at 22:00.

Wifi

Eduroam is available at the location.

Contact

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

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Keynote Lecture 1

Gianluca Corno

(National Research Council of Italy – Water Research Institute (CNR-IRSA)

Integrating ecological theory and evolutionary principles to comprehend the intricate cycle of antibiotic resistance

The abuse and misuse of antibiotics in human and veterinary medicine over the last century have led to the current situation where the problem of antibiotic resistance is global and, in perspective, potentially devastating in the coming decades. Despite a series of actions promoted by various global institutions, the scale of the problem, antibiotic consumption, and the number of deaths attributable to resistant infections are constantly increasing, to the point where the issue can be defined as a "hidden pandemic". However, antibiotic resistance is a phenotypic trait much older than the era of human antibiotic use and is mediated in nature by the concurrent action of various ecological factors such as competition for resources. The co-evolution of antibiotic-producing microorganisms and others that develop resistance systems is present throughout the history of bacterial evolution. The peculiar evolutionary speed of bacteria, capable of both vertical and horizontal gene transmission, along with the massive use of synthetic or semi-synthetic antibiotics (absent in nature), has promoted the rapid development and widespread distribution of resistance mechanisms against all currently known antibiotics. To address the problem, it is necessary to understand the so-called "cycle of antibiotic resistance," i.e., how resistances pass from a human or an animal to food, the environment, and then back to other humans, with a perspective of "one-health" or, better yet, "global-health."

Knowledge of ecological theory and evolution, often lacking in human and veterinary medicine, and the application of these as a background for implementing measures to reduce and contain resistance, are essential to overcome this challenge, crucial for the future of humanity.

Gianluca Corno is a Researcher at the CNR-IRSA Verbania and the Coordinator of the Molecular Ecology Group, MEG. He uses microbes as model organisms to test general ecological theories such as community response to natural stressors, interactions prey-predators, competition and/or cooperation between species, resistance and resilience of microbial communities. He tries to define trends and ecological models to apply the ecological theory to concrete problems associated with bacteria (mostly in marine and freshwaters, but also in soils and human gut) including microbial blooms, antibiotic resistance, and spread of pathogenic bacteria.

Keynote Lecture 2

Bianca Vienni-Baptista

(ETH Zurich)

Pathways to inter- and transdisciplinary research for sustainable futures: opportunities and challenges

Interdisciplinary and Transdisciplinary research are considered of central importance to academia, policy and practice. This talk will give an overview of what interdisciplinarity and transdisciplinarity are and why they hold important for sustainable futures. Finding sustainable solutions to the social, cultural, political, economic, and health challenges we currently face demands that we do things differently, that we work collaboratively and that we embrace transdisciplinary research — across and between all disciplines— like never before. This talk will present key issues and pathways for fostering inter- and transdisciplinary research focusing on the integration between disciplines and partners. It provides concrete guidance on the opportunities that inter- and transdisciplinarity offer to co-produce knowledge for sustainable development and introduces some resources available to orient teams in designing and implementing such collaborations.

Bianca Vienni-Baptista holds a PhD in Cultural Studies and a Habilitation (Venia Legendi) on the anthropology of science and technology from ETH Zurich. She is group leader and lecturer at the Transdisciplinarity Lab (Department of Environmental Systems Science, ETH Zurich). Her research focuses on the study of inter- and transdisciplinary knowledge production processes. As a result, she is interested in methods and tools, as well as concepts and theories, as means of achieving transformative and developmental change. Together with her team, she investigates the specific conditions for transdisciplinary research and implements participatory co-production processes for sustainable development.

Oral Presentations

Petra Lukender

Review on the coleoid diversity from the Carnian Polzberg Konservat-Lagerstätte (Late Triassic, Northern Calcareous Alps).

Petra Lukeneder[1]*, Dirk Fuchs[2], Alexander Lukeneder[3]

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Although coleoid cephalopods are widespread from the Palaeozoic throughout the geological time scale, their fossil record is incomplete and thus the various palaeobiological aspects are insufficiently understood. The extinct group of the belemnoid Phragmoteuthida is thought to be closely related to the stem group of the ten-armed Decabrachia and eight-armed Octobrachia. The well-known, almost complete specimens of *Phragmoteuthis bisinuata* from the Carnian Polzberg *Konservat-Lagerstätte* near Lunz am See (Lower Austria) and Cave del Predil (Julian Alps, Northern Italy) come from historical excavations, but of course these specimens do not reflect the entire belemnoid assemblage within this Triassic environment. In order to obtain a more complete picture of the coleoid fauna within the Reifling Basin, 430 coleoid specimens from Polzberg and, for comparisons, 60 fossils from Cave del Predil were studied in detail. The phragmocones and proostraca, parts of the living chambers, arm hooks, cephalic cartilages, ink sacs and even jaws, attributed to this coleoid fauna were recorded, measured and evaluated taxonomically. New, surprising finds from the Polzberg *Konservat-Lagerstätte* challenge the previous assumption of a monospecific composition of the coleoid Polzberg fauna. The presence of phragmocones with small opening angles, characteristic dorsal crests and growth lines of the final (body) chamber combined with non-tripartite proostraca and curved arm hooks indicate the presence of the basal coleoid group comprising the rostrum-less "*Mojsisovicsteuthis* Group".

A newly excavated, exceptionally preserved phragmoteuthid fossil with an entire arm crown indicates the presence of ten differentiated arms within this group for the first time. Additionally various fossils are assumed to belong to still undescribed phragmoteuthid species. Our results confirm that the coleoid diversity from the Polzberg *Konservat-Lagerstätte* and Cave del Predil is higher than previously thought and must be treated in a much more differentiated way. Especially the high variability of the cephalic cartilages and hook shapes in the Phragmoteuthida needs further attention for a detailed assessment of the species.

Susanne Reier

Exploring the Impact of Paleohydrology and Underground Migration on the Population Genetic Structure of the minnow Phoxinus lumaireul (Schinz, 1840)

Susanne Reier[1,2], Luise Kruckenhauser[2,3], Min Chai[1], Anja Palandačić[1,4]

[1]First Zoological Department, Vienna Museum of Natural History, 1010 Vienna, Austria; [2]Department of Evolutionary Biology, University of Vienna, 1030 Vienna, Austria; [3]Central Research Laboratories, Natural History Museum Vienna, 1010 Vienna, Austria; [4]Department of Biology, Biotechnical Faculty, University of Ljubljana, 1000 Ljubljana, Slovenia.

The Dinaric karst on the Balkan peninsula harbors a remarkable variety of European biodiversity. Karst landscapes, known for intricate underground water systems interconnected with surface water, are prevalent in this region.

A biologically-oriented exploration of these subterranean connections involves analyzing the genetic relationships among aquatic organisms inhabiting the studied karst system. By examining genetic population structure, insights not only into aquatic relationships but also into the ecology of the organism under investigation can be gained.

In our preliminary study, we sampled several populations of the minnow species *Phoxinus lumaireul* in the Slovenian Dinaric karst. Genetic markers (COI, cytb, RPS7) revealed a natural population structure influenced by historical and current gene flow, rather than human translocations. Our ongoing research utilizes genome-wide ddRAD-seq data to compare populations linked through underground connections. Our goal is to determine whether minnows utilize underground water connections or if the karst serves as a barrier to gene flow. Furthermore, we examine how paleohydrology has shaped the current genetic structure. The rapid hydrological changes in the Dinaric karst impact species distribution and adaptation.

Our results shed light on the divergence of different genetic lineages of *P. lumaireul* in the Dinaric karst, providing valuable insights into the intricate dynamics of biodiversity in this unique region. Understanding genetics and historical adaptations underscores the importance of preserving karst landscapes, particularly due to their vulnerability to human impact, emphasizing the necessity for protective measures.

Silvia Basanta

The evolution of signaling at the fetal-maternal interface

Silvia Basanta[1], Daniel Stadtmauer[2,3], Mihaela Pavlicev[1], Gunter P. Wagner[1,3]

[1]Evolutionary Biology, University of Vienna; [2]Konrad Lorenz Institute; [3]Ecology and Evolutionary Biology, Yale University.

The evolution of eutherian pregnancy entailed several signaling milestones, including signals for maternal recognition of pregnancy or specialized and intimate cell-cell communication between maternal and trophoblast cell types. We approach the evolution of signaling in pregnancy by looking into the interrelatedness of three endocrine systems: the luteal phase of the ovarian cycle, implantation, and the final establishment of a fetal-maternal interface. These three systems show a progression from a maternal-only type of signaling to one in which an essential part of the endocrine control of pregnancy and the homeostatic maintenance of a newly formed tissue shifted to being placental. We use a comparative, single-cell-based cell-cell communication study encompassing different species (the opossum as the outgroup for ancestral state reconstruction, the tenrec as a basally branching eutherian, and the mouse and guinea pig) to understand the evolution of this pregnancy-specific signaling. Our key questions include how the cell type inventory and cell-cell interaction network changed and evolved in eutherians.

Sanjay Narayanaswamy

Germ layer morphogenetic behavior and boundary formation in self-organizing gastruloids of Nematostella vectensis

Sanjay Narayanaswamy[1], Franziska Haas[1], Emmanuel Haillot [1], UlrichTechnau[1]

[1]University of Vienna, Department of Neuroscience and Developmental Biology, 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-dependent mechanism, FoxA+ endodermal cells are gathering around the mesodermal clusters to later form a primary pole, which eventually becomes 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.

Paul Knabl

Developmental roles of BMP signaling in Cnidaria

Paul Knabl[1], Grigory Genikhovich[1]

[1]Department of Neuroscience and Developmental Biology, University of Vienna.

In Bilateria (worms, insects, molluscs, vertebrates, etc.), Bone Morphogenetic Protein (BMP) signaling is involved in a myriad of developmental processes, including dorso-ventral body axis patterning, as well as the survival, homeostasis and differentiation of cells. BMP signaling is also important for the development of Cnidaria (jellyfish, sea anemones and corals), the phylogenetic sister group of Bilateria. During development of the sea anemone *Nematostella*, BMP signaling is remarkably dynamic: in the embryo, it forms a signaling gradient governing the formation of a secondary body axis, like it does in many Bilateria. Then, once the body axis is established and patterned, BMP signaling switches to a non-graded activity and becomes broadly detectable in the gastric folds of the polyp. In this study, we investigated different developmental roles of BMP in a cnidarian. 1) To better understand the processes of axis patterning regulated by graded BMP signals, we used chromatin immunoprecipitation followed by Illumina sequencing to generate a genome-wide list of direct BMP signaling gene targets in the embryo. Analyses of identified targets revealed many genes involved in secondary axis patterning. The comparison of the *Nematostella* BMP signaling targets with the similar datasets from two bilaterian model species showed little overlap, however, we find several targets conserved between the sea anemone, the frog and the fruit fly. 2) To unravel the function of BMP signaling unrelated to axis patterning, we documented the diversity of BMP signaling domains in adult *Nematostella* polyps and generated an atlas of the signaling activity using an antibody against its effector, pSMAD1/5. Then, we combined the pharmacological attenuation of BMP activity with tissue-specific RNA-Seq and showed that BMP signaling mostly controls other developmental regulators, including a large fraction of neuronal genes. Utilizing transgenic reporter lines, we identified some of the cell populations with active BMP signaling, including distinct neuronal subpopulations (expressing *elav*, *soxB2* and *nanos1*) adjacent to the longitudinal muscle regions. Altogether, our study highlights interesting similarities but also differences of processes regulated by BMP signals in Cnidaria and Bilateria.

Oliver Link

The medusa neuromuscular system: A gate for understanding evolutionary events that led to cell-type diversification.

Oliver Link[1], Alison G. Cole[1], Stefan Jahnel[1], Juan Daniel Montenegro[1], Ulrich Technau[1]

[1]University of Vienna, Department of Neurosciences and Developmental Biology.

Cell-type complexity is required to achieve body plan diversity in all animals but reached its climax in the Bilateria. To gain a basic understanding of mechanisms that led to diverse body plans across bilateral symmetric animals it is advantageous to take a deeper look into their phylogenetic sister group, the cnidarians. In contrast to Bilateria, cnidarians typically possess 2 germ-layers but already show astonishing cell-type complexity. Especially their free-swimming medusa, or so-called "jellyfish" develop cell-types like striated muscles and corresponding motor neurons which enable a free-swimming lifestyle and are not present in sessile stages like anemones or corals. However, the development and evolution of these cell-types is poorly understood. In the scyphozoan moon-jellyfish *Aurelia coerulea*, striated muscles as well as neurons that form the motor nerve net and the eyes (rhopalia) emerge during metagenesis, a transition from an asexual polyp to a sexual reproducing free-swimming medusa through a process called strobilation. We used single-cell RNA sequencing for all life-stages that cover this transition and validated cell-type diversity via phalloidin stains, immunohistochemistry and in situ hybridization to be able to identify the molecular profiles of cell-types along this transition. With this reference atlas for cell-types in the moon-jellyfish we try to infer the developmental origin of medusa cell-types via trajectory analysis and functional experiments. Further we generated single-cell RNAseq data sets for other medusozoans like the hydrozoan *Clytia hemisphaerica* and the cubozoan *Tripedalia cystophora* to compare molecular profiles from cell-types of interest. Subsequently, we want to compare these molecular cell profiles between cnidarians and ctenophores which were recently shown to be the sister group to all other animals to gain insights in the evolution of those cell-types across metazoans. Therefore, we generated a single-cell RNAseq dataset from *Euplokamis dunlapae,* the only ctenophore found so far that possesses striated muscles. Our results from the moon-jellyfish Aurelia *coerulea* indicate different developmental origins for medusa muscles and neurons. Whereas neurons might emerge from a yet unidentified possible stem cell population, striated muscles might remodel from a smooth muscle precursor. We also found a shared contractile complex for medusa smooth and striated muscles which differs from our knowledge in Bilateria. In a broader sense this could be a feature of all muscles in basally branching animals.

Stefano Mari

Ecological significance of the detour test: inhibitory control, personality, and ecological performance in brown trout

Stefano Mari[1,2], Libor Zàvork[1,2]

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[1]University of Vienna, [2]Wassercluster Lunz.

The detour test, a classical paradigm for studying inhibitory control and cognitive flexibility in animals, involves obstructing a direct path to a resource (e.g., food, social group, shelter) to assess the ability of an animal to suppress impulsive behavior and find an alternative route. Performance in the inhibitory control detour test (ICDT) is widely recognized as a correlate of cognitive abilities and ecologically relevant traits in mammals and birds. While analogous ICDT performance has been demonstrated in fish, these studies took place in controlled laboratory conditions, which limits their ecological informative value. Moreover, studies on different fish species differ in how ICDT performance correlates with the personality traits from fast-slow axis (i.e., boldness, exploration, activity). According to the speed-accuracy trade-off of animal cognition, animal personality and cognitive flexibility are linked together so that bold individuals have lower cognitive flexibility and performance in the ICDT then their shy conspecifics. These differences in cognitive and personality traits can influence the ecological performance of individuals.

In this talk, I show how we filled these gaps by investigating the interplay between ICDT performance, personality tested in controlled laboratory conditions and diet composition through evaluations of stomach contents analyses in brown trout *Salmo trutta,* whose samples were taken after a period of rearing in semi-natural stream mesocosms conditions.

According to our hypothesis, higher inhibitory control capacities should correspond to shy personalities and facilitate novel prey consumption in new environments—so a higher biomass in their stomach content is expected—and positively correlate with a higher prey diversity and cryptic prey consumption than less performing, bolder individuals.

Carlos Antonio Perez Rizquez

Role of Ferritin(s) in nodule formation and the symbiont induced stay-green effect upon drought

Carlos Pérez-Rízquez[1], Lisa Carolin Bilz[1], Leila Afjehi-Sadat[2], Manuel González-Guerrero[3], Stefanie Wienkoop[1]

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[1]Plant-Microsymbiont Interaction Group, Functional and Evolutionary Ecology, University of Vienna, Vienna, Austria; [2]Mass Spectrometry (Core Facility), University of Vienna, Vienna, Austria; [3]Centro de Biotecnología y Genómica de Plantas, Universidad Politécnica de Madrid (UPM)-Instituto Nacional de Investigación y Tecnología Agraria y Alimentaria (INIA/CSIC), Madrid, Spain.

The symbiotic relationship between nitrogen-fixing rhizobacteria and legumes play a crucial role in enhancing plant tolerance to drought stress. Previous research has proven that this symbiosis triggers a phenotype known as symbiont induced stay-green (SISG), which delays leaf senescence in response to drought and facilitates quicker recovery from desiccation. Ferritin, an Fe-storage and distribution protein, known to be involved in drought stress and leaf senescence, seemed to play a major role in this stay-green phenotype. Their levels were enhanced during symbiosis compared to non-symbiotic *Medicago truncatula* (Jemalong) plants.

Here, we show that Ferritins are additionally involved in nodule formation. Knockdown mutants exhibited reduced nodulation while function was retained. Hence, ferritin supports the formation of the symbiotic relationship and symbiosis, vice versa, induces the levels of Ferritin. As a consequence, ferritins are not only regulated by rhizobia but are also regulating symbiosis. In order to decipher the dynamics of the different isoforms of Ferritin in this relation(s), we further analysed the absolute amount of ferritin isoforms in leaves of *M. truncatula* wildtype R108. For this, we used the Mass Western approach and compared protein levels upon symbiosis and drought. We will discuss the data with a critical analysis of the Mass Western approach.

Giulia Marchioro

Investigating responses of coral fluorescent proteins to light gradients using confocal laser scanning microscopy

Giulia M. Marchioro[1,2], Johanna Sonnleitner[1,2], David Coelho[3], Michael Schagerl2, Luise Kruckenhauser[1,2], Daniel Abed-Navandi[4], Thibault Bouderlique[5], Igor Adameyko[5,6], Pedro R. Frade[1,7]

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GFP-like proteins or fluorescent proteins (FPs) are highly abundant and diverse in reef-building corals and can be categorized based on emission-excitation properties. A well-supported hypothesis is that FPs modulate light use by the coral's photoautotrophic endosymbionts, either by shading them from excessive irradiance (shallow water) or by re-emitting light at photosynthetically-active wavelengths in low light (deep water). To test this, we investigated the role of host FPs in light modulation over depth on Curaçao reefs for different species in the coral genus *Madracis (M. senaria, M. decactis, and M. pharensis),* by combining confocal laser scanning microscopy (CLSM) on histological sections with symbiont photobiology analyses (cell and pigment concentrations, photochemical activity). Our CLSM approach, developed by analyzing the temporal response of FPs under controlled light conditions in an aquarium setting, allows to effectively characterize the distribution and intensity of different FP groups at the cellular/tissue level. Our findings indicate higher fluorescence intensity in green FPs (GFP) and a higher ratio of GFP to symbiont chlorophyll concentration at 5-10m depth as compared to 20-25m depth. In contrast, there was no significant variation in symbiont physiology along a depth gradient, but rather in tissue orientation (top/side of colonies).

In summary, the results indicate that the animal component regulates the response to depth-light gradients, while the symbiont mediates the light response to tissue orientation for acclimatization. Possible variation in coral green FPs may be the result of acclimatization to irradiance spectral changes with depth. This factor will be investigated in future analyses of reciprocal depth transplantations and bleached samples of the genus *Madracis.* In general, our work illustrates how animal and symbiont are integrated at the tissue and cellular level to maximize the performance of the coral holobiont.

Thomas Pribasnig

The biofilm lifestyle of ammonia-oxidizing archaea: An understudied mode of growth and activity

Thomas Pribasnig[1], Maximilian Dreer[1], Logan Hodgskiss[1], Melina Kerou[1] and Christa Schleper[1]

[1]Department of Functional and Evolutionary Ecology, University of Vienna, Djerassiplatz 1, 1030 Vienna, Austria.

Ammonia-oxidizing archaea (AOA) are ubiquitously distributed in soil and aquatic environments and through their autotrophic growth contribute significantly to both the global nitrogen and carbon cycles. Although, there is a continuously increasing number of axenic isolates available, comparably little is known about ecophysiological aspects and growth modes of AOA. In this study, *Nitrososphaera viennensis* was grown as a continuous culture in a bioreactor, where biofilm formation was observed under high flow rates. In order to better characterize growth in biofilm compared to planktonic growth, we performed a transcriptome study based on RNA-seq and were able to identify significantly distinct expression patterns between both growth modes, including (among others) genes for EPS production and adhesion being highly expressed in the biofilm. We then expanded our investigations to four strains of AOA representing different families *(Nitrososphaeraceae and Nitrosopumilaceae)* and ecosystems (terrestrial and marine) to explore how widespread the ability to form biofilms is amongst the diversity of AOA. While these strains showed differing ability to form biofilms, soil strains exhibited strongest biofilm formation. Our comparative analyses involving scanning electron microscopy (SEM), staining of biofilm extra-polysaccharides and transcriptional analysis during growth in a biofilm, reveals distinct biofilm-forming abilities of AOA strains reflecting their phylogenetic distribution and ecological niches.

Marcel Seifert

Green thumbs for sustainable investments and greenwashing identification: Cultivating sustainable finance literacy beyond advanced financial literacy

Marcel Seifert[1,2,3], Stefan Palan[4], Florian Spitzer[1], Erich Kirchler[5], Aja Ropret Homar[1] & Katharina Gangl[1]

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Sustainable investments that consider Environmental, Social and Governance criteria are instrumental for the sustainability transition but require enhanced knowledge, i.e., sustainable finance literacy. Nevertheless, widely used measures for quantifying financial literacy ignore the sustainability aspect and efforts to investigate the relationship between sustainable finance literacy and investment decisions remain scarce. In Study 1 (preregistered) we develop and validate a measurement instrument for sustainable finance literacy in collaboration with 12 Austrian experts, using a representative sample of 1,047 participants. In Study 2 (preregistered), we investigate its relationship with investment behavior by conducting an incentivized investment decision with a representative sample of 1,510 participants. Based on Study 1, we propose a 7-item measurement item for sustainable finance literacy. Participants answer about half of the sustainable finance literacy questions correctly. Study 2 shows that sustainable finance literacy robustly relates to higher stock market participation, more sustainable investments and less greenwashed investments in the incentivized investment decision, also among participants without investment experience. Participants with higher levels sustainable finance literacy are four times more likely to identify a greenwashed fund and have fewer misperceptions about sustainable investments. While sustainable finance literacy correlates with advanced financial literacy, we find significantly higher effect sizes and additional variance explained in the outcome variables compared to advanced financial literacy. Thus, sustainable finance literacy is a complementary concept to advanced financial literacy. The results allow to determine the importance of sustainable financial literacy for the sustainability transition. Based on the measurement instrument, academics and practitioners (e.g., for financial advisors) can adopt their financial advice to potential investors.

Karen Kölzer

Pollen diversity in honey from Apis mellifera along the urban-suburban gradient in a Central European metropolis

Karen Koelzer[1,2], Martina Weber[1], Alexandra Ribartis[2]

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Urban beekeeping has become a popular trend in many cities worldwide. Green spaces such as parks, private gardens, and road verges provide pollinators with diverse floral resources. Pollen analysis with light microscopy is a valuable tool to identify foraging plants of honeybees and allow to determine the botanical and geographical origin of honey. However, urban areas with their high diversity of ornamental, non-native plants pose a specific challenge in authenticity checks. Because they are also exceedingly affected by climate warming, many municipalities have started using adapted planting regimes to adapt to heat and drought.

With the aim to characterize the "urban", pollen in honey from eighteen apiaries across Vienna, Austria, was microscopically analysed over three consecutive years. Pollen grains were counted out to 500 per sample to determine the relative abundances of each pollen type. Differences in the pollen spectra were qualitatively and quantitatively examined according to year, extraction time and extent of urban built-up area within the typical 3 km flight radius of honeybees.

A total of 202 plant taxa could be identified, of which 48% to genus level and 25% to species level. The median number of pollen types per sample was 46. Overall, out of 71 identified ornamental plant taxa, 41 were non-native. Woody species were major contributors of pollen and nectar for urban honeybees, including the invasive Ailanthus altissima, which was the predominant pollen type in 15 out of 50 samples. Other non-native trees important for mass foraging included *Gleditsia triacanthos, Sophora japonica, Koelreuteria paniculata* and *Liriodendron tulipifera.*

This research evaluates bee-friendly municipal and private planting regimes in urban areas. The results suggest potential synergies between climate-adaptive taxa, pollinator ecology, and food security in cities.

Anna-Maria Salgado Gschwandner

Seasonal dynamics of plankton communities in four subalpine lakes

Anna-Maria Salgado Gschwandner[1,2], Simon Vitecek[1,2], Robert Ptacnik[1,2]

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Based on the island biogeographic model, lakes can be considered as islands surrounded by a terrestrial matrix. Following the island biogeographic model, lakes, which are geographically closer to each other are ecologically better connected through dispersal and should have higher biodiversity and stability through the ability to regeneration faster than remote lakes. Ecosystem stability is of growing concern with climate change. Lakes and their plankton communities tend to respond highly sensitive to global warming. Their resilience in response to stressors is expected to be linked to the biodiversity of their communities.

For 2.5 years, I sampled four subalpine lakes in Austria on a monthly basis. Two of them are rather isolated in the landscape, the other two are part of a larger cluster (Salzkammergut) and represent the two connected lakes in this study. In addition to abiotic data, I collected phytoplankton, zooplankton and bacterioplankton samples to investigate species abundance and compositional changes over the seasons, and to assess if "remoteness" links to the stability of these lake ecosystems.

The community composition of bacterioplankton is significantly different between the lakes, while no difference in their metabolic activity was notable. Preliminary results for Zooplankton indicate that more rare taxa occur in the remote lakes, while no general difference was found between the lakes within their diversity. Simultaneously, I observed reduced compositional stability in the more remote lakes compared to the connected ones.

Florian Danzinger

Development of the strategic framework for the restoration of degraded ecosystems and landscapes for Austria

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In 2011, the European Union published an EU Biodiversity Strategy for the period 2011–2020. The goals and measures of this strategy are based on the so-called Aichi Targets.

Target 2 of the EU Biodiversity Strategy calls for the restoration of at least 15% of degraded ecosystems by 2020. This target and the corresponding action for the restoration of ecosystems were also set out in the EU Biodiversity Strategy 2030 and are included accordingly in the national implementation of the Austrian Biodiversity Strategy 2030+. The very current European Commission's proposal for a Nature Restoration Law is the first continent-wide, comprehensive law of its kind. It is a key element of the EU Biodiversity Strategy, which calls for binding targets for the restoration of degraded ecosystems.

In the course of the present study, a strategic framework was developed as a preparatory measure (Action 6a according to the EU Biodiversity Strategy) to set prioritieZs for the restoration of degraded ecosystems and landscapes in order to achieve the 15% target. This also included the identification of individual landscape areas that are to be prioritised for restoration.

A geographically explicit map of biotope types at national level served as the main basis for the development of the strategic framework.

Since the planning of restoration measures, along with the setting of restoration priorities, requires knowledge of the state of the ecosystems, the next step was to assess their current state and to perform a classification into four levels of degradation. The intrinsic characteristics of ecosystems, but in particular the heterogeneity of available and relevant basic data, made different methodological approaches necessary.

The costs necessary to achieve the 15% target were calculated separately for each of the ecosystems: forests, surface waters and open land. The resulting costs depend heavily on the target. Different scenarios were therefore calculated.

The implementation of the 15% target is assumed to be achieved within the 2020–2050 timeframe. The estimated costs of the implementation of restoration measures to achieve the 15% target in Austria are approximately 10.7 billion euros for all ecosystems and ecosystem groups, excluding urban ecosystems and those characterised by settlement.

Poster Presentations

Pratiksha Acharya – P1

Influence of resource diversity on the microbial processing of fine particulate organic matter during leaf breakdown in streams

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Leaf litter decomposition (LLD) is an essential ecosystem function in headwater streams, which can be influenced by leaf diversity and preconditioning of the leaves. However, how resource diversity is affecting LLD and the microbial decomposition of fine particulate organic matter (FPOM) produced during LLD is not well known. We hypothesized that leaf litter diversity influences the composition of the produced FPOM and associated microbial functional responses. In laboratory microcosms, we fed alder, beech, and maple leaves and their mixtures, preconditioned under anoxic and oxic conditions to caddisfly larvae *(Sericostoma sp.)* for 24 days. Every four days, we measured the production, composition, and microbial activities of the produced FPOM, i.e., manually shredded fine leaves and shredder egesta. The shredded leaf particles showed significantly different microbial activities with higher microbial respiration but lower bacterial production on shredded alder and maple leaves following oxic compared to anoxic preconditioning. Therefore, anoxic preconditioning increased microbial growth efficiencies on shredded leaf particles. Bacterial production on faecal pellets from shredders that fed on oxic preconditioned leaves was lower than on anoxic ones, similar to the shredded leaf particles, suggesting that the gut passage does not change the microbial growth efficiencies observed on the shredded leaf particles. However, this difference was only significant in the early experimental phase whereas no differences in bacterial production on faecal pellets were found after 24 days. Hence, these results emphasize that microbial decomposition of FPOM produced during LLD depends on leaf species and preconditioning, however, modulated by the duration of the decomposition.

Fariha Naz Apon – P2

How nickel induced changes in cell wall components trigger growth responses via members of the Catharanthus roseus RECEPTOR LIKE KINASES 1 LIKE (CrRLK1L) gene family

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Nickel (Ni^{2+}) is an essential microelement for plants. In agricultural soils, Ni^{2+} ion concentration range between 10–40 µg/g soil. However, this concentration is higher as 1 mg/g in serpentine soils and around mining areas. Due to human activities and agricultural practices, the amount of Ni^{2+} ion release into soils rises thus imposing environmental concerns. We and others have recently shown that Ni^{2+} ions inhibit cell elongation in hypocotyl and root growth in *Arabidopsis thaliana*. To understand how Ni^{2+} inhibits growth, we focused to the effect of Ni^{2+} on modifications of cell wall component pectin. Pectins and in particular the homogalacturonans (HGs) are highly methylated and acetylated and the degree of these modifications is controlled by 67 pectin methylesterases (PMEs) and 76 PME inhibitors (PMEIs). To determine if Ni^{2+} exposure is changing their expression, RT-qPCR was conducted for the whole gene family of PMEs and PMEIs. 18 PME genes were at least 2-fold upregulated while only six were downregulated. An opposite picture emerged for the PMEI genes where only one was upregulated and 13 were downregulated. These results indicate that the balance between PME and PMEI activity was shifted towards PME and thus demethylation of pectins. This result was corroborated by PME activity assays showing that Ni^{2+} exposure of seedlings induced PME activity up to 3.5-fold. Time course experiments further demonstrated that PME activity was induced within two hours of Ni^{2+} exposure. Changes in pectin methylation levels are a prerequisite for the production of pectin derived signaling molecules like pectates and oligogalacturonides (OGs). These signaling molecules are ligands of the *Catharanthus roseus* RECEPTOR LIKE KINASES 1 LIKE (*Cr*RLK1L) family. We have previously shown that members of this cell wall integrity sensors mediate growth responses upon Ni^{2+} exposure. We will present data where PME activity in *Cr*RLK1L mutants point to their role in suppressing demethylation of pectins. A model will be proposed and discussed how Ni^{2+} ion induce cell wall modifications leading to signaling events resulting in growth adjustments.

Pamela Baur – P3

Diurnal patterns of CH4 fluxes in a subsaline reed ecosystem analyzed for each emission pathway and season

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Wetlands dominated by reed *(Phragmites australis)* naturally release methane (CH_4), which is formed in the sediment and transported to the atmosphere via different pathways. Annually, about 15% of the net carbon fixed by wetlands may be released to the atmosphere as CH_4. However, little is known about the quantification of the different pathways of CH_4 emissions in reed belts, especially of Central European and subsaline wetland ecosystems, and their contribution depending on season and time of day.

The reed belt of Lake Neusiedl is the largest coherent reed ecosystem in Europe after the Danube Delta, a wetland of international importance (RAMSAR and UNESCO site) and the study site for this research. The reed belt forms a dynamic mosaic of water, reed and sediment patches and has a subsaline character.

In order to investigate the different emission pathways of CH_4, intensive 24-hour measurement campaigns were conducted in the reed belt of Lake Neusiedl every 3 months (seasonally) for one year in 2021/2022.

Various chamber measurement systems were used to capture these pathways: ebullition traps for the ebullition of gas bubbles from supersaturated sediments, floating chambers

for the molecular diffusion transport at the water-atmosphere interface, sediment chambers for the molecular diffusion transport at the sediment-atmosphere interface and vegetation chambers for the plant-mediated transport of *P. australis.*

CH_4 concentrations and stable carbon isotope values of CH_4 ($\delta^{13}C$-CH_4) and carbon dioxide ($\delta^{13}C$-CO_2) were measured using cavity ring-down spectroscopy (Picarro G2201-i). With the help of $\delta^{13}C$-CH_4, biological and geological sources of CH_4 emissions can be distinguished and the mechanisms of CH_4 production and oxidation can be investigated. In addition, sediment and water samples were taken in each campaign and analyzed for various parameters such as TOC, sulfate, nitrate, ammonium and phosphate.

In this study, we quantified the different pathways of CH_4 emissions, assessed the underlying factors responsible for seasonal variation, and investigated whether the reed ecosystem exhibits a diurnal cycle of CH_4 emissions depending on the season and emission pathway.

Filip Paul Boanca – P4

Can Microbes Inform about the Vulnerability of Spring Waters — Assessment of Microbial Communities and Water Quality in Austrian Springs

Filip Paul Boanca[1], Magdalena Seelig[2], Clemens Karwautz[1], Winkler Gerfried[2], Christian Griebler[1]

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Springs are vital water sources, and their vulnerability to environmental changes, particularly climate change, is a growing concern. The PhD project focuses on the assessment of microbial communities and water quality pattern in Austrian springs, with an emphasis on understanding the vulnerability of spring waters.

The first aim of the study is to characterize springs based on their spatial and temporal dynamics in terms of physical and chemical characteristics. This involves a detailed analysis of various parameters such as temperature, pH, conductivity, nutrients, and the concentration of major ions. These characteristics provide valuable insights into their geological background and hydrological conditions, as well as their catchment areas.

A key aspect of the project is the phylogenetic and functional composition of microbial communities in spring waters. Microbes are integral components of aquatic ecosystems and can serve as sensitive indicators of environmental conditions including changes. By comparing the physical-chemical characteristics with microbial communities' members, we aim to explore the potential of individual microbes as environmental tracers.

The research comprises two parts: a local to regional study in the province of Styria, where three springs are sampled monthly, and a national study sampling 90 springs across Austria in two campaigns, one in the spring season and one in autumn, the hydrological extremes.

In summary, this research seeks to enhance our understanding of the vulnerability of spring waters to anthropogenic pressures such as climate change. The findings will provide a most needed knowledge base for future water resources management and contribute to the sustainable use of these vital resources.

Gilles Colling – P5

Factors and trajectories of alien plant species accumulation in arable fields

Gilles Colling[1], Franz Essl[1], Stefan Dullinger[1], Michael Glaser[1]

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[1]University of Vienna

Biological invasions pose a significant threat to global ecosystems, impacting biodiversity, economics, and human welfare. We investigated the accumulation of alien species in arable fields across a study region covering ten countries in Central Europe over a time period from 1930 to 2020. We used an extensive dataset compiled from the newly available AgriWeedClim database and applied general mixed-effect models to analyze the probability of plots containing at least one alien species and the ratio, and relative abundance of alien species within plots.

Our study's findings demonstrate a remarkable increase in the presence of alien species at two distinct spatial scales: within individual agricultural plots, where an upsurge in alien species is recorded per plot, and at the inter-plot level, reflecting a broader pattern of proliferation. Towards the end of our study period, nearly 70% of plots within arable fields contained at least one alien species, indicating a substantial spatial spread. At the plot level, both the ratio and relative abundance of alien species more than doubled. However, these metrics were considerably lower and remained below 10% throughout our study period, indicating a discrepancy in accumulation trends between the two spatial scales.

Our study shows an increase in the presence of alien species across scales in agricultural landscapes, with the potential to homogenize regional weed communities. We anticipate a growing dominance of alien species in local communities into the future, posing a substantial threat to the regional biodiversity.

Maximilian Dreer – P6

Ammonia Oxidizing Archaea Cultivated from Human Skin

Maximilian Dreer[1], Ülkü Yükse[1], Logan Hodgskiss[1], Melina Kerou[1], Rafael Ponce[1], Christa Schleper[1]

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[1]University of Vienna

Ammonia oxidizing archaea (AOA) play a crucial role in the global nitrogen cycle by converting ammonia to nitrite. They are part of the nitrifying communities in marine, freshwater and terrestrial ecosystems and outnumber ammonia oxidizing bacteria in many environments. Interestingly, only AOA but not AOB or comammox bacteria have been discovered as part of the human skin microbiome using molecular techniques. However, the significance of these finding has also been disputed. Here we present the cultivation of AOA from three different human individuals. Each enrichment contains a distinct and novel AOA species, belonging to the genus *Nitrosocosmicus,* members of which are found in diverse terrestrial environments. The organisms oxidize stoichiometrically ammonia to nitrite which coincides with cell growth. Light microscopy and scanning electron microscopy images show their spherical cell morphology as well as their preference to form aggregates like other representatives of this genus. Comparative genomics shows their ability to produce extracellular polymeric substances (EPS) and reveals metabolic features unique to the skin-derived strains, such as e.g. the potential to oxidize compounds encountered on the skin surface. The potential beneficial role of AOA on human skin is intriguing considering that nitric oxide (NO), an important signaling molecule involved in diverse processes such as neuronal signaling, immune response and wound healing in humans, is produced during the ammonia oxidation process. While the influence of AOA on human health remains to be elucidated, we unequivocally show that they are present and culturable from human skin.

Salvador Espada-Hinojosa – P7

Descent rather than life style explains the functional trait distribution in thiotrophic gammaproteobacteria

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Thiotrophic symbiotic bacteria are a widespread representative of the symbiotic habit. Two different clear cases separate them as for lifestyle, whether they show horizontal or vertical transmission. Genomes and metagenome assembled genomes increasing availability enable deeper inquiries about their phylogeny, their physiology, and their evolution. Bacterial phylogeny is for long deeply troubled, challenged by the complications of departure from pure similarity by descent initial darwinian postulate. Functional potential capabilities as inferred from the genomes benefit from the use of coarser levels of integration such as metabolic pathways and traits, based on gene content prediction and annotation. Using 16S rRNA gene trees, phylogenetic conservatism of microbial traits has been proposed in the past. Here we show that these single gene 16S trees have limited power to reliably unveil internal phylogenetic nodes, limited only to the shallow levels of the tree, close to the tips, and not beyond the family level. Nevertheless, a combination of concatenation and multispecies coalescent core genome trees succeeds to find agreement in most internal nodes of the statistical central trend species tree hypothesis, shedding light at the level of family diversification, but not for orders. Genomic features are also addressed, and we validate Sach's

postulate of vertically transmitted symbionts having smaller genomes than free-living closer relatives, and horizontally transmitted symbionts bigger ones. Descent proves related with trait distribution as the outcome of a Mantel test, and a NMDS ordination corroborates it, while no apparent pattern of traits content signature emerges for lifestyle.

Christian Geier – P8

Flower-insect interactions in the Paleogene inferred from in situ and adhered pollen

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Several Eocene and Oligocene maar lake structures in Central Europe offer unique windows into past ecosystems. Both faunal and floral remains enable the reconstruction of a subtropical climate in the Eocene, followed by cooler temperatures in the Oligocene. Evidence for flower-insect interactions are rare in the fossil record and investigations on pollination biology in the Paleogene are almost completely absent. By extracting in situ and adhered pollen from both flowers and insects from the same geological formations links can be drawn between these organism groups. Fossils are screened with epifluorescence stereomicroscopes and pollen is extracted using tiny needles. The

pollen is investigated using light- and scanning electron microscopy (LM & SEM), sometimes even with transmission electron microscopy (TEM). Since pollen morphology is relatively conservative and specific to species, genera, or families, the in situ and adhered pollen can be used to: (1) assign previously unidentified flowers to a modern group and (2) conclude which plants the insects visited prior to death and deposition into the sediment. Applying this methodology, several hundred fossils from three German localities of Messel (middle Eocene, ~48 Ma), Eckfeld (middle Eocene, ~44 Ma) and Enspel (late Oligocene, ~24 Ma) were investigated. Among these were over 1700 flowers (638 with pollen) and over 1500 insects (273 with pollen). The flowers can be affiliated to over 50 families and include members of Anacardiace-ae, Araliace-ae, Chloranthaceae, Cornaceae, Euphorbiacae, Fabaceae, Hamamelidaceae, Juglandaceae, Malvaceae, Nympheales, Onagraceae, Rosace-ae, Rutaceae, Sapotaceae, and Vitaceae. Within the insects, Coleoptera are most abundant, followed by Hymenoptera and Diptera, and only a handful of Lepidoptera are present in the collections. Several examples show a close relationship between insects and flowers already in the Paleogene: (1) *Parthenocissus* (Vitaceae) was detected in all four mayor pollinator groups, especially flies; (2) *Apiformes* (Hymenoptera) show a close relationship to the subfamily of Tilioideae (Malvaceae); (3) *Ludwigia* (Onagraceae) was visited by Buprestidae and Scarabaeidae (Coleoptera).

Michelle Hämmerle – P9

Monkeypox virus genomes from orangutan museum specimens linked to the outbreak in the Rotterdam Zoo in 1965

Michelle Hämmerle[1,2], Aigerim Rymbekova[1,2], Pere Gelabert[1,2], Susanna Sawyer[1,2], Olivia Cheronet[1,2], Paolo Bernardi[1], Sébastien Calvignac-Spencer[3,4], Martin Kuhlwilm[1,2]*, Meriam Guellil[1,2]*, Ron Pinhasi[1,2]*, *These authors contributed equally.

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The Monkeypox virus (*Orthopoxvirus* genus, *Poxviridae* family) is a large double-stranded DNA zoonotic virus first identified in 1958 in macaques. The first human case was reported in 1970, and recent outbreaks have attracted wide public attention to the virus. Monkeypox virus (MPXV) is also among the viruses known to infect non-human great ape populations, which have suffered a substantial population decrease over the last decades. Museomics is well-placed to open a window on this lost diversity for both host and microbial DNA.

Here, we report findings related to four orangutan (*Pongo spec.*) specimens from 1965 that were originally reported to be wild animals from Sumatra. We could recover complete and partial MPXV genomes from those individuals and show that the genomes are highly similar to one sequenced from a MPXV outbreak in the Rotterdam Zoo. The outbreak severely affected orangutans kept at the facility, and six out of ten infected animals died. Given the concordance of the dates and circumstances combined with the genetic evidence, we are confident that we

identified some of these animals within our museum specimens.

In conclusion, we could link the MPXV infection of these orangutans to a specific outbreak, further highlighting the significance of museum specimens to investigate historical outbreaks.

Sonja Hoxha – P10

Characterization of biogeochemical self – purification processes in the Vjosa River network with a focus on different spatial and temporal scales

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Together with its tributaries the Vjosa River represents a large and dynamic running water ecosystem characterized by a near natural flow regime and largely undisturbed hydromorphological dynamics. Due to the low degree of anthropogenic disturbance (e.g. the lack of dams and regulation), the Vjosa River is a hot spot of aquatic and terrestrial biodiversity. The river ecosystem not only consists of the visible river channels but, even more important, of the bed sediments in the hyporheic zone and the riparian corridor. Moreover, in connection with the shallow aquifer the river system carries water even during long drought periods and, on the other hand, mitigates floods by floodplain inundation. Taken all together, the river network provides essential ecosystem services, with a huge water purification capacity of exceptional importance for biodiversity and human needs.

The project targets key biogeochemical processes involved in water purification in a qualitative and quantitative manner. The spatio-temporal distribution and transformation of different carbon (e.g. DOC, DIC, CO_2, CH_4), nitrogen (e.g. NO_3^-, NO_2^-, NH_4^+), and phosphorus (e.g. PO_4^{3-},

Ptot) species will be studied in microcosms (i.e. flow-through sediment systems) and river sections of various dimensions (mesoscale to macroscale) that allow a good quantification of material import, transformation, attenuation, and export. Together with key physico-chemical conditions, water and sediment microbial communities will be analyzed in terms of composition and functions by means of modern molecular tools.

Results from this study will contribute to a significant improvement of our understanding of river functioning from the micro – to the catchment scale as a basis for in depth evaluation of future management options, in the light of the sustainable development goals and above all, highlight the importance of the Vjosa River, as a rare refence system for other rivers in Europe.

Ekin Kaplan – P11

ReSurveyEurope: a database of resampled vegetation plots in Europe

Ilona Knollová[1], Milan Chytrý[1], Helge Bruelheide[2,3], Stefan Dullinger[4], Ute Jandt[2,3], Markus Bernhardt-Römermann[3,5], Idoia Biurrun[6], Francesco de Bello[7,8], Michael Glaser[9,10], Stephan M. Hennekens[11], Florian Jansen[12], Borja Jiménez Alfaro[13], Daniel Kadaš[1], Ekin Kaplan[9,10], Klára Klinkovská[1], Anna Kuzemko[1,14], Bernd Lenzner[10], Harald Pauli[15,16], Marta Gaia Sperandii[1], Kris Verheyen[17], Manuela Winkler[15,16], all data contributors##, Franz Essl[10]*

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Aims: We introduce ReSurveyEurope – a new data source of resurveyed vegetation plots in Europe, compiled by a collaborative network of vegetation scientists. We describe the scope of this initiative, provide an overview of currently available data, governance, data contribution rules, and accessibility. In addition, we outline further steps, including potential research questions.

Results: ReSurveyEurope includes resurveyed vegetation plots from all habitats. Version 1.0 of ReSurveyEurope contains 283,725 observations (i.e. individual surveys of each plot) from 79,454 plots sampled in 442 independent resurvey projects included in 256 datasets. Of these, 62,404 (78%) are permanent plots, i.e. marked in situ, or located with GPS, which allow for high spatial accuracy in resurvey. The remaining 17,050 (22%) plots are from studies in which plots from the initial survey could not be exactly relocated. Four datasets, which together account for 28,470 (35%) plots, provide only presence/absence information on plant species, while the remaining 50,984 (65%) plots contain cover information (e.g. percentage cover or cover-abundance classes such as variants of the Braun-Blanquet scale). The oldest plots were

sampled in 1911 in the Swiss Alps, while most plots were sampled between 1950 and 2022.

Conclusions: ReSurveyEurope is a new resource to address a wide range of research questions on fine-scale changes in European vegetation. The initiative is devoted to an inclusive and transparent governance and data usage approach, based on slightly adapted rules of the well-established European Vegetation Archive (EVA). ReSurveyEurope data are ready for use, and proposals for analyses of the dataset can be submitted at any time to the coordinators. Still, further data contributions are highly welcome.

Val Karavaeva – P12

Comparative genomics of heme biosynthesis in prokaryotes

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Modified metallated tetrapyrroles are large macromolecular cycles that are essential to many biological processes, e.g. electron transfer and microbial energy conservation solutions. Central to these processes are hemes *b*, which are found across all domains of life. For a long time, it has been assumed that heme biosynthesis exists as a single conserved pathway in all organisms able to produce hemes. However, with time, additional pathways for heme biosynthesis came into light. Currently, there are three known heme biosynthesis pathways, named after the key intermediate compound before the formation of heme *b*.

Although the biosynthesis of hemes has been studied for over half a century, no large-scale analysis of distribution and evolution of different pathways has been conducted. In addition, the focus of research was placed predominantly on heme biosynthesis and acquisition within

eukaryotes or well-studied prokaryotes, leaving these pathways within the less studied and/or newly discovered prokaryotic lineages without resolution. With the advent of metagenomics and sequencing technology in the last decade, it became increasingly necessary to conduct genomic analyses on a large scale to obtain a fuller picture of the metagenomics-derived organismal diversity. This project intends to fill this gap by using methods of comparative genomics on metagenomic data to resolve the distribution, composition, and evolution of hemes biosynthesis pathways in prokaryotes. Here, we present the analysis of taxonomic distribution and composition of heme biosynthesis pathways across 35,000 prokaryotic assemblies. The data is presented in the c ontext of evolution.

Nicole Krause – P13

Stable chromosome configuration and loop-based polarization in animal symbionts

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Chromosome partitioning precedes the division of the cytoplasm, and its evolution is linked with the positioning of the division plane. So far, bacterial chromosome biology has heavily focused on transversally dividing, free-living ones. However, we determined the chromosome organization of three longitudinally dividing Neisseriaceae exclusively inhabiting the oral cavity of mammals. We showed that in all three multicellular bacteria the origin of DNA replication is invariably located at the host-attached (proximal) pole. Additionally, 3C-seq revealed loop-based folding of the *ori* region

in *Alysiella filiformis* and *Simonsiella muelleri*. Moreover, genes involved in cell motility, piliation and signal transduction mechanisms were specifically looped when transcriptionally and translationally active cells adhered to a substrate, but not when floating in liquid. Overall, we propose that proximal positioning of the *ori* and loop-based folding of its surrounding DNA may mediate localized translation of proteins involved in host colonization and thereby symbiotic bacteria.

Katharina Mason – P14

Small snails, big rocks and huge trees – a phylogenetic revision of the door snail Montenegrina (Mollusca: Gastropoda: Clausiliidae)

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Montenegrina is a hyper-diverse land snail genus that is specialised on limestone and has a very restricted distribution range in the western part of the Balkan Peninsula. As common in molluscs, the existing systematics of *Montenegrina* was established mainly based on conchological traits. To extensively revise the taxonomy, a comprehensive phylogenetic study based on three mitochondrial markers *cytochrome c oxidase subunit 1, 16S rRNA, 12S rRNA (COI, 16S, 12S)* was conducted. In the resulting tree, about half of the species and subspecies are monophyletic, but several remained paraphyletic. To gain better insight into the incongruencies, anatomical features like specific genital structures were analysed as well. Combining the results, some of the paraphylies could be reasonably resolved by

taxonomic changes by reassigning subspecies or raising them to species level. However, in other cases, also introgression even between distant clades could be the reason for the paraphylies. This integrative taxonomic approach led to a revised taxonomy of *Montenegrina* with 110 valid taxa, raising the number of species from 29 (conchologically based) to 69 species. As a next step, population genetic analysis based on newly established microsatellite markers will be performed, helping to get insights into population structure and testing for possible gene flow between selected populations.

Andrea Mrnjavac – P15

Slower X: theory and data

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Sex-linked and autosomal loci experience different selective pressures and demographic trajectories, leading to distinct evolutionary dynamics. Models of sex chromosome evolution typically assume that X (or Z) chromosomes are hemizygous in males, as Y (or W) chromosomes usually degenerate. However, in young non-recombining regions, Y chromosomes often have many functional genes, and many X-linked loci are therefore diploid. Here we provide the first theoretical model of diploid X loci with non-recombining but functional gametologs on the Y, and show that they exhibit Slower-X (Slower-Z) effect, that is, reduced efficiency of selection. This is in contrast with the Faster-X effect expected for hemizygous X loci. Furthermore, we provide the first empirical evidence of reduced efficacy of selection in a young non-recombining region of the *Schistosoma japonicum* Z chromosome, directly supporting the relevance of our Slower-X model for understanding early sex chromosome evolution.

Anastasiia Padalko – P16

Fusion/Fission Protein Families Identification in Archaea

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The majority of new archaeal lineages remain without a cultivated representative, but the scarce experimental data from the cultivated organisms shows they harbour distinct functional repertoire.

To unveil the ecological as well as evolutionary impact of Archaea from metagenomics we need a set of computational methods and in-depth analysis. The genome-wide fusion protein screening is meant to aid protein functional annotation. A fusion protein is defined as a protein consisting of two or more domain originally encoded by different genes. If the gene splits, then the process is called fission. Fusion identification is required for proper phylogenetic reconstruction and metabolic pathway completeness assessment. Functional mappings between fused and unfused proteins might partially fill the gaps in the metabolic models.

In the archaeal genome-wide screening we identified 1927 fusion/fission protein clusters in both new and well-studied lineages. The identified fusion/fission families belong to all types of metabolism, genetic and cellular processes. In our approach, several experimentally validated proteins known to have undergone fusion/fission events were also identified. However, more than a half of the protein families identified remains poorly characterised on either fused or unfused side.

To distinguish fusion from fission events, we implemented the assignment based on a combination of numeric and taxonomic

features. As a result, we retrieved more than 300 high-confidence fusion clusters with enrichment in energy metabolism and cofactor biosynthesis, while fissions prevailed in genetic information processing and central carbon metabolism. After bacterial mappings, out of the identified 1927 clusters, 8% of families turned out to be unique for archaea, corresponding to events that occurred at different depths of the archaeal tree.

John Lester Pide – P17

Intrinsic potential and activity of nitrate turnover examined for different hydrogeological aquifer settings

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Nitrate is one of the most serious contaminants in groundwater, frequently deteriorating water quality and its use as drinking water. However, nitrate can, at specific environmental conditions, be removed within the subsurface environment via natural biogeochemical processes, such as denitrification and dissimilatory nitrate reduction to ammonium (DNRA). Nitrate reduction mostly depends on two key factors, i.e. the prevalence of hypoxic or anoxic conditions and the availability of a suitable electron donor, be it organic or inorganic. For a long time, research concentrated mainly on the nitrate attenuation potential and activity in groundwater, ignoring the aquifers' sediment matrix. We hypothesize that the sedimentary deposits host the major potential for nitrate reduction, carrying the majority of microorganisms as well as different sources of electron donors. It is further assumed that the diverse hydrogeological settings harbor different sources and of varying amounts of electron donors. Microbial communities harboring the metabolic potential for nitrate

reduction are believed to be ubiquitously present. At locations where physicochemical conditions favor nitrate reduction, we may expect microbes involved in these processes to be more abundant and highly active, leading to a fast nitrate removal from groundwater. In repeated field campaigns, fresh sediments and groundwater were collected by drilling from shallow aquifers different in geological background and physico-chemical conditions. Subsequently, flow-through sediment column and batch experiments were carried out in a temperature-controlled climate room at 12°C, to mimic ambient groundwater temperature. Our goal is to understand the overall potential and in situ activity of nitrate removal in different shallow aquifers related to their nitrate load, redox conditions, hydrogeology, and microbial community characteristics.

Emily Pigott – P18

Re-assessing faunal and possible hominin remains from the Middle to Upper Palaeolithic sites of Crimea and beyond, using more recent protocols for radiocarbon dating and ZooMS

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The Crimean Peninsula contains numerous important archaeological Palaeolithic sites. It has been considered a potential Neanderthal refugium in Eurasia prior to their disappearance or assimilation, and subsequent replacement by Homo sapiens. This understanding is primarily drawn from lithic technological analysis and radiocarbon dating. However, recent developments in radiocarbon dating suggest that many of the previously obtained radiocarbon dates from Crimean sites may be too young. The chronological sequence from the site of Kabazi II is a case in point. Differences between dates of

bulk collagen, and those of single amino acids, range up to 10,000 radiocarbon years. These discrepancies are argued to arise from sample contamination and its lack of removal in bulk collagen dating. This project involves a critical re-evaluation of results from seven Palaeolithic archaeological sites in the Crimean Peninsula; Kabazi II, Siuren I, Buran-Kaya III, Zakalnaya V and Zakalnaya VI, Kabazi V and Starosele. Analysis of radiocarbon results from various sites, suggest that some radiocarbon dates may be too young, which has been indicated in the stratigraphy and lithic assemblages. The research project will involve innovative protocols in future chronometric work, such as hydroxyproline and XAD for radiocarbon dating, there is potential for constructing robust and accurate chronologies. Zooarchaeology by mass spectrometry (ZooMS) will also be conducted on unidentified fragmented remains, to give an overview of the palaeo-environment and possible recovery of hominin remains. In evaluation, improved dating accuracy and ZooMS holds the promise of significant additional insights into the prehistoric sequence of the Crimean Peninsula and its potential role as a refugium for Neanderthals, prior to their disappearance.

Christian Pruckner – P19

RESTORESEAS – Using microbes to protect and restore biodiversity

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Marine forests are ecosystems based on a key group of organisms consisting of kelp for-ests, seagrass meadows, or coral gardens. These organisms provide numerous ecosystem ser-vices and are the backbone of biodiversity-rich ecosystems. Losing these key organ-isms and the habitats they support leads to a significant

ecological tipping point, where ecosystems are irreversibly changed. Critical nursery, shelter, and feeding grounds for species that provide humans with food security would be in jeopardy. Additionally, it leads to the loss of numerous other crucial ecosystem functions, such as counteracting climate change through carbon sequestration.

The internationally funded project RESTORE-SEAS (Marine Forests of animals, plants. and algae: nature-based tools to protect and restore biodiversity) aims to assess large-scale suitabil-ity and needs for conservation and restoration of marine forests, including fore-casts for the future conditions. It also aims to test critical sizes for ecosystem stability and conditions and thresholds for tipping points. Another objective is to evaluate the significance of species and genetic diversity (integrating microbiomes) as well as func-tional diversity, including functional genetic diversity, and the diversity and role of pathogens. In addition, it aims to quantify the long-term outcomes of conservation and restoration approaches. To achieve this, efficient ecosystem function indicators based on de-scriptors of total biodiversity using eDNA of the water and sediment will be de-veloped. These approaches will be tested across diverse eco-systems, including deep coral gardens, seagrass meadows, algal forests, symbiont and pathogen communities, and distinct oceanic regions. The restoration of such marine habitats presents a signifi-cant challenge, and this pioneering initi-ative is anticipated to serve as a model for the global marine researcher community, not only by demonstrating the educational and upscaling potential of ecosocial approaches.

My task involves examining the compositional and functional diversity of the microbial community of the cold-water coral (CWC), *Desmophyllum pertusum,* as well as its potential use in restoration projects to boost the success of larval settlement and metamor-phosis. In situ characterization and in vitro screening of CWC

microbiomes will reveal the microbial composition and genetic makeup required for probiotics studies focused on inducing larval settlement in CWCs. This will pave the way for up-scale propagation and rearing of sexually derived colonies. Ultimately, artificial reef structures incorporat-ing reared colonies can be utilized to restore destroyed reef sites.

Aigerim Rymbekova – P20

A meta-analysis of ancient and present-day Central Eurasian genome data to revise ancestries from archaic hominins

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Central Eurasia is a region which experienced extensive migration from both Western and Eastern Eurasia throughout history and has been home to modern humans and the archaic hominins since at least the Late Pleistocene. Introgression from Neandertals and Denisovans has shaped the evolutionary history of Eurasian populations with selection and phenotypic traits. While European populations have been extensively studied, archaic introgression has not been addressed in previous studies on Central Eurasia. However, as East Asian populations carry introgressed variation from possibly several Denisovan-like lineages, Central Eurasian populations also carry ancestries from various sources and might expose a unique set of archaic variation.

Archaic ancestry represents a minor fraction of modern human genomes, hence reconstruction of the temporal landscape of archaic introgression in Central Eurasia requires multiple genomes sampled at different points in time. We used whole-genome sequencing data from present-day and ancient individuals from Central Eurasia to assess the variation in the individual genomes using a local ancestry inference tool, admixfrog, and inferred genomic regions in a "human-typical", "Neandertal-typical" or "Denisovan-typical" state. This allowed us to estimate the proportion of introgressed material from each archaic source along with genes and genetic variants inherited from archaic hominins during Bronze and Iron Age as well as in the present.

Inferring introgressed regions in Central Eurasians, and connecting the variation within these regions to potential phenotypic and disease outcomes is valuable to understand the impact and importance of such admixture in comparison to other populations from different parts of Eurasia.

Daniel Saavedra – P21

Multifunctional alkaline phosphatases drive the phosphorus cycle in the ocean

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Phosphorus, an essential nutrient, plays a crucial role in limiting productivity within marine ecosystems. To overcome this limitation, organisms use alkaline phosphatases (APases) to obtain phosphate from organic compounds. Although traditionally viewed as isoenzymes with specific roles, recent investigations have uncovered the multi-functional nature of one type of APase, the PhoA family. However, the prevalence of enzyme multi-functionality across all APase families remains unexplored, as does the determination of the dominant APases and the microbial taxa expressing them in the oceanic water column. In this study, we combined the generation of recombinant proteins, enzymatic kinetics assays, proteomics of a key marine bacterium, and bioinformatic quantification of global ocean gene expression and secretion pathways of the main APase families (PhoA, PhoD, PhoX and PafA). Our findings revealed that all major APase families are actively expressed in the global ocean and are dominated by *Alteromonas,* particularly in the deep ocean. We then obtained purified recombinant APases of *Alteromonas mediterranea* and tested their kinetic characteristics. We found that all APases without exception exhibited multi-functional activities, with different substrate affinities likely indicative of distinct ecological strategies. A proteomic experiment with *Alteromonas mediterranea* revealed which specific proteins were regulated under phosphorus-limitation. Collectively, our findings underscore the widespread relevance of APases utilization in the global ocean, revealing how microbes use a set of multi-functional alkaline phosphatase families to acquire phosphorus, while ultimately highlighting the role of multi-functional enzymes in marine biogeochemical cycles.

Luigi Schillaci – P22

Combined or alone, how are heavy metals more harmful to mosses?

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Increasing pollution in the environment calls for the precise determination of metal accumulation in plants as they are at the base of the food chain. Mosses are often employed as biomonitors for the presence of heavy metals in soil, air and water, and moreover provide good models for testing metal adsorption. However, combinations of metals and their subcellular accumulation over time are rarely studied.

In our case, we studied two different varieties of mosses, *Pohlia drummondii* and *Physcomitrium patens,* and analyzed in the presence of different heavy metals, $CuCl_2$, $MnCl_2$, $FeCl_2$, and Sbacetate, alone and in combination. We are interested how different moss species may react and performed growth studies in controlled conditions on solid agar contaminated with heavy metals. In addition, physiological analyses after immersion in a water solution containing heavy metals were done. Taking advantage of the high resolution at a synchrotron beamline, we are investigating the adsorption, localization and toxicity of various metals inside cells over time.

Brina Zagorc – P23

Integrating Multidisciplinary Methods to Investigate the Lives of Nonadults in Early Medieval Sites from North Eastern Croatia

Brina Zagorc[1,2], Magdalena Blanz[2,3], Anita Rapan Papeša[4], Hrvoje Vulić[4], Mario Novak[5], Andrea Rimpf[6], Zrinka Premužić[5], Mario Carić[5], Tajana Trbojević Vukičević[6], David Reich[7,8,9], Maria Ivanova Bieg[2,3], Pere Gelabert[1,2], Susanna Sawyer[1,2], Ron Pinhasi[1,2]

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This paper presents a comparative study of two Late Avar sites in North Eastern Croatia, Nuštar and Šarengrad Klopare, to gain insights into the lives of the nonadult populations. We utilize an interdisciplinary approach, combining paleogenetic, palaeodietary, osteological, and paleopathological methods to provide a comprehensive understanding of the upbringing and overall health of the nonadult population. In our study, 36 nonadults and adults from Nuštar and 18 nonadults from Šarengrad Klopare were analyzed for kinship and molecular sex using established ancient DNA pipelines and protocols. For stable isotope ratio analysis ($\delta^{13}C$ and $\delta^{15}N$), we analysed bone collagen from both sites using the same individuals as in the previous analyses, in addition to 10 animal bones from Nuštar as dietary references. Furthermore, to enhance our understanding of the dietary habits at the sites, we also included additional samples of adults, resulting in a total of 55 nonadults and adults from Nuštar and 86 nonadults and adults from Šarengrad Klopare.

Our findings shed light on questions of kinship, molecular sex, and diet, and provide a deeper understanding of the relationships between these factors and mortality rates, disease, and preferential sex-related treatment at the mentioned sites. The comparison between the two sites enhances our understanding of the time period and area, providing valuable insights into how populations lived, how they were impacted by external factors, and how they responded to these impacts.

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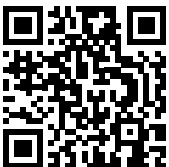|		
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