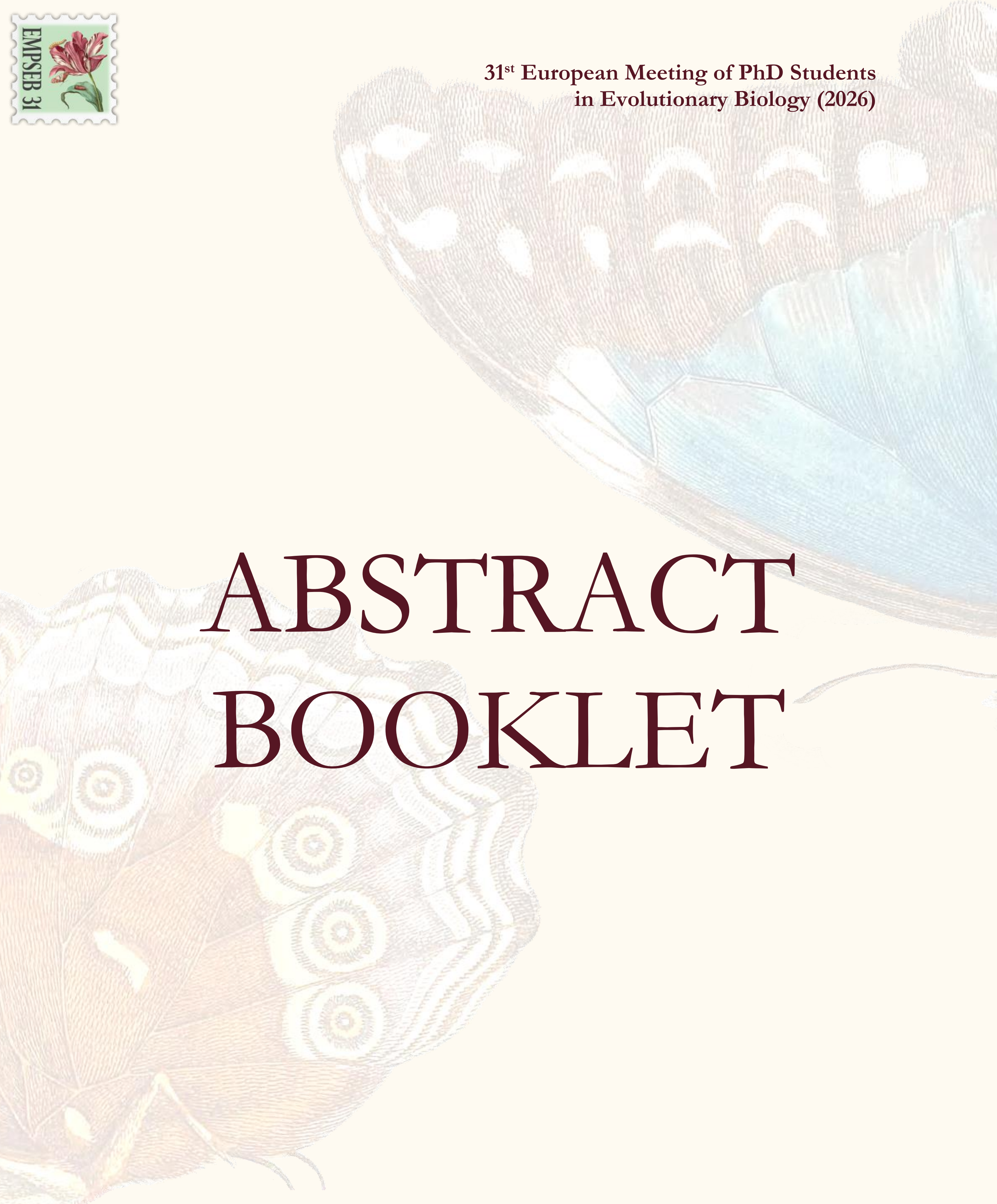
EMPSEB 31

31st European Meeting of PhD Students
in Evolutionary Biology (2026)



ABSTRACT BOOKLET

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31st European Meeting of PhD Students
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Session 1A – Genome Evolution and Structural Variation

10:15 – 10:30

Dennis Vlegels, *University of Cambridge, United Kingdom*

Initial evidence that pyrrolizidine alkaloids shape the mutational landscape of Ithomiine butterflies

Chromosomal rearrangements, such as fusions, fissions and inversions, play a key role in genome evolution and speciation. However, the mechanisms that generate karyotypic diversity are not well understood. The nymphalid butterfly tribe Ithomiini has exceptionally dynamic karyotypes, with chromosome numbers ranging from 5 to over 120 — far exceeding the typical range of 29–32 observed in butterflies and moths (order: Lepidoptera). Members of the Ithomiini tribe sequester pyrrolizidine alkaloids (PAs), which are plant-derived compounds used for chemical defence. Although PA foraging is restricted to adult males, substantial quantities are transferred to females via the spermatophore during mating, thereby exposing their reproductive tissues to these compounds. PAs are also potent genotoxins capable of inducing DNA damage, including characteristic base substitutions and chromosomal breaks. This raises the hypothesis that PA exposure contributes to genome instability in Ithomiini. To investigate this, we analysed mutational signatures in 100 chromosome-scale genomes from Ithomiini and Arctiini (tiger moths), which have evolved PA utilisation independently, as well as from non-PA-using Heliconii. We used heterozygous germline SNPs as a proxy for mutational processes. PA-using lineages showed consistent enrichment of PA-associated G:C ⟶ T:A transversions relative to non-PA-using lineages, with the strongest effects observed in genomic regions under weaker purifying selection. Principal component analyses revealed convergence in mutational signatures between PA-using Ithomiini and the phylogenetically distant Arctiini, suggesting the existence of shared nucleotide-level mutational processes associated with PA exposure. However, the Arctiini have relatively stable karyotypes, suggesting that they may have developed lineage-specific adaptations for detoxification or DNA repair to mitigate chromosomal damage. Together, these results provide initial evidence of a link between chemical ecology and genome-wide mutational processes, offering new insight into the origins of karyotypic evolution.

10:30 – 10:45

Diana Catherine Gonzalez, *Leibniz Institute for the Analysis of Biodiversity Change, Germany*

Genetic diversity and evolutionary dynamics of the germline-restricted chromosome and other maternally inherited elements in the zebra finch

Programmed DNA elimination, although rare across vertebrates, is widespread among *Passeriformes* (~6,700 species), where most species carry a germline-restricted chromosome (GRC) that is confined to reproductive tissues and absent in the soma. In the zebra finch (*Taeniopygia guttata*), the GRC is typically present as a single copy in males and removed during spermatogenesis, resulting in predominantly maternal inheritance. Females, in contrast, harbor two nearly identical copies, suggesting limited or no recombination, similar to the behavior of other female-specific elements such as the W chromosome. Despite its broad distribution and apparent biological importance, the evolutionary history of the GRC remains poorly resolved, especially when compared with traditional maternally inherited elements like mitochondrial DNA (mtDNA) and the W chromosome. Recent findings indicate that the zebra finch GRC shows exceptionally low genetic diversity and, in rare cases, can even be paternally inherited. In this study, I investigate the evolutionary dynamics of the GRC by analyzing not only SNP-level diversity but also structural variants and copy number variation across multiple captive zebra finch lineages. I further contrast phylogenetic and population genetic patterns of the GRC with those of the W chromosome and mtDNA to assess how processes such as Hill–Robertson interference might differentially shape these genomes. By integrating three largely maternally inherited elements within a comparative framework, this work sheds new light on the origins and maintenance of genetic variation in songbirds and on the forces influencing the long-term evolution of the GRC.

10:45 – 11:00

Ioannis Chrysostomakis, *Leibniz Institute for the Analysis of Biodiversity Change, Germany*
Long-read genome assemblies of museum samples

Museum collections worldwide contain thousands of specimens, many from species that are extinct, endangered, or otherwise inaccessible, making the collection of fresh material for genomic analyses difficult or impossible. In this project, we developed wet- and dry-lab techniques to analyze whole genome sequences from museum samples with unique traits, showcasing how museums can be leveraged to improve our understanding of the genetics of vulnerable and rare species using high-quality, long-read data. As part of broader efforts to sequence all life on earth, we explored the genomic potential of particularly interesting vertebrates from wet museum collections that cannot be sampled in the field.

We produced genome assemblies from PacBio long-read HiFi sequencing and performed comparative gene annotation to understand the genomic underpinnings of phenotypic diversity. As a case study, we sequenced a pair of recently diverged catfish species exhibiting a marine-to-freshwater transition. This analysis revealed how transposable elements and genome architecture can diverge in closely related species and accompany rapid adaptations in these systems. Our findings underscore both the potential and limitations of using museum samples compared to fresh specimens. This research not only delivers well-annotated reference genomes from museum collections but also offers a roadmap for unlocking their genomic potential, demonstrating that historical specimens can yield insights into evolutionary processes and biodiversity that would otherwise remain inaccessible.

11:00 – 11:15
Marzena Marszałek, *Jagiellonian University, Poland*
How yeast deals with harmful mutations: transcriptomic insight

Gene expression regulation is a major determinant of phenotypic variation and fitness. In natural populations, organisms experience environmental and genetic perturbations that challenge their cellular homeostasis. Because broad transcriptional responses can be metabolically costly and disruptive, selection may favor regulatory mechanisms that buffer the effects of a specific gene disruption. One such mechanism is genetic compensation: mutant mRNA degradation via nonsense-mediated decay (NMD) triggers upregulation of related genes or the wild-type allele in heterozygous mutations. Since NMD primarily targets transcripts carrying premature-termination codons – protein-truncating variants (PTVs), these mutations constitute natural substrates for genetic compensation. However, previous studies indicate that compensation may be gene-specific rather than universal, and its prevalence remains poorly understood.

To address this gap, we used population-level transcriptomic data for 282 natural *Saccharomyces cerevisiae* isolates to investigate the prevalence of NMD and genetic compensation in heterozygous PTVs. We screened heterozygous PTVs and employed allele-specific expression analysis. The NMD signal was assessed by examining the relative fraction of the defective allele, while potential compensatory responses were evaluated through differential gene expression analysis. We found NMD evidence acting on a subset of PTV-containing transcripts; however, we did not find widespread compensation. Instead, many genes harboring PTVs exhibited reduced overall expression. Because truncated protein may be cytotoxic, downregulation of PTV-bearing genes may represent an adaptive regulatory strategy. Alternatively, the observed PTVs may occur in genes of low importance and therefore are not strongly constrained by purifying selection, reducing the need for compensatory upregulation.

11:15 – 11:30

Paula Mora-Rojas, *University of Edinburgh, United Kingdom*

Here you see me, here you don't: genomic and transcriptomic insights into island colour polymorphism in *Oophaga pumilio*

Oophaga pumilio is a neotropical poison frog that exhibits extraordinary colour polymorphism, particularly within the Bocas del Toro archipelago of Panama, where island populations range from cryptic to aposematic phenotypes. This system provides a powerful natural framework for studying the evolutionary interplay between natural and sexual selection. Genomic investigation of these traits has been hindered by the absence of a high-quality reference genome, as amphibian genomes are typically large and repeat-rich. Previous short-read assembly of *O. pumilio* (~6.7 Gb; ~70% repetitive) is highly fragmented and likely incomplete, limiting downstream analyses. We generated a chromosome-level genome assembly from a single male individual using PacBio HiFi long-reads (12× haploid coverage) and Hi-C data for scaffolding. Assembly was performed with hifiasm in Hi-C mode, followed by the Omni-C pipeline, YaHS scaffolding, and manual curation. The final assembly spans 6.98 Gb across 10 chromosome-level scaffolds, with an N50 of 810.9 Mb and an L50 of four scaffolds, representing a substantial improvement in contiguity and completeness. Repeat content was estimated at 53.7%, and gene annotation using BRAKER3 and TOGA yielded a comprehensive set of gene models. Using this genomic resource, we analyse population structure and island colonisation history across six Bocas del Toro islands using low-coverage whole-genome sequencing. We integrate these data with RNA-seq analyses of skin from the same individuals to characterise expression differences associated with cryptic and aposematic colouration. Complementary transcriptomes from eye, brain, and liver tissues further enable investigation of colour perception and alkaloid metabolism pathways underlying antipredator strategies.

11:30 – 11:45

Suhaas Sehgal, *University of Lausanne, Switzerland*

A comparison of selection on autosomes and the young X chromosome in diploid *Mercurialis* species

The evolutionary dynamics of proto-X and Y chromosomes during early divergence—when most genes remain functional but recombination is suppressed—have been explored theoretically. A recent model (the "slow-X" hypothesis) predicted that genes on young X chromosomes should exhibit lower adaptive substitution rates than autosomal genes due to their smaller effective population size and the ‘masking’ of their gene products by their Y-linked allelic homologs in males, while they remain functional. Accordingly, young X-linked genes should tend to accumulate deleterious mutations faster than autosomal genes. We tested these predictions in the dioecious plant *Mercurialis annua* and its sister species *M. huetii*, for which we are assembling a haplotype-phased genome. These species have young sex chromosomes with a large non-recombining region on the Y, where most genes are still intact, allowing us to evaluate the slow-X hypothesis. Although autosomal and young X-linked genes show similar divergence between species, X-linked genes segregate a higher proportion of non-synonymous polymorphisms. Selection tests indicate lower adaptive potential on the X chromosomes, and the distribution of fitness effects is skewed toward deleterious mutations with few or no beneficial ones. Overall, these results support the predictions of the slow-X effect.

Session 1B – Adaptation and Urban Evolution

10:15 – 10:30

Fatima Jlil, *Aarhus University, Denmark*

The adaptation landscape of low-dispersive arthropods across time and space

Spatiotemporal signatures of selection reveal how the recolonisation of a habitat, in combination with contemporary population dynamics, shapes the adaptive landscape of a species, i.e. the spatiotemporal mosaic of selection. We investigated the adaptation landscape of six *Collembola* species across Denmark and identified a northward post-glacial recolonisation history that strongly influences the spatial distribution of adaptive signals. We found that a significant proportion of selective sweeps were due to shared ancestry rather than independent convergent evolution. These ancestral sweeps are broader than younger, population-specific sweeps, which supports the expectation of temporal changes in selection intensity. Depending on its level and population demography, patterns of gene flow can hinder or promote adaptation: while high gene flow can rescue small populations but prevent local adaptation, low gene flow may allow local adaptation but increase extinction risks in small populations. We identified varying levels of gene flow among species over the past ~4000 years, ranging from stable to decreasing or fully interrupted. We predict that these patterns will be reflected in the adaptation landscapes of different species. The patterns of selection identified in light of declining gene flow rates are consistent with different selection regimes acting during the early colonisation of Denmark following Pleistocene glaciations, as well as with current selection acting on increasingly isolated populations. Integrating genetic and demographic analyses suggests a decline in the adaptive potential of these soil-dwelling arthropods, likely driven by intensive land use and habitat fragmentation, which cause reductions in gene flow.

10:30 – 10:45

Nils Sternberg, *Leibniz Institute for the Analysis of Biodiversity Change, Germany*

Ecological niche differentiation drives distribution in cryptic Phoxinus species

Eurasian minnows of the genus *Phoxinus* (Leuciscidae) are a prominent case of cryptic diversity. This is evident between the genetically distinct yet morphologically similar *Phoxinus phoxinus* and *P. csikii* in Central Europe. The distribution ranges of the two species overlap in the Sieg system, a right-sided tributary of the Rhine River near Bonn (Germany). Despite the occurrence of a natural hybrid zone within the Sieg drainage, allopatric populations of both species were found to exist in geographically separated regions. While *P. csikii* inhabits the more mountainous regions, *P. phoxinus* is found in the foothill regions of the basin. We aimed at identifying factors related to these distribution patterns. Since environmental variation and species-specific niche preferences are key factors driving species distribution, we hypothesise that the geographical distribution of the two *Phoxinus* species within the Sieg basin might be driven by their ecology. Hence, we investigated each species' ecological niche, focussing on their dietary, trophic, and habitat ecology. The two species differed in niche breadth and habitat utilisation, showing distinct preferences for microhabitat conditions like flow velocity, depth and substrate composition across life stages. Both juvenile and adult *P. phoxinus* preferred a wider range of flow velocities and depths than their *P. csikii* equivalents. *P. phoxinus* also appeared to avoid habitats with higher cobble densities, habitats that were preferred by *P. csikii.* The suitability of preferred habitats was generally greater for *P. csikii*, indicating a more intense preferred habitat utilisation. Furthermore, we found substantial differences in dietary composition, feeding strategy, and trophic position. While *P. csikii* is a primary consumer, characterised by specialized feeding on Aufwuchs, *P. phoxinus* is a secondary consumer with a generalised feeding strategy, utilising a wide range of aquatic insects. Our findings demonstrate that the two *Phoxinus* species differ substantially in their ecological niche. In particular, species-specific habitat preferences could be a key factor driving the distribution of *P. csikii* and *P. phoxinus* in the Sieg basin.

10:45 – 11:00

Emily Ann Dovydaitis, *Martin-Luther-Universität Halle-Wittenberg, Germany*

Impacts of urbanization and agriculture on bumblebee genetic diversity

Populations rely on genetic diversity to adapt to environmental change and persist in the long-term. This includes adapting to changes brought about by human impacts. Understanding the extent to which population genetic processes are associated with environmental factors across species is a powerful way to examine the processes maintaining patterns of biodiversity. The field of macrogenetics addresses these types of questions by synthesizing publicly available data to study population genetics at broad spatial and taxonomic scales. Here we examine how land use, namely urbanization and agriculture, are associated with genetic diversity in bumblebees. Found mostly across the Northern Hemisphere, bumblebees thrive in areas with high floral diversity (e.g., grasslands and meadows). They are important pollinators of both wild plants and commercial crops. Although many species are generalist foragers, capable of adapting to life in farmlands or cities, their populations are declining. The loss of food plants and exposure to pesticides are common culprits for their decline.

We used a compilation of publicly archived microsatellite data consisting of 4620 individuals sampled across 243 populations and 14 species of bumblebee (Apidae: *Bombus*) to test whether human-driven landscape change consistently affected the genetic diversity of bumblebee populations. Overall, we detected no consistent relationships between land use metrics and genetic diversity using Bayesian hierarchical models. Instead, genetic diversity had variable relationships with land use predictors across species. Our results suggest that, rather than consistently reducing genetic diversity, genetic responses to urbanization and agriculture in bumblebees tend to be species-specific.

11:00 – 11:15

Ana Sofía Torres Lara, *University of Bremen, Germany*

Urban evolution of seasonal plasticity across latitudes in *Pieris napi* butterflies

Urbanization imposes novel environmental conditions that can drive adaptive responses in urban populations. While adaptation to urban environments has been documented across different taxa, most studies have considered a small number of cities, limiting our ability to assess whether evolutionary responses are consistent across geographic regions.

Urbanization can affect seasonal plasticity, a trait that organisms rely on to time their life cycles based on environmental cues. The urban heat island effect increases temperatures and can extend the growing season, while light pollution can alter perceived photoperiods. These factors may disrupt life cycles by affecting the timing of key developmental decisions, such as when to enter diapause during winter. Because natural photoperiod varies across latitudes, the impact of these urban stressors may also differ geographically, emphasizing the need for replicated studies across multiple cities and latitudinal gradients.

To address this, we collected wild female *Pieris napi* butterflies from ten cities at different latitudes across Europe and their rural counterparts. Offspring were reared in a common garden experiment under different photoperiod treatments to assess urban evolution of plasticity in development path (diapause or direct development). Preliminary analyses indicate large variation among urban–rural pairs in the frequency of diapause, with no clear latitudinal pattern. These results suggest that urban populations may respond to local conditions in different ways rather than exhibiting consistent parallel evolution across Europe. Our study highlights the importance of studying multiple cities across broad latitudinal ranges to better understand how urbanization shapes seasonal plasticity and evolutionary responses in natural populations.

11:15 – 11:30

Juho Kökkö, *University of Helsinki, Finland*

The dispersal ability of urban *Pieris napi* butterflies might not have evolved, but could still be distinct

Cityscapes are becoming an increasingly common environment worldwide. The differences between urban and rural areas are often stark, and many species have had to adapt to living in cities. One challenge that organisms face in urban environments is dispersal. Environmental factors such as habitat fragmentation, limited resources and extreme temperatures all affect the costs of dispersal, and these factors tend to be more pronounced in urban areas. While previous research suggests that these factors can cause evolutionary changes in dispersal, relatively little attention has been given to linking dispersal evolution specifically to urban environments. In our experiment, we attempt to detect the evolution of dispersal ability by comparing the offspring of *Pieris napi* butterflies from urban and rural areas around the Helsinki metropolitan area in Finland in a common garden experiment. We measured flight metabolic rates under different temperatures, as well as wing size, as proxies for dispersal ability. We did not detect any differences in metabolic rates between urban and rural populations. However, flight metabolic rates did correlate positively with measurement temperatures to a certain extent. Our results therefore suggest that urban evolution in *P. napi* dispersal ability may not have occurred, but that temperature likely plays a significant role in the butterfly’s dispersal success. Consequently, anthropogenic environmental temperature shifts, such as climate change and the urban heat island effect, may impact butterfly dispersal ability, even in the absence of an evolved urban response. Further analysis of wing size metrics will provide an additional perspective on the data.

11:30 – 11:45

Charlotte Andrew, *University of Cambridge, United Kingdom*

Regulation of pitcher fluid volume and properties in six ecologically distinct Bornean *Nepenthes* species

Nepenthes is a species-rich carnivorous plant genus with fluid-filled pitchers that predominantly capture and digest arthropod prey. Pitchers vary in morphology, diet, trapping mechanisms and lifespan across species. Their open fluid pools are susceptible to weather-dependent flooding and evaporation. We hypothesised that species more exposed to fluid level fluctuations and reliant on fluid-based prey capture would show stronger regulation of pitcher fluid volume and composition. In Bornean *Nepenthes* species with diverse traits and ecological strategies (*N. rafflesiana*, *N. hemsleyana*, *N. gracilis*, *N. ampullaria*, *N. albomarginata*, *N. bicalcarata*), we quantified natural fluid fluctuations and how prey capture efficiency depends on pitcher fluid level. We experimentally manipulated fluid volume and concentration and monitored pitchers’ regulatory responses over time. *Nepenthes* species differed in their fluid regulation and how fluid level affected capture performance. Prey capture in species with waxy inner walls and/or conical pitchers declined at high fluid levels, facilitating prey escape. Species with steep peristomes retained prey efficiently regardless of fluid level. All species re-secreted fluid after removal but at varying rates, and all except *N. bicalcarata* reduced excess volumes, likely by fluid absorption. Reduced need for fluid regulation may be associated with traits such as large, horizontal lids and sheltered habitats that buffer fluid fluctuations, or alternative nutrient sources (leaf litter in *N. ampullaria*; bat faeces in *N. hemsleyana*) that reduce reliance on active prey capture. Closely related species showed similar regulation abilities. This study highlights ecological diversity across *Nepenthes* and demonstrates how their capture mechanisms are shaped by environmental conditions.

Session 2A – Hybridization and Speciation

13:30 – 13:45

Emma Laval, *Aix-Marseille University, France and Masaryk University, Czech Republic*

Hybrid speciation in leuciscid species, or how much information is in the caudal fin?

Hybrid lineages provide a unique opportunity to uncover how genomes evolve during speciation. In French river systems, natural hybridisation occurs between two distantly related leuciscid fishes, *Parachondrostoma toxostoma* and *Telestes souffia*, which separated over 15 million years ago, yet still produce viable offspring. To explore how regulatory processes shape hybrid genomes, we performed a transcriptome-wide analysis of parental species and first-generation hybrids. RNA was isolated from caudal fin tissue and sequenced to quantify gene expression, identify regulatory divergence and determine patterns of expression inheritance. All individuals were raised in controlled mesocosms to minimise environmental variation.
Analysis of 14,809 orthologous genes revealed that the majority retained similar expression levels in hybrids and in the parental species, suggesting that regulatory stability plays a key role in hybrid viability. Nonetheless, a subset of genes showed strong parental bias, with expression favoring the *P. toxostoma* genome twice as often as the *T. souffia* genome. In addition, many genes exhibited either additive or transgressive expression, indicating that novel regulatory interactions arise immediately following hybridisation. Overall, our findings show that hybrid genomes are shaped by a balance between conserved regulatory mechanisms that ensure survival and novel expression patterns that may drive phenotypic diversification. We also demonstrate that sampling caudal fin tissue provides a non-lethal and efficient way to study genome-wide regulatory dynamics in freshwater fish hybrids.

13:45 – 14:00

Titouan Bouinier, *Collège de France, France*

Sex chromosome systems shape the evolution of reproductive isolation

Understanding the speciation process remains a central challenge in evolutionary ecology. Completed speciation usually involves an initial divergence, reinforcement processes and long-term co-existence of incipient species. A common approach to estimate the progress of speciation relies on measures of reproductive isolation driven by the accumulation of genetic and/or ecological barriers. Such an approach is especially relevant when studying sympatric speciation, where gene flow can occur throughout the speciation process without any geographical limitation. Differences in mating systems may influence the evolution of reproductive isolation between incipient species. Sex chromosomes (XY or ZW) are indeed assumed to play a peculiar role in the reduction of gene flow, notably because heterogametic hybrids tend to exhibit reduced fitness relative to their homogametic counterparts. The sex of the heterogametic individuals can differ depending on the clade, with males being heterogametic in *Drosophila* (XY) and females in *Lepidoptera* (ZW). Since females usually exert stronger mate preferences than males in most species, sex chromosome systems (XY or ZW) likely influence both pre- and post-zygotic barriers between species. To test the effect of sex-chromosome systems on the evolution of reproductive isolation between diverging species, we developed a mathematical model assuming two divergent populations, where females are the choosy sex and heterogametic hybrids are non-viable. Using series expansions, we simplified and solved the population equations to estimate differences in hybrid populations between XY and ZW systems. We then compared the level of hybridization that occurs under different levels of female choosiness.

14:00 – 14:15

Vitali Razumov, *University of Innsbruck, Germany*

Patterns of taxonomic change and hybrid genome evolution in the *Daphnia longispina* complex

Secondary contact and hybridization of diverged lineages can lead to various evolutionary outcomes, especially during periods of ecological disruption. The *Daphnia longispina* complex, occupying different ecological niches in peri-Alpine lakes, has faced substantial changes due to historical eutrophication and recent climate shifts, and serves as an ideal model to study the patterns and evolutionary consequences of hybridization. This project investigates the spatial and ecological factors influencing the distribution and genome evolution of the *Daphnia longispina* complex and their hybrids in peri-Alpine lakes. I assess whether hybridization has left a permanent mark on the genomes of these species after several decades of ecological change and identify mechanisms driving hybrid genome evolution. For this, I collected *Daphnia* samples along with measurements of abiotic and biotic factors from 43 peri-Alpine lakes. Together with historical data, I analyse ecological data to assess past and present environmental variation across these lakes. From the collected samples, I generated whole-genome resequencing data for >20 individuals per lake. Using these data, I identify the current taxonomic composition and genomic regions affected by hybridization to better understand the drivers and repeatability of hybrid genome evolution. This project sheds light on environmental and spatial factors shaping hybridization and genome evolution, setting the stage for investigating the eco-evolutionary consequences of hybridization. By integrating genomic data with environmental and historical variables, I contribute to our understanding of the dynamics of ecological change and hybridization and inform conservation strategies for aquatic ecosystems.

14:15 – 14:30

Nikita Tikhomirov, *VIB-UGent Center for Plant Systems Biology, Belgium*

Genomics of adaptation in the largest aquatic plant genus on Earth

Adaptation implies preferential survival of certain genotypes in an environment. The environment and individual phenotypes vary across time and space; therefore, different means of adaptation may be available for each group of organisms. Exploring the continuum of adaptations available under varying environments and phenotypes encourages population genomic research across the tree of life. We advance this research by studying genomic diversity in *Potamogeton*, an aquatic monocot genus with ~80 species found on all five continents in fresh waters of varying chemistry. Roughly half of these species are polyploids, providing an opportunity to study polyploidy both as a means of adaptation and as a condition that itself requires adaptation.
We assembled five reference genomes of the Potamogetonaceae family and described the history of polyploidization in the genus. All *Potamogeton* polyploids arose through whole-genome hybridization rather than duplication, with most species descending from a shared polyploidization event ~8 Mya. This set of reference genomes is used to analyse short-read data from ~500 herbarium samples across most *Potamogeton* species, leveraging patterns of diversity and divergence to identify signatures of natural selection. Our work provides valuable data for a globally widespread group of aquatic plants and contributes robust methods for analysing population genomic data across ploidy levels.

14:30 – 14:45

Temitope Oriowo, *Leibniz Institute for the Analysis of Biodiversity Change, Germany*

Hybridisation and sex chromosome turnover drive divergence in Phoxinus

The minnow genus *Phoxinus* (family Leuciscidae) is widespread across Eurasia and occupies various freshwater habitats. Although it was once considered monotypic (*P. phoxinus*), the genus has undergone taxonomic revision. It now includes at least 25 valid species, many of which are morphologically cryptic and can mainly be identified through DNA barcoding. This complex evolutionary history, along with the ecological diversity within the genus, makes *Phoxinus* an excellent model for studying how historical processes influence divergence and hybridization in freshwater fish. This study explores species relationships, patterns of genomic admixture, and variation in sex determination in European *Phoxinus* populations, especially those from the Rhine drainage. Whole-genome and mitochondrial data identify four distinct species, each with clear geographic structure and different levels of intraspecific diversity. In the Rhine system, we found a hybrid zone between *P. csikii* and *P. phoxinus*, likely formed after post-glacial secondary contact. Nuclear genomic data (i.e., SNPs) show a strong admixture gradient from upstream to downstream, with *P. csikii* ancestry dominating upstream and *P. phoxinus* increasing downstream. Yet mitochondrial haplotypes often contradict nuclear ancestry, suggesting female-biased *P. csikii* colonization in the Middle Rhine, followed by *P. phoxinus* introgression in the Lower Rhine. Moreover, differences in sex-determination systems between the two species suggest that sex chromosome turnover may contribute to mito-nuclear discordance and help sustain reproductive isolation despite ongoing gene flow. Our analyses show homomorphic sex chromosomes in both species, with no significant sex-biased coverage differences. In *P. phoxinus*, male-specific heterozygosity uncovers two sex-linked regions on chromosomes 3 and 12. Population-specific patterns point to an XX/XY sex determination system and geographic variation in sex determination. Conversely, females of *P. csikii* display sex-linked signals on chromosome 3, consistent with a ZZ/ZW system. Male-specific sequences in *P. phoxinus* and female-specific sequences in *P. csikii* confirm the existence of distinct sex-specific genomic regions. Overall, these findings highlight the *Phoxinus* genus as a natural model for studying divergence with gene flow, where hybridization, colonization history, and sex chromosome evolution collectively influence speciation processes.

Session 2B – Sexual Selection and Reproductive Evolution

13:30 – 13:45

Agnes Szwarczynska, *Imperial College London, United Kingdom*

Do early birds catch a worm?

In seasonal breeders such as birds, late-season reproduction in temperate regions often results in smaller clutches and reduced offspring survival, primarily due to declining environmental conditions. While the fitness consequences of reproductive timing are well documented, its association with the gut microbiota—an important determinant of health and fitness—remains underexplored. Addressing this gap is increasingly important, as climate change is expected to shift breeding phenology and expose more birds to unfavourable conditions. Climate-driven phenological mismatches may alter prey availability, potentially affecting host diet and associated microbial communities. To assess whether seasonal shifts in environmental conditions shape gut microbiota, I studied wild blue tits (*Cyanistes caeruleus*), a species with a time-sensitive dependence on Lepidoptera larvae, across the breeding season. I used cloacal swabs as proxies for gut microbiota from early- and late-breeding females and their chicks. Contrary to my predictions, microbial alpha diversity and community composition did not vary with breeding phenology in females. In chicks, however, gut microbiota composition shifted over the season toward communities characterised by fewer rare taxa and a higher prevalence of taxa from the Enterobacterales order. These findings suggest that phenological effects in females may be overshadowed by inter-individual variation or differences in habitat quality. In contrast, hatching time influences gut microbiota in chicks. Further work is needed to link these changes to microbial functional roles and to test causal relationships with host health.

13:45 – 14:00

Yi Sun, *Johannes Gutenberg University Mainz, Germany*

Why do young females copy mate choice of old ones, despite males displaying honest signals?

Mate copying is a common mating strategy among females of lekking species. This is a surprising observation, as the time males spend displaying on the lek already provides females with an easily recognizable signal of male stamina, which is itself likely to be an honest indicator of genetic quality. In a well-studied lekking population—the black grouse (*Lyrurus tetrix*) of Finland—copying is most frequent among young females, suggesting that older females possess valuable social information that younger ones do not. We investigate whether this pattern could stem from fidelity to previous mates, a factor that at first glance complicates information gathering. Females mating with the same male across years raises the intriguing possibility that older females have information about male quality, as continued presence may signal the carriage of advantageous viability alleles. Here, I present an individual-based model that explores whether recognition of males across years can lead to the evolution of age-specific mate copying, particularly when across-year male presence covaries with lek attendance stamina within a season. By systematically varying factors such as male and female lek fidelity and the covariance between within- and between-season male presence, I demonstrate the conditions under which such an evolutionary response is most likely, as well as those under which mate copying should not be expected. While model development is ongoing, I predict a priori that high lek fidelity should favor beneficial copying early in life, but that these benefits will gradually erode as females accumulate social information, leading to age-specific mating strategies”.

14:00 – 14:15

Eva Adina Baumgarten, *Johannes Gutenberg University Mainz, Germany*

Evolution of sex-specific gene expression and regulation in a haplodiploid pollinator

Distinct sexes are found in many organisms and can exhibit differences in a range of traits, including morphological, behavioural, physiological, as well as patterns of gene expression. These differences are especially pronounced in haplodiploid organisms, in which females and males differ in ploidy, creating fundamental contrasts in genome architecture and gene expression landscapes. However, our understanding of whether ploidy leads to differences in gene expression and regulation, as well as the relative strength of evolutionary processes, remains fragmented in haplodiploids. First, using mason bees (*Osmia* spp.), we employ long- and short-read transcriptomics to characterise differences in gene expression amplitude and splicing between the sexes. Second, by combining transcriptomic data with whole-genome sequencing, we assess whether splice variants arise from evolutionary processes such as selection or drift, and how they contribute to sex-biased expression. Collectively, our study will shed light on the evolution and expression of transcript isoform diversity in an ecologically important group of haplodiploid pollinators. Furthermore, it will improve our understanding of how gene expression patterns diverge between sexes with differing ploidy, and how conserved these patterns are across species. These findings highlight the role of gene expression and regulation as a potential substrate of evolutionary change and provide insight into how sex-specific pressures, selection, and drift interact to shape haplodiploid systems.

14:15 – 14:30

Giulia Lin, *ETH Zürich, Switzerland*

Is there one haplotype to rule them all? Mitochondrial Patterns in a Sexual-Asexual Species

Potamopyrgus antipodarum is a model system used to study the "queen of problems" in evolutionary biology: the maintenance of sexual reproduction. This species exhibits two distinct reproductive strategies: diploid individuals reproduce sexually, while triploids reproduce asexually via apomixis. A previous study (Paczesniak et al. 2013) reported mitonuclear discordance among *P. antipodarum* populations from different lakes in New Zealand, identifying a mitochondrial haplotype (1A) strongly associated with asexual, triploid snails across multiple lakes. We set out to collect a large sample of wild snails, focusing particularly on populations in the South Island of New Zealand, with the aim of extending the previous dataset and increasing representation of sexual populations. We collected snails from 47 lakes across the South Island (N > 10,000). This dataset is the largest and most geographically representative to date for this species and, combined with advanced sequencing technologies targeting nearly the entire mitochondrial genome, enables in-depth analyses addressing the following questions: i) What is the geographical distribution of mitochondrial lineages, and how does it relate to nuclear genetic structure? ii) Is the previously observed association between haplotype 1A and asexuality supported at this broader scale? iii) Are there additional mitochondrial markers strongly associated with reproductive mode? By integrating large-scale field sampling with advanced genomic tools, we aim to shed light on the genetic and ecological factors contributing to the emergence and spread of asexual lineages in *P. antipodarum*.

14:30 – 14:45

Tomáš Pavlica, *Institute of Animal Physiology and Genetics, Libchov, Czech Republic*

When you don't give a damn: unprecedented degree of inter-individual karyotype variability and sex chromosome evolution in banjo catfish *Bunocephalus aloikae*

The Neotropical region represents the world's largest freshwater ichthyofauna (>6,200 species). Yet, this biodiversity is likely underestimated due to the existence of cryptic (morphologically indistinguishable) species revealed by molecular and cytogenetic methods. Neotropical fishes also exhibit a remarkable variety of sex chromosome systems with both male and female heterogamety, including standard and derived systems with varying degrees of differentiation. These features make Neotropical fishes, such as the genus *Bunocephalus*, excellent models for studying chromosome-related evolutionary questions. *Bunocephalus* includes cryptic species, and previous studies have identified significant inter-population differences in diploid numbers (2n) and suggested an X1X1X2X2/X1Y1X2Y2 sex chromosome system for *B. coracoideus*. Here, we analysed chromosomes of eight males and six females of *B. aloikae* using molecular cytogenetics through hybridization of whole-genome, whole-chromosome, and repetitive DNA probes. Phylogenetic analyses placed the studied individuals within the same clade, yet we uncovered striking intraspecific karyotype diversity, similar to that observed in the closely related *B. coracoideus*. None of the individuals shared identical karyotype traits, differing in 2n (47–51), synteny block organization, presence of multivalents during meiosis, and heterochromatic male-linked supernumerary (B) chromosomes. These observations imply multiple independent translocations, centric fusions, and fissions occurring at varying degrees among individuals. Comparative genomic hybridization further suggested the possible existence of multiple sex chromosomes forming a tetravalent during meiosis, although this scenario requires further investigation. These results highlight *Bunocephalus* as a promising model for studying tolerance to large-scale genome rearrangements and the role of chromosomal changes in reproductive isolation.

Session 3A – Host-Microbe Interactions and Immune Evolution

16:15 – 16:30

Debapriya Dari, *Indian Institute of Science Education and Research, Mohali, India*

Ecological implications of bacterial co-infection in a model insect host (*Drosophila melanogaster*)

Hosts and pathogens exist within complex ecological communities; therefore, co-infections—where a single host is simultaneously infected by multiple pathogens—are common in the wild. Previous research shows that co-infections elicit distinct immunological and physiological host responses compared to single infections. The ecological consequences of co-infection, and their effects on host fitness, are therefore expected to differ from those of single infections. However, this idea remains empirically underexplored, as most studies have focused primarily on immunological processes. Using fruit flies (*Drosophila melanogaster*) and their bacterial pathogens (*Enterococcus faecalis* and *Pseudomonas entomophila*), we examine whether co-infection affects host survival and reproduction, susceptibility to abiotic stressors, and other ecologically relevant traits in ways that differ from single infection. We first measured post-infection lifespan of females and males—either fed ad libitum or starved—that were infected (via septic injury) individually with each bacterium or co-infected, alongside uninfected and sham-infected controls.

We find that co-infection consistently and significantly increases mortality rates compared with both single-infection treatments. However, the effects of infection—both single and co-infection—are sex- and nutrition-specific. Females with ad libitum nutrition exhibit reductions in both median and maximum lifespan. Starved females and males from both nutritional treatments exhibit reductions in median lifespan only. Starvation increases overall mortality, but this effect is least pronounced in co-infected flies, as mortality is already high under ad libitum conditions. We are further exploring whether co-infection affects host (a) susceptibility to cold stress, (b) locomotor activity, and (c) reproductive output differently than single infection.

16:30 – 16:45

Théo Ulve, *University of Poitiers, France*

A virus feminizes carriers in a pill bug

Maternally transmitted endosymbionts can manipulate host reproduction in different ways, including cytoplasmic incompatibility, male killing, and feminization of carriers. Feminization is particularly striking because the symbiont can act as a new sex determinant, potentially replacing feminizing sex chromosomes (X or W) and causing strong sex-ratio biases. To date, only a few feminizing symbionts are known: two bacteria (*Wolbachia* and *Cardinium*) and some microsporids, which infect arthropods, especially crustaceans. In terrestrial isopods (commonly known as pill bugs), feminizing *Wolbachia* strains infect many species and induce female-biased sex ratios. Lineages lacking *Wolbachia* have their sex determined by Mendelian chromosomes and therefore produce balanced sex ratios. In the pill bug *Armadillidium arcangelii*, females collected from several populations produce strongly biased sex ratios. Identification of sex chromosomes revealed that all individuals in these populations were genetically male. However, total DNA sequencing of ovaries did not detect any microbial agent capable of inducing feminization. Through a combination of crossing experiments and RNA sequencing, we found that sex-ratio biases are caused by an RNA virus whose genome comprises four genes. This virus is specific to females of a single matriline, indicating a unique acquisition event followed by strict maternal transmission of a de facto feminizing virus.

16:45 - 17:00

Tereza Anna Javůrková, *Landscape Research Institute, Průhonice, Czech Republic*

Pathogen-driven selection in Alnus glutinosa: assessing resistance to Phytophthora × alni

The hybrid pathogen *Phytophthora* × *alni* has caused a severe decline of *Alnus glutinosa* in many European riparian ecosystems. This situation creates strong selection pressure on natural alder populations and raises questions about their adaptive potential. The presented research builds on newly bred alder genotypes that are expected to exhibit increased resistance to the pathogen. The main objective is to determine and verify the level of resistance in these genotypes. Resistance is assessed through controlled inoculation experiments conducted both in vivo and in vitro. Physiological and biochemical defence responses will be analysed. In parallel, micropropagation protocols are being optimised to enable stable multiplication of selected genotypes for further testing and potential restoration use. This approach allows evaluation of resistance stability while maintaining genetic variability. From an evolutionary perspective, this study contributes to understanding how pathogen-driven selection influences long-lived tree species and how adaptive variation can be identified and supported in breeding and conservation programmes aimed at restoring degraded riparian habitats. This research is financed from the state budget by the Technology Agency of the Czech Republic and the Ministry of the Environment of the Czech Republic within the "Prostedí pro život" ("Environment for Life") Programme, project SS02030018 Center for Landscape and Biodiversity (DivLand) and by institutional support VUK-IP-00027073 for the long-term conceptual development of the research organization.

17:00 - 17:15

Shivali, *University of South Bohemia, Czech Republic*

Exploring microbial and functional adaptations in termitophilous beetles within microbe-termite-termitophile tripartite symbiotic system

Social insects often acquire gut microbial symbionts from the environment or other species during interspecific interactions. Such horizontal microbial transfer can drive rapid adaptation to new diets or habitats. Termites are among the most striking examples of the critical role that insect gut microbiomes play in adaptation to specific dietary niches. A diverse range of arthropods live with termites, forming a variety of symbiotic relationships. The obligate inhabitants of termite nests are called termitophiles; among them, rove beetles (Aleocharinae) represent the most diverse and abundant group. These beetles have independently transitioned from a free-living to a termitophilous lifestyle multiple times. The cohabitation of termites and termitophilous beetles raises the possibility of gut microbial exchange between them, a question that has not yet been systematically addressed.

In this project, I explore microbiome composition across a globally sampled Illumina short-read dataset of termitophilous beetles and their termite hosts. Using a metagenomics pipeline, I generate bins representing distinct microbial taxa. Preliminary data suggest that, aside from abundant intracellular bacteria (*Wolbachia*), the guts of some termitophilous beetles host members of the Enterobacteriaceae and Oxalobacteraceae families. Additionally, I investigate gut functional adaptations in termitophilous beetles using a comparative morphological approach based on X-ray microtomography. Assuming that termitophilous beetles share similar diets and gut microbiomes with their hosts, their gut structure may have evolved convergently to resemble that of termites rather than that of free-living beetles. To test this, I am constructing 3D models of beetle guts to compare termitophilous species with their free-living relatives.

17:15 - 17:30

Maxence Remérand, *Université Paris-Saclay, France*

Plant-plant-pathogen interactions in heterogeneous fields: complementary approaches of modelling and field experimentation on wheat cultivar mixtures

Varietal mixtures represent an important but underused agronomic tool for increasing and stabilizing yield, particularly under reduced pesticide use. Such mixtures are known to improve disease control through both ecophysiological and epidemiological processes. However, the impact of diseases on plant–plant competition, and conversely the influence of this competition on pathogen virulence evolution, remain poorly studied from both modelling and experimental perspectives. We coupled a Lotka–Volterra model of plant growth and competition with an S(E)IR epidemiological model to explore disease dynamics in heterogeneous fields with competing plants. This approach allowed us to identify regions of parameter space that enable effective control of disease progression. In parallel, we conducted a field experiment over two years using four wheat varieties differing in disease resistance and competitive ability. Each cultivar was grown under fungicide-treated and untreated conditions, both in monocultures and in binary mixtures. We analysed yield and disease severity in mixtures versus monocultures and applied a biodiversity–ecosystem functioning framework to partition yield into selection and plasticity components, highlighting the role of disease in shaping varietal competition. By combining modelling and empirical approaches, we demonstrate how a better understanding of plant–plant–pathogen interactions can inform more effective deployment of varietal mixtures for sustainable disease control.

17:30 - 17:45
Leopold Preuß, *Martin-Luther-Universität Halle-Wittenberg, Germany*
Of Bees and BOOMs – The evolution of a nutritional mutualism between *Wolbachia* and solitary bees

The intracellular endosymbiont *Wolbachia* is found in approximately 40% of arthropod species. It often acts as a reproductive parasite, exerting negative fitness effects on its host, although it can be beneficial in certain host species. A recent analysis of more than 200 *Wolbachia* genomes revealed the presence of a biotin synthesis operon (BOOM) in 14 strains from different insect hosts. Strikingly, eight of these strains were symbionts of solitary bees. Although solitary bees are a diverse and ecologically important group of insects, the role and evolution of biotin (vitamin B7) supplementation by *Wolbachia* in bees remains enigmatic. The aim of this study is to investigate the distribution and evolutionary history of BOOM in order to elucidate the potential function of *Wolbachia* in solitary bees. A screen of over 150 bee species revealed BOOM to be present in 23% of cases. Phylogenetic analysis of newly sequenced *Wolbachia* genomes showed that two distinct clades of the BOOM exist in bee-associated *Wolbachia*. Finally, bacteriophages were identified as likely mechanisms for the lateral transfer of BOOM genes between *Wolbachia* strains. Altogether, these findings indicate a dynamic evolutionary history of an intricate association between solitary bees and *Wolbachia*, suggesting a potential role as a nutritional mutualist.

Session 3B – Evolutionary Theory and Modelling I

16:15 - 16:30
Akanksha Singh, *Max Planck Institute for Evolutionary Biology, Plön, Germany*
Fixation probability on metapopulations with asymmetric migration

A metapopulation consists of a group of subpopulations connected through migration. Classical results show that mutants have identical fixation probabilities in metapopulations where migrant inflow is exactly balanced by migrant outflow for every deme; such structures are known as circulations. However, real populations are unlikely to conform to perfect circulations. In this study, we systematically introduce asymmetric migration patterns into metapopulation structures and investigate their effects on fixation probabilities. We find that both the degree distribution of the metapopulation network and the magnitude of migration asymmetry influence fixation probabilities in multiple ways, most notably through the emergence of suppressors of selection (SoS) and amplifiers of selection (AoS). SoS increase the fixation probability of deleterious mutants and decrease that of beneficial mutants, whereas AoS have the opposite effect relative to circulations. In degree-homogeneous metapopulation structures, migration asymmetry typically generates SoS. In contrast, introducing low levels of asymmetry in degree-heterogeneous structures produces SoS and AoS in roughly equal proportions. Increasing migration asymmetry generally raises the likelihood of generating SoS. The strongest AoS arise when migration is biased toward high-degree demes, whereas the strongest SoS occur when migration is biased toward low-degree demes. These findings highlight the importance of population structure and migration asymmetry in shaping fixation probabilities and have implications for experimental design and conservation strategies.

16:30 - 16:45
Suzie Tallon, *Université de Montpellier, France*
Sex chromosome recombination suppression: articulating sex-antagonistic and regulatory theories

Recombination arrest between sex chromosomes is a central step in their differentiation and subsequent degeneration. The classical sexually antagonistic (SA) theory proposes that loci with opposite fitness effects in males and females favor the suppression of recombination around the sex-determining locus. More recent theoretical work has suggested an alternative mechanism in which recombination arrest and degeneration arise from the coevolution of gene expression regulators, with dosage compensation stabilizing Y-linked inversions. Using theoretical modelling, we re-examine the contribution of sexually

antagonistic loci to the maintenance of recombination suppression, in the presence or absence of regulatory variation. We first focus on inversions carrying a single SA locus and explore their dynamics across a range of conditions, including the position of the SA locus along the chromosome, population size, rates of recombination reversion, and the average effect of deleterious mutations.
We find that, in the absence of regulatory variation, recombination suppression driven by a single SA locus is temporary. In all tested scenarios, reversions restoring recombination are eventually favored, preventing the long-term maintenance of recombination suppression. This pattern remains robust across parameter values. In the presence of regulatory evolution, however, SA selection accelerates recombination arrest by increasing the fitness advantage of inversions. We also investigate more complex scenarios in which regulatory evolution is limited or involves buffering effects, as well as cases with multiple SA loci. These results show that sexually antagonistic selection alone is generally insufficient to ensure durable recombination arrest and help clarify the processes required to explain the evolution and persistence of recombination suppression.

16:45 - 17:00

István Oszoli, *Eötvös Loránd Tudományegyetem, Hungary*

Investigating the stability of positive pairwise interactions in a lattice-based modell

Eukaryogenesis can be divided into two major phases based on the number of participating species in a syntrophic interaction. We hypothesize that eukaryotes emerged from two species with strong metabolic cross-dependency within a biofilm. In the early stages of eukaryogenesis, positive pairwise interactions must arise within a multispecies syntrophic community. In later stages, a stable positive interaction between two prokaryotic species has already formed, which must persist despite competition from non-cooperative (null) mutants. We investigated two scenarios using a two-dimensional lattice model: cross-feeding and cross-facilitation. In the cross-feeding scenario, cells produce a metabolite that inhibits their own growth but increases the fitness of the partner type. In the cross-facilitation scenario, cells secrete enzymes that persist in the environment for a limited time and promote the growth of both types. The model includes six types: A, B, A*, B*, an enzyme producer, and its corresponding null mutant. Our main question is under which conditions pairwise interactions remain resistant to invasion by mutant types. Our results show that types A and B can coexist in a diffuse spatial pattern across the lattice. However, following the emergence of mutants, the A* and B* types consistently outcompete the cooperative types. In future work, we plan to incorporate gene loss and gain to investigate the effects of horizontal gene transfer (HGT) and the Black Queen hypothesis. We also aim to include negative interactions (e.g., antibiotic production) to better understand their impact on the stability of cooperative interactions.

17:00 – 17:15

Mona Huguenin, *Stockholm University, Sweden*

Effects of reference genome divergence on phylogenetic and population genomic inference

The reference genome forms the backbone of many evolutionary analyses, but its choice can strongly influence genomic inferences through reference bias. Reference bias arises because reads more similar to the reference genome are more likely to map successfully than reads carrying alternative alleles. Although several studies have quantified reference bias, its magnitude and direction vary across datasets and study systems. Here, we investigate how reference genome divergence affects population genomic inferences in the bird genus *Pachycephala*, a rapidly diversifying clade representing one of the most geographically widespread and complex avian radiations in the Indo-Pacific region. Using a whole-genome resequencing dataset, we aligned reads to multiple reference genomes, including *Pachycephala* references and increasingly divergent outgroup genomes. For each reference, we generated independent variant callsets and inferred phylogenetic relationships, alongside population genomic statistics (e.g., FST, DXY, π, Ne) and reticulation metrics used to detect hybridization and introgression. By repeating these analyses across reference genomes of increasing divergence, we assess how reference bias affects phylogenetic inference, population genomic statistics, and the detection of reticulation. Our results highlight the importance of careful reference genome selection for robust genomic inference.

17:15 - 17:30

Florian Robert Schmidt, *Swedish Museum of Natural History, Sweden*

Understanding the impact of bottlenecks on time-calibrated trees using simulated data

Estimating divergence times has traditionally relied on coalescent-based phylogenies, particularly when fossil records are unavailable. These approaches typically assume neutral models and demographic stability within the clade. However, population bottlenecks—such as those caused by founder effects during island colonization—can substantially alter genetic diversity and bias divergence time estimates. Overestimating island colonization events may therefore lead to incorrect biogeographic inferences. We simulated demographic scenarios to investigate the effects of founder events associated with island dispersal, both with and without selection, and compared these to neutral scenarios. To provide an alternative to classical estimation approaches, we introduce a methodology based on ancestral recombination graphs (ARGs) to infer divergence times.
By analysing deep branch lengths in simulated datasets, we quantified the extent to which bottleneck events distort time-calibrated phylogenies. Our results demonstrate that phylogenetic methods based on standard neutral coalescent models tend to underestimate the impact of founder effects. These findings highlight the need to account for demographic history when inferring divergence times and provide a framework for improving the accuracy of phylogenetic and biogeographic analyses.

17:30 - 17:45

Kathryn Bullough, *University of Exeter, United Kingdom*

Weber's Law of proportional processing influences the coevolution of ornaments and preferences in models of sexual selection

Mating preferences are often influenced by the magnitude of sexual signals, which indicate signaller quality. While these signals are often assumed to be perceived linearly by receivers, increasing evidence suggests that stimulus perception may be shaped by nonlinear perceptual adaptations and constraints. One example is proportional processing (Weber's Law), where discrimination between signals depends on their proportional rather than absolute differences. Weber's Law has the potential to fundamentally alter sexual selection by changing the evolutionary dynamics between male traits and female preferences, potentially driving signal limitation, exaggeration, or diversification—an issue that has been debated for decades. Here, I explore the evolutionary outcomes of incorporating Weber's Law into long-term sexual selection using individual-based models. The results show that including Weber's Law affects the coevolution of male ornaments and female preferences. Depending on the costs of female choice, this can lead either to reduced signal exaggeration or to increased exaggeration and diversification of both traits and preferences. These findings highlight the importance of incorporating female perception and cognitive processing into models of sexual selection to better predict the evolutionary dynamics of traits and preferences.

Session 4A – Evolution during Climate Change and Environmental Stress

13:30 – 13:45

Aindrila Das, *Indian Institute of Science Education and Research, Mohali, India*

Do reproductive traits and thermal fertility limits evolve in *Drosophila melanogaster* populations selected for resistance to extreme thermal stress?

Global warming and increasing temperature extremes threaten tropical ectotherms living near their upper thermal limits, making them especially vulnerable to climate change. Temperature strongly influences both survival and reproduction in ectotherms. While stress responses such as heat shock proteins may provide cross-tolerance, it remains unclear whether adaptation to one type of thermal stress enhances resilience to another. Notably, male fertility can be impaired by heat before lethal temperatures are reached, underscoring the importance of fertility thermal limits (FTL). We investigated whether adaptation to cold shock in *Drosophila melanogaster* enhances resistance to heat stress in reproductive traits. Flies were exposed to heat shock across a range of temperatures (35–38°C) and durations (30 minutes to 4 hours), with longer exposures (≥3 hours) causing high mortality. Following standardization, selected and control populations were subjected to a 30-minute heat shock at 38°C. Cold shock adaptation did not confer cross-tolerance in reproductive traits. Although heat-shocked flies exhibited increased mating within 24 hours, no significant differences were observed in fecundity, survival, or egg hatchability. However, only 50% of larvae from heat-shocked parents successfully pupated, and eggs laid 24 hours later showed delayed development. No evidence of male sterility prior to mortality was detected, suggesting minimal disparity between fertility thermal limits (FTL) and critical thermal limits (CTL) in this system. These findings highlight the stressor-specific nature of thermal adaptation and support treating FTL and CTL as distinct, species-specific thresholds.

13:45 – 14:00

Romane Gout, *Martin-Luther-Universität Halle-Wittenberg, Germany*

Reproductive ruin in a warming world: a meta-analysis of the effects of temperature on gamete quality

Human-induced climate change is dramatically altering the global thermal environment. Recent decades have been characterized by rising summer temperatures and increasing frequency, duration, and intensity of extreme heat events (i.e., heatwaves), with further intensification predicted in the coming decades. The range of temperatures that organisms can physiologically tolerate strongly influences their spatial and temporal distributions; therefore, heatwaves can threaten population persistence. Thermal tolerance studies have traditionally focused on survival under extreme heat, often overlooking critical sub-lethal effects. Increasing evidence shows that high temperatures can impair fertility traits—such as sperm and egg number and viability—leading to infertility and reproductive failure. Consequently, thermal limits to reproduction, rather than lethal temperature limits, may play a key role in determining species distributions.

To address this, we conducted a systematic review and meta-analysis to assess how extreme heat affects primary sexual traits across a broad range of non-human animal taxa. We screened over 1,600 studies and incorporated data from an existing systematic map examining the relationship between temperature and reproduction. Our meta-analysis reveals widespread negative effects of high temperatures on gamete quality. For example, in endothermic animals, elevated temperatures are associated with declines in sperm concentration and motility. These findings suggest that heatwaves may pose a significant but underappreciated threat to the reproductive health of wild populations and, consequently, to global biodiversity.

14:00 – 14:15

Vinayaka Hegde, *University of Innsbruck, Germany*

Phenotypic selection on heatwave responses of *Lymnaea stagnalis* snails

Human-induced climate change is increasing the frequency and intensity of extreme weather events, such as summer heatwaves, which can disrupt natural biological processes. Our study investigates phenotypic selection on organismal responses to heatwaves. Specifically, we examined (1) how responses of juvenile *Lymnaea stagnalis* snails to heatwaves vary among individuals, (2) whether this variation reflects differences in fitness, and (3) whether heatwave-mediated selection is influenced by ecological conditions, namely food availability. We exposed approximately 500 juvenile snails (initial shell length: 6–7 mm) to a one-week experimental heatwave (27°C), followed by four weeks at a benign temperature (17°C). Snails were maintained under two resource conditions (ad libitum vs. reduced food supply), and performance was measured as growth rate, a key fitness-related trait influencing reproductive potential. Shell length was measured at the start and end of the heatwave to quantify heatwave response, and again three weeks post-heatwave to assess recovery and final size as a proxy for fitness. Snails increased their growth rate during the heatwave, with stronger effects under ad libitum feeding. Growth rates returned to baseline levels after the heatwave. Selection gradient analysis revealed stabilizing selection on heatwave responses: individuals with intermediate growth rates achieved higher final sizes than those with either low or high growth rates. This pattern was consistent across both food treatments. To assess whether selection on heatwave responses varies across life stages, we conducted a parallel experiment on adult *L. stagnalis*, measuring growth rate, immune function, and reproductive output. Results from this experiment will be available by the time of the conference.

14:15 – 14:30

Melina Sophia Welling, *University of Hamburg, Germany*

The bog of eternal stench? Community effects on evolutionary responses of bog microalgal communities to climate warming

Rapid evolutionary responses to climate warming are increasingly documented in aquatic photosynthesising microorganisms, yet most experimental studies examine adaptation in monocultures. In bog ecosystems—important for global carbon cycling—evolutionary trajectories unfold within complex communities that experience recurring environmental disturbances and restoration under climate change. This raises fundamental evolutionary questions: how predictable are community and evolutionary responses to warming, how does community complexity shape these responses, and to what extent are evolutionary and ecological outcomes re-established following disturbance? I address these questions using five species of Zygnematophyceae isolated from Hamburg bogs. Zygnematophyceae are freshwater microalgae and the closest relatives of land plants, acting as key primary producers in bog ecosystems. Despite their ecological importance, their evolutionary responses to warming remain poorly understood.

I will characterise thermal performance curves of these Zygnematophyceae species and quantify fitness-related traits, including growth, photosynthetic efficiency, and nutrient uptake. Based on these data, I will conduct experimental evolution over approximately 100 generations under elevated temperature in replicated selection regimes that vary in environmental stability and community complexity, including monocultures and two types of artificial communities. One community type will evolve continuously, while the other will be periodically reset, enabling tests of evolutionary and ecological repeatability. I expect warming to drive rapid evolutionary change in thermal performance, with species differing in both the magnitude and direction of trait evolution. Community context is predicted to modify these trajectories by altering selection pressures, potentially reducing predictability and promoting alternative evolutionary outcomes.

14:30 – 14:45

Sofia Costa, *University of Lisbon, Portugal*

Surviving the heat: plastic consequences of thermal stress on spider mite reproduction

Although survival is widely used to assess thermal effects on organisms, reproduction is generally more sensitive to high temperatures and may better predict population responses to climate change. However, how temperature simultaneously affects male and female reproductive traits remains poorly understood. To address this, we first measured heat tolerance in the spider mite *Tetranychus cinnabarinus*, a haplodiploid species in which only the first mate fertilizes the female, making it particularly vulnerable to heat-induced declines in male fertility. We then tested how sub-lethal temperatures (that impair fertility but not survival) affect reproduction. Males and females reared under control or sub-lethal temperature conditions were paired, and their fertility, mating behaviour, and offspring paternity were assessed. Both female and male fertility declined at high temperatures, resulting in fewer offspring and a male-biased sex ratio. In haplodiploid systems, reduced male fertility directly limits daughter production, in contrast to diploid organisms. Pairings involving heat-stressed individuals also showed increased mating latency. However, when females initially paired with heat-stressed males remated, mating latency decreased and paternity was redistributed among multiple males. This restored the offspring sex ratio, but not total offspring number. This shift from single to multiple paternity, along with altered mating behaviour, is likely to affect interactions within and between the sexes, with potential consequences for sexual selection and sexual conflict. Whether such behavioural adjustments are sufficient to prevent population decline or extinction remains an open question.

14:45 – 15:00

Šimon Roubal, *Masaryk University, Czech Republic*

De novo domestication of Camelina sativa for sustainable oilseed production in a changing climate

Camelina sativa is an emerging crop with high potential for sustainable agriculture, aviation biofuels, and climate-resilient production. Its broader utilization, however, is limited by an extreme domestication bottleneck and very low genetic diversity. In our previous work, we resolved the evolutionary origin of this allohexaploid species and identified its parental genomes, demonstrating that *C. sativa* arose through hybridization between *C. intermedia* and *C. hispida*. Here, we present a genome-driven de novo domestication strategy that follows the evolutionary history of *C. sativa* to deliberately recreate and expand its genetic diversity. We generated synthetic allohexaploid lines through controlled interspecific hybridization and polyploidization, and performed high-fidelity long-read genome sequencing using PacBio HiFi technology on the synthetic lines and their parental species. HiFi assemblies enabled accurate reconstruction of chromosome-scale genome structure and detailed comparative analyses of homoeologous subgenomes. Our results reveal high synteny between the synthetic lines, parental genomes, and the cultivated *C. sativa*, indicating rapid genome stabilization after polyploid formation. Only a limited number of post-hybridization chromosomal rearrangements were detected, primarily associated with subgenome fusion and structural fine-tuning rather than large-scale genome reshuffling. These findings provide direct insight into the mechanisms shaping polyploid genome architecture during crop origin. Beyond evolutionary insight, these de novo synthesized *Camelina* lines constitute a practical pre-breeding resource that expands the genetic space of the crop beyond domestication constraints. This approach opens a realistic pathway toward climate-resilient, low-input oilseed improvement and sustainable diversification of agricultural production.

Session 4B – Phylogeny and Diversification

13:30 – 13:45

Lauren Amillicent Young, *Czech University of Life Sciences, Czech Republic*

Phylogeography of the North American Desert species, Chenopodium fremontii

The North American A-genome diploid species of the genus *Chenopodium* (Amaranthaceae) provide a unique model for examining the roles of orogenic activity and Quaternary climate change in plant diversification. This study focuses on *Chenopodium fremontii*, a desert and montane species distributed from the Rocky Mountains to the Sierra Nevada and across the Great Basin. We hypothesize that Neogene orogenic activity initiated speciation events within North American *Chenopodium*, and that Pleistocene glacial–interglacial cycles shaped current phylogeographic patterns through refugial isolation.

Genomic data were generated using RADseq from more than 130 individuals representing over 40 populations across the United States, Canada, and Mexico. Population structure and relationships were inferred using phylogenetic analyses and sparse non-negative matrix factorization (SNMF). To integrate genetic patterns with environmental history, ecological niche models (ENMs) were constructed using over 450 verified herbarium and field occurrence records to estimate past and present habitat suitability and stability. ENM results suggest geographically structured areas of long-term habitat stability consistent with hypothesized Pleistocene refugia, while genomic analyses indicate regional genetic differentiation within *C. fremontii*. Together, these findings provide insight into how geological history and climate dynamics have shaped diversification in North American desert plants and contribute to a broader understanding of evolutionary processes within the genus *Chenopodium*.

13:45 – 14:00

Pauline Jennert Orschel, *Leipzig University, Germany*

Untangling Mahogany mysteries: phylogenomics shed light on the complex evolution and taxonomy of the timber genera *Toona* and *Cedrela*

The pantropically distributed mahogany family (Meliaceae Juss.) comprises ecologically, economically, and culturally important tree lineages valued worldwide for timber and medicinal uses. Despite this importance, effective long-term conservation is constrained by persistent taxonomic uncertainty and an incomplete understanding of evolutionary relationships within the family. The Asian–Australasian genus *Toona* (Endl.) M.Roem., closely related to the Neotropical *Cedrela* P.Browne, exemplifies these challenges. Species boundaries, distributions, and even total species numbers remain unresolved, likely reflecting a complex evolutionary history that cannot be fully captured by traditional morphology-based taxonomy or standard phylogenetic approaches. Recent phylogenomic studies of Meliaceae have revealed relationships that are incongruent with earlier Sanger sequencing-based reconstructions and suggest the influence of ancient hybridization, polyploidization, and gene duplication events. Building on these insights, we use Hyb-Seq data targeting nuclear single-copy genes (Angiosperms353 probe set) to present the most comprehensive phylogenomic analysis of the sister genera *Toona* and *Cedrela* to date. By integrating phylogenomic evidence with traditional morphological data in an integrative taxonomic framework, we address long-standing taxonomic challenges in *Toona* and provide a substantially improved basis for species delimitation and conservation.

14:00 – 14:15

Tim David, *Université de Montpellier, France*

A complete time-calibrated phylogeny of the most speciose seabird genus supports a non-adaptive radiation scenario

Phylogenomic studies have considerably increased our knowledge of the evolutionary relationships among many organisms in recent years. However, the biology and conservation status of some taxa make them difficult to sample, which can hinder the reconstruction of their evolutionary history and limit our understanding of their taxonomic status. The genus *Pterodroma* is the most species-rich seabird genus and one of the most threatened. Its breeding populations are restricted to remote oceanic islands, with some populations numbering only a few dozen pairs. In this study, we compiled mitochondrial sequences from public databases, generated new sequences from fresh and museum specimens, and re-used existing genomic datasets to assemble a comprehensive sampling of the genus, totalling 2,052 sequences.

We successfully sampled all extant taxa and nearly all known populations, including some recently extinct ones. By integrating these data with recent phylogenomic datasets, we reconstructed the first exhaustive phylogeny of the genus *Pterodroma*. We then investigated how biogeographic history and diversification dynamics have contributed to the high species diversity of this genus relative to its closest relatives. Our results support a predominant role of climatic events during the Late Tertiary in driving diversification in gadfly petrels. We find a steady increase in speciation rates over time, rather than a rapid, punctuated radiation. Finally, the phylogenetic placement of extinct specimens reveals that several highly differentiated lineages have already been lost due to human activities.

14:15 – 14:30

Yara Maquitico Rocha, *Universidad Nacional Autónoma de México, Mexico*

Behavioral diversity in hunting fireflies (Coleoptera: Lampyridae: Photurinae), the first step to understanding its evolution

Most fireflies do not feed as adults, relying instead on resources accumulated during the larval stage. However, a small group within the subfamily Photurinae, comprising the genera *Photuris*, *Bicellonycha*, and *Pyrogaster*, includes species with predatory females. Unlike other fireflies, these females are considered specialist predators because they typically prey on males of other firefly species. Although most behavioural observations of photurines come from species in the United States, the majority of Photurinae species are distributed in the Neotropics. In Mexico, we have documented substantially greater behavioural diversity than previously reported, a diversity that is only beginning to be explored.

Here, we describe the behavioural diversity observed in Photurinae species in Mexico based on five years of field observations, focusing on species of the genera *Photuris* and *Bicellonycha*. Our findings significantly expand the known behavioural repertoire of photurines, including previously unreported behaviours. Notably, we identified a strictly cannibalistic species of *Bicellonycha* that uses bioluminescence to hunt, sometimes even during mating. We also observed species in both genera in which females do not exhibit predatory behaviour, as well as a novel repertoire of predatory strategies in adult *Photuris*. According to recent phylogenetic studies of the family Lampyridae, photurines evolved from a non-carnivorous ancestor. However, their behavioural diversification appears to be linked, at least in part, to metabolic adaptations that differ among genera. These findings provide new insights into the evolution of behavioural diversity within *Photurinae*.

14:30 – 14:45

Samuel Nestor Meckoni, *University of Bonn, Germany*

Genetic insights into Lentibulariaceae carnivory evolution

The plant family Lentibulariaceae comprises exclusively carnivorous species, making it an intriguing system for studying the evolution of plant carnivory. Notably, its three genera exhibit distinct trapping mechanisms: *Pinguicula* uses sticky leaves, *Genlisea* employs fish-trap-like structures, and *Utricularia* possesses bladder-shaped, vacuum-driven suction traps. The ubiquity of carnivory within Lentibulariaceae raises questions about its evolutionary origins. Genetic changes in the most recent common ancestor may have facilitated the emergence of carnivory in this lineage. For instance, duplication of protease genes—enzymes involved in prey digestion—could have played a key role in this transition. Recent advances in long-read sequencing have provided new insights into Lentibulariaceae genomes, enabling more comprehensive bioinformatic analyses across a broader range of species and candidate genes. Integrative approaches combining transcriptomic data and synteny analyses can strengthen inferences drawn from comparisons with closely related non-carnivorous species. Furthermore, including distantly related carnivorous plant lineages in comparative analyses may help identify general evolutionary mechanisms underlying the emergence of carnivory. Together, this work aims to elucidate the genetic and evolutionary processes that gave rise to carnivory in plants.

14:45 – 15:00

Zuzana Rottová, *Landscape Research Institute, Průhonice, Czech Republic*

Biotechnological approaches to the conservation of *Daphne cneorum* L.

Glacial relict species provide valuable systems for understanding how past climate oscillations, range fragmentation, and population bottlenecks shape genetic diversity. *Daphne cneorum* L. (Thymelaeaceae) is a chamaephyte persisting in Central Europe in small, isolated populations that likely represent remnants of its pre-glacial range. Its occurrence at the Czech range margin, together with its patch-forming clonal growth, makes it an ideal model for testing whether peripheral populations exhibit reduced genetic diversity and stronger structure due to drift and limited dispersal, or whether some populations retain high diversity through long-term persistence or admixture. By combining genome-wide genotyping, cytotype screening, and propagation experiments, we aim to link evolutionary history with conservation outcomes. We will quantify intra- and inter-population genetic diversity using DArTseq genotyping of more than 500 samples (ca. 450 from Czech populations and ~70 from neighbouring countries). Ploidy variation will be assessed via flow cytometry to support karyological interpretation and identify atypical cytotypes (e.g., triploids). In parallel, we will optimise conservation propagation by testing phytochemical regulators (CDK/cytokinin-related inhibitors) and refining rooting, acclimatisation, and cultivation protocols. This includes comparisons between long-term in vitro genebank material and current in vivo samples. We expect edge-of-range populations to exhibit clonality (polycorm “patches”) and potentially reduced diversity, but we will test whether some peripheral populations retain unexpectedly high variation. Preliminary trials indicate that at least one compound enhances shoot multiplication; additional compounds will be evaluated for shoot formation and rooting. This project will inform a national conservation programme by identifying genetically valuable populations and genotypes for protection and reinforcement, and by developing robust in vitro and in vivo propagation protocols. The partial results presented were obtained within project SQ01020054: “Determination of genetic variability, monitoring of ecosystem changes, and growth physiology in the critically endangered species *Daphne cneorum* using modern methods” funded by the Technology Agency of the Czech Republic.

Session 5A – Experimental Evolution

15:30 – 15:45

Gabin Calmet, *INSA Lyon, France*

Evolution of spatial organization in bacterial colonies

Multicellularity has evolved independently in several lineages, including bacteria. For instance, the obligate multicellular bacterium *Streptomyces coelicolor* specialises cells that secrete antibiotics at specific stages of its life cycle, while *Bacillus subtilis* biofilms exhibit cell differentiation, division of labour, and spatial organisation. These colony-level developmental dynamics are governed by complex gene regulatory networks (GRNs) that enable robust growth and organisation. Despite these insights, the selective drivers of bacterial multicellularity and the evolution of bacterial development remain poorly understood. We address these questions using a computational evolutionary framework. We model a population of bacterial cells that can replicate, deposit antibiotics, and sporulate on a discrete two-dimensional grid. These behaviours are controlled by GRNs encoded in linear genomes consisting of genes and upstream promoters. Genes can function as transcription factors (TFs) or as simplified modules for antibiotic production, growth, or sporulation. TFs bind to promoters to activate or repress gene expression, thereby shaping colony development. The model operates in discrete “seasons”: during each cycle, cells compete through growth and antibiotic secretion, but only sporulating cells contribute to the next generation. Selection therefore directly favours successful sporulation, while colony-level developmental dynamics emerge indirectly through competitive interactions. Genomic mutations—including duplications, deletions, and changes in TF binding strength—can rewire GRNs and generate diverse phenotypic outcomes. Overall, this model demonstrates how developmental programs regulating growth, antibiosis, and sporulation can evolve through emergent colony-level selection and the cumulative effects of genomic mutations.

15:45 – 16:00

Soumya Panyam, *Universitat de Valencia, Spain*

Environmental variation affects the adaptive value of male harm

Male harm refers to the phenomenon whereby interactions with males reduce female fitness. It is widespread across the animal kingdom and can impose substantial costs on populations by affecting adaptation rates, evolutionary rescue, demography, and population viability. The persistence of male harm, despite these costs, is often attributed to the assumption that harmful traits are adaptive for males; however, this hypothesis has rarely been tested directly. Recent evidence suggests that ecological context can modulate the effects of male harm through both plastic responses within generations and adaptive responses over evolutionary timescales. Yet, how natural environmental variation influences the relationship between male harm and male fitness remains poorly understood. To address this, we investigated the relationship between male reproductive success and their capacity to harm females across a natural thermal range. Using isogenic lines derived from a wild population of *Drosophila melanogaster*, we measured male harm and reproductive success at three temperatures (20°C, 24°C, and 28°C). We found a positive relationship between male harm and reproductive success at higher temperatures (24°C and 28°C), but not at 20°C. Additionally, both male harm and reproductive success varied substantially across temperatures. These findings challenge the assumption that male harm is universally favoured by selection and highlight the importance of environmental heterogeneity in maintaining phenotypic variation in traits linked to reproductive success.

16:00 – 16:15

Emily M. Booms, *Leibniz Institute of Freshwater Ecology and Inland Fisheries, Germany*

Limited effect of evolutionary history on density-trait responses to salinity of Colpidium striatum populations

Natural communities are strongly affected by human-induced environmental change. Populations can respond through both ecological (changes in density) and evolutionary (changes in traits) processes. Importantly, species do not exist in isolation but interact with other species, which can influence how they respond and evolve under abiotic stressors. In this study, we tested whether populations of the freshwater ciliate *Colpidium striatum* that evolved under no, slow, or fast increases in salinity—either in the absence or presence of competitors—differ in their density and trait dynamics. Using common garden experiments under low- and high-salinity conditions, we quantified population density and key morphological traits. We found that higher contemporary salinity led to significantly lower population densities, smaller cell sizes, and rounder cell shapes. Effects of evolutionary history were detected in some traits but were generally weak and transient. Overall, past environmental change and ecological interactions had subtle effects on the coupled density–trait responses of *Colpidium* populations under changing conditions. These results highlight the importance of identifying when environmental change and species interactions meaningfully influence evolutionary trajectories.

16:15 – 16:30

Triveni Shelke, *Indian Institute of Technology, New Delhi, India*

Evolutionary responses of *Pseudomonas entomophila* to insect-associated thermal stress reveal enhanced fitness and virulence

The widespread incidence of insecticide resistance among pests highlights the need to better understand insect–insecticide interactions. Bacterial species with insecticidal properties offer promising alternatives, and studying insect–pathogen dynamics can provide key insights for developing sustainable control strategies. Experimental evolution is a powerful approach to investigate how pathogens adapt under host-driven environmental selection pressures. *Pseudomonas entomophila* (Pe), an entomopathogen, grows optimally at 30°C, whereas insect hosts typically experience temperatures ranging from 18°C to 30°C. We found that *Drosophila melanogaster* infected with Pe exhibited lower mortality at 18°C than at 30°C, consistent with reduced bacterial growth at lower temperatures. To test adaptive responses, we subjected Pe to thermal selection using serial transfer, gradually reducing the temperature from 30°C to 18°C over 120 days. The evolved bacteria showed improved growth under low-temperature conditions and increased virulence, as indicated by higher mortality in infected flies. Physiological assays revealed enhanced protease activity in evolved strains compared to the ancestor at 18°C. Genomic analyses identified mutations in genes associated with host interaction, secretion systems, and motility regulation.

Despite the relatively small number of genetic changes, we observed differential DNA methylation (6mA) in genes related to the cell periphery, transmembrane processes, and ATP binding. These patterns suggest that epigenetic regulation may contribute to adaptive responses affecting cellular interfaces and metabolism. Overall, our findings indicate that insect-associated thermal stress can drive the evolution of increased virulence in *Pseudomonas entomophila*, with important implications for the development of sustainable pest management strategies.

16:30 – 16:45

Piyumi Sandaruwani De Alwis, *University of Konstanz, Germany*

One parasite, many defences: evolutionary routes of algal resistance

Host resistance drives coevolution between hosts and parasites, fuelling reciprocal adaptation and diversification in both partners. A key aspect of host defence is the ability to evolve multiple resistance mechanisms against a specific parasite. When these mechanisms target different stages of infection, they can alter selection pressures on the parasite. Additionally, resistance mechanisms may differ in their fitness costs, with consequences for host life-history traits and population dynamics. Together, these factors can influence the trajectory of host–parasite coevolution. This study uses an alga–virus model system to investigate the divergent evolution of resistance and its potential effects on subsequent coevolutionary dynamics. In previous work with the green alga *Chlorella variabilis* and the virus PBCV-1, we generated a panel of 22 algal clones that independently evolved resistance to the virus. Preliminary results indicate that these clones exhibit at least three distinct resistance strategies, based on differences in susceptibility to viral resistance-breaking. Here, we assess whether these resistant *Chlorella* clones employ different mechanisms of resistance. Specifically, we test whether resistance occurs at different stages of the viral life cycle: adsorption to the host cell, depolarisation and genome entry, or release of progeny virions. We also examine whether the fitness costs associated with resistance differ among clones. This study will provide the first insights into the diversity of resistance mechanisms in *Chlorella* algae and establish a foundation for understanding how variation in host resistance strategies shapes host–parasite coevolution.

16:45 – 17:00
Arya Dhiman, *Indian Institute of Science Education and Research, Mohali, India*

Shifting the balance: how sex ratios shape sexual selection and fitness in Drosophila melanogaster

Sexual selection is a major evolutionary force, but its effects depend strongly on the intensity of mating competition experienced by males and females. Manipulating adult sex ratio provides a powerful way to experimentally alter sexual selection and examine its consequences for fitness-related traits. In this study, I investigate how different levels of mating competition influence courtship behaviour, mortality, and reproductive success in *Drosophila melanogaster*. I established three selection treatments: male-biased (M), female-biased (F), and control (C). Two sex-ratio treatments were used to vary the strength of sexual selection: a high-bias treatment (1:3) and a moderate-bias treatment (1:2). Each treatment consisted of replicated population cages, with flies sorted into the required sex ratios on day 12 post-egg collection, once all individuals had eclosed and reached sexual maturity. Flies were maintained under these conditions until day 21. Multiple assays were conducted over a nine-day interaction period. Courtship activity was measured every six hours by counting courting males within fixed observation zones in each cage, providing a proxy for mating effort and potential mate harm. Sex-specific mortality was recorded daily. Female reproductive output was estimated by counting eggs laid on alternate days (days 14, 16, 18, and 20). To assess offspring viability, collected eggs were incubated and measures of egg-to-pupa viability, pupal counts, sex-specific eclosion, and pupa-to-adult survival were recorded. This experimental design enables the simultaneous assessment of behavioural, survival, and reproductive consequences of altered sex ratios. The study provides insights into how varying intensities of sexual selection shape fitness components and sex-specific trade-offs, improving our understanding of the evolutionary consequences of mating competition.

Session 5B – Evolutionary Theory and Modelling II

15:30 – 15:45
Nicholas Armeni, *University of Helsinki, Finland*

Ecosystems on the scale of a byte: when predation and dispersal shape eco-evolutionary dynamics

Climate change is shifting environmental conditions and increasing extinction risk. Persistence under ongoing change depends not only on selection and dispersal, but also on species interactions that can modify both demography and adaptation. Predation is typically viewed as purely detrimental because it reduces prey abundance. However, theory suggests that predators can sometimes promote persistence by selectively removing maladapted individuals ("selective push") and by generating compensatory demographic responses (hydra effects). Most existing theory focuses on single panmictic populations and may therefore overlook key dynamics in spatially structured systems. Here, I use an individual-based, genetically explicit simulation model (NEMO-age), extended to include a predation life-cycle stage, to test how selective predation and dispersal jointly shape prey responses to gradual directional environmental change.
I simulate a stage-structured prey population across a 100-patch landscape that is either environmentally homogeneous or structured along clines of varying steepness. Predation is phenotype-dependent, with maladapted individuals experiencing higher mortality. I vary predation intensity, migration rate, and the strength of stabilizing selection, and quantify outcomes including population abundance, mean fitness, additive genetic variance, and trait–optimum mismatch. Predation effects are strongly context-dependent. Under strong stabilizing selection, predation reduces trait lag and can increase prey abundance. As selection weakens, predation increasingly acts as an additional mortality source, leading to reduced fitness, increased trait lag, and greater population declines, particularly in low-connectivity systems. Higher migration can partially buffer these effects, but outcomes depend on environmental heterogeneity, which mediates the balance between dispersal-driven maladaptation and selective filtering. These

results highlight the complex interplay between predation, dispersal, and selection in determining population persistence under environmental change.

15:45 – 16:00

Katarzyna Potera, *Jagiellonian University, Poland*

Experimental test of equations for the probability of beneficial allele fixation

When a newly arisen mutation is beneficial, it may spread through a population and eventually become fixed. The probability of fixation can be estimated using theoretical models, most notably Haldane's approximation, which predicts fixation probability as approximately twice the selection coefficient. Kimura's equation extends this framework by incorporating initial allele frequency and effective population size. However, both models rely on simplifying assumptions that are rarely met in natural or experimental populations, and empirical tests have yielded inconsistent results. Here, I use strains of *Saccharomyces cerevisiae* to experimentally test these theoretical predictions under controlled conditions, with precisely defined selection coefficients, initial mutant frequencies, and large population sizes across multiple replicates. Single cells carrying a beneficial allele were introduced into a background population via cell sorting. Populations were propagated in batch culture under two bottleneck regimes for at least 600 generations, and allele frequencies were tracked using flow cytometry. In many cases, background populations evolved before the beneficial allele reached frequencies sufficient for fixation. Comparing the proportion of populations in which the beneficial allele fixed with theoretical expectations revealed that bottleneck size, rather than selection coefficient, plays a dominant role in determining allele fate. These results indicate that neither Haldane's nor Kimura's approximations adequately predict fixation dynamics in microbial populations, highlighting the importance of demographic processes in shaping evolutionary outcomes.

16:00 – 16:15

Elisa Barreiro-Docío, *Universidade de Vigo, Spain*

Benchmarking Nuclear eDNA: Comparing SNP-based Allele Frequencies from Water Samples vs. Tissue-derived Data

Monitoring wild populations is often limited by incomplete and non-random sampling, resulting in biased estimates of genetic diversity. Environmental DNA (eDNA) offers a non-invasive alternative, but most population-level applications rely on mitochondrial markers, which provide limited resolution for genomic inference. Capturing nuclear variation is therefore essential for assessing intraspecific diversity and demographic processes. Effective population size (Ne) is a key parameter in conservation genetics, reflecting the strength of genetic drift and the rate of genome-wide diversity loss. To determine the genomic resolution required for robust Ne estimation, we performed allele frequency-based simulations using a 220K SNP array developed for Atlantic salmon (*Salmo salar*). These simulations indicated that approximately 1,000 nuclear SNPs are sufficient to estimate Ne with accuracy comparable to that obtained using the full dataset.

Based on these results, we developed a targeted approach to recover nuclear variation from water samples. We designed species-specific primers amplifying fragments ≤300 base pairs, each containing at least two informative SNPs. The panel was validated using controlled tank experiments with salmon populations of known genotype. Using multiplex PCR to amplify these targets from water-derived eDNA, we compared allele frequency estimates with those obtained from tissue samples. Our results demonstrate that nuclear SNPs can be reliably recovered from environmental samples, producing allele frequency estimates that closely match tissue-based data. Together, these findings show that nuclear SNP-based eDNA approaches enable scalable, non-invasive inference of population genetic diversity, with direct applications in evolutionary biology and conservation genetics.

16:15 – 16:30

Chandan Relekar Thukaram, *University of Lübeck, Germany*

Inference of interactions in the gut microbiome

Deciphering interactions within gut microbial communities is challenging due to constant microbial turnover, environmental fluctuations driven by diet and host responses, and limitations in sampling. Non-invasive sampling typically provides only snapshot data, while the number of available time points is often limited, constraining inference. In such non-ideal conditions, Bayesian approaches offer a powerful framework for parameter inference by enabling partial reconstruction of system dynamics while explicitly quantifying uncertainty. In this study, we fit stochastic population dynamics models to both simulated and empirical microbiome datasets. We investigate whether incorporating higher-order statistical moments—specifically variance and covariance—into the fitting procedure improves parameter inference by leveraging information that is typically discarded. Most existing approaches rely on regression-based methods that provide point estimates, or, when using Bayesian techniques, focus primarily on fitting mean behaviour. By contrast, our approach integrates both mean and higher-order moments expected under demographic stochasticity in the model. Using simulated datasets, we demonstrate that incorporating higher-order moments can significantly improve parameter inference in certain scenarios, as shown across hundreds of time-series datasets generated with randomized model parameters. These results highlight the potential of moment-based Bayesian inference to extract more information from sparse and noisy microbiome data, improving our ability to characterise complex microbial dynamics.

16:30 – 16:45

Robin von Allmen, *Stockholm University, Sweden*

Segment anything: employing SAM3 by META semi-automated measurements of image data

Artificial intelligence (AI) has become an increasingly important tool in evolutionary biology, particularly for analysing large datasets. However, many studies—especially those involving morphological data—still rely on small to medium-sized datasets, which often do not justify the development or application of complex machine learning models. The latest version of the Segment Anything Model (SAM3) offers enhanced performance and integrates text prompts, enabling segmentation of objects in images based on both visual and natural language inputs. To date, SAM3 has been primarily applied to large, public, or non-research datasets, and its utility for smaller, research-focused datasets remains largely unexplored. In this pilot study, we developed and tested a web-based application to evaluate SAM3 performance against manual morphological measurements and tracking. We used a diverse set of datasets, including published high-resolution images of pollen, fish sperm, and foraminifera, as well as unpublished video recordings of fish in their natural habitat and experimental recordings of butterflies and bumblebees in controlled environments. Across all datasets, SAM3 achieved high recall (>95%), missing only a small number of objects of interest. However, precision and overall accuracy were lower compared to human annotations. Despite this, the tool substantially accelerates data processing and reduces manual workload. These results demonstrate that SAM3 can effectively support the analysis of small and medium-sized morphological datasets without the need for large training datasets or model fine-tuning, offering a practical and accessible approach for evolutionary research.

16:45 – 17:00

Ríona Burke, *University of Exeter, United Kingdom*

Genetic and non-genetic inheritance through multiple paternal and maternal channels

Non-genetic inheritance (NGI) refers to the transmission of phenotypic information from parents to offspring, and even across multiple generations. It plays a key role in shaping organismal phenotypes and can influence evolutionary trajectories. However, the extent of its evolutionary significance remains debated, particularly when considering the combined contributions of maternal and paternal effects. To address this, we extend classical evolutionary models of gene regulatory network (GRN) inheritance by incorporating multiple channels of parental transmission. First, both parents contribute equally to the offspring's genome, forming a diploid zygote. Second, both parents may transmit gene expression products—such as small RNAs—to the zygote, representing a form of molecular inheritance beyond DNA sequence. Third, maternal effects influence offspring development through resource allocation, including ovum size and parental care, which can affect both the relative contribution of parental small RNAs and the strength of stabilizing selection around an optimal phenotype. By integrating these multiple inheritance pathways, our framework provides a more comprehensive approach to studying NGI. This model enables the generation of formal predictions about how different inheritance channels interact to shape evolutionary dynamics. Overall, this work contributes a novel perspective on the role of non-genetic inheritance and offers a foundation for understanding its impact on evolutionary processes.

Session 6A – Genome Evolution and Structural Variation II

17:15 – 17:30

Aryadevi Anitha Shaji, *Leibniz Institute for the Analysis of Biodiversity Change, Germany*

Genomic insights into biodiversity decline in endangered Hallig beetle, *Pseudaplemonus limonii*

The accelerating global decline in biodiversity underscores the urgent need for refined conservation strategies. While traditional approaches focus on species monitoring and habitat protection, genomic data can reveal early signatures of population decline before demographic changes become detectable. Despite this potential, most conservation genomics studies have focused on a limited number of flagship or model species, leaving the majority of taxa understudied. The Hallig beetle, *Pseudaplemonus limonii*, is a small weevil in the subfamily Apioninae within the hyperdiverse superfamily Curculionoidea, which comprises more than 62,000 described species. Despite this diversity, genomic resources for this group remain scarce: only 106 genome assemblies are currently available for Curculionidae, of which just 47 are chromosome-level, and no reference genome has previously been generated for the genus *Pseudaplemonus*. Here, we present a high-quality, chromosome-resolved reference genome for *P. limonii* and use it to investigate the genomic consequences of its recent population decline in Germany. We sequenced 20 contemporary individuals and 20 historical specimens collected from the same population prior to the documented decline, enabling a direct temporal comparison. Using these data, we assess multiple genomic indicators of population decline, including mutation load, nucleotide diversity, inbreeding levels, and gene copy number variation. By integrating historical and modern genomes, we quantify genetic erosion and identify genomic signatures of population bottlenecks. This study demonstrates how combining museum genomics with high-quality reference genomes can provide powerful insights into biodiversity loss in non-model, endangered insects, offering a scalable framework for genomics-informed conservation across diverse taxa.

17:30 – 17:45

Elisabeth Stryckmans, *Université de Montpellier, France*

Cis-regulatory variation and the expression of the load

Diploidy is characterized by the presence of two copies of each gene, one of maternal and one of paternal origin. Balanced expression of these alleles (1:1) is often considered a baseline state. However, mutations in cis-regulatory elements can disrupt this balance, leading to allele-specific expression (ASE), where one allele is consistently over- or under-expressed. Although ASE is widespread in eukaryotes, as shown by population-scale transcriptomic data, a unified theoretical framework to predict its prevalence and evolutionary consequences is still lacking. Multiple evolutionary processes can contribute to ASE, including genetic drift, stabilizing selection on expression levels, and direct selection on cis-regulatory variants. Additionally, a regulatory "runaway" process has been proposed, whereby homologous cis-regulatory elements compete within diploid genomes, promoting the spread of increasingly strong regulatory variants. This process may be counterbalanced by compensatory mutations in trans-regulators that maintain overall expression near an optimal level. However, such dynamics could generate characteristic genetic associations, with weaker cis-regulatory alleles more likely to be linked to deleterious coding mutations. Here, we test for signatures of this cis-regulatory runaway process. We analyse RNA-seq data from three human populations to examine the relationship between ASE and the presence of deleterious mutations, estimated using SIFT conservation scores. This approach allows us to evaluate how cis-regulatory variation and ASE influence the exposure of deleterious mutations to natural selection. Our results provide new insights into the evolutionary dynamics of gene regulation and the role of ASE in shaping genetic load in natural populations.

17:45 – 18:00

Daniela Eugenia Nerelli, *University of Trieste, Italy*

Gene dispensability reveals an open pangenome in the genus Mytilus

Declining sequencing costs and the increasing availability of genome assemblies have revealed that a single reference genome is insufficient to capture the full extent of genetic diversity within a species. This limitation is particularly evident in bivalves, which exhibit exceptionally high levels of heterozygosity and structural variation. Copy number variation, chromosomal rearrangements, and presence/absence variants (PAVs) can reshape gene content, generating a flexible genomic fraction that may contribute to adaptation and evolutionary diversification. These observations have led to the development of pangenomes, which encompass the full complement of genomic sequences present across individuals of a species. Hemizygous regions—where a DNA segment is present on only one homologous chromosome—provide indirect evidence of PAVs and offer a proxy for estimating gene dispensability. Such regions have been reported in bivalves and appear widespread, to varying degrees, across other molluscs, suggesting that open pangenomes may represent a common genomic architecture in these organisms. However, the evolutionary implications of this pattern remain poorly understood. To investigate the relationship between hemizygosity, structural variation, and pangenome openness, we combined a broad comparative analysis across major invertebrate groups with a focused study of the genus *Mytilus*. By integrating genomic data from multiple species, we reconstructed a non-redundant gene repertoire and identified extensive PAVs both within and among species. Gene content variability clearly differentiates species within *Mytilus* and supports the hypothesis that mussels possess an open pangenome. Overall, our results reinforce the view that pangenomes represent an evolutionarily significant genomic architecture, with structural variation acting as a key driver of diversification.

18:00 – 18:15

Bin Zhao, *Trinity College Dublin, Ireland*

Evolution of histone mRNA 3’ end processing machinery in eukaryotes

Replication-dependent histone mRNAs in metazoans are uniquely characterised by a conserved stem–loop (SL) structure at their 3 end, which is recognised by the stem-loop binding protein (SLBP) to regulate histone mRNA metabolism. Outside animals, however, the distribution, composition, and evolutionary history of this pathway remain poorly understood. In particular, fungi are widely assumed to have lost SLBP–SL-dependent processing. Here, we combine large-scale homology searches, domain and structure prediction, and genome-wide motif analyses across diverse eukaryotic lineages to reconstruct the evolution of histone mRNA 3-end processing machinery. We show that SLBP, SL motifs, and core U7-associated factors are far more broadly conserved across protists, plants, and early-branching opisthokonts than previously recognised, challenging earlier assumptions of widespread loss. In fungi, we identify a clade-specific, stepwise transition from SLBP–SL–U7 snRNP-dependent processing to canonical polyadenylation. Early-diverging fungal lineages retain SLBP with a conserved RNA-binding domain, weak but detectable SL motifs, and partial sets of U7 snRNP components. Together with the presence of non-canonical poly(A) polymerases, these findings are consistent with an ancestral intermediate state characterised by SLBP-dependent but U7-independent polyadenylated histone mRNAs. Our results redefine the evolutionary trajectory of histone mRNA 3-end processing, positioning fungi as key intermediates in the transition from SLBP–SL–U7-mediated regulation to canonical poly(A)-based control. More broadly, they reveal a deeply conserved continuum of RNA 3-end regulation across eukaryotes.

18:15 – 18:30

Zeynep Oguzhan, *University of Copenhagen, Denmark*

Did flight loss relax genome size constraints in birds?

Genome size and its role in genome evolution have long been debated in evolutionary biology, with distinct patterns emerging across taxonomic groups. Birds exhibit a notably constrained range of genome sizes, often attributed to the energetic demands of flight. Here, we investigate whether the loss of flight relaxes this constraint. We compiled short-read sequencing data from 61 bird species across 27 families, including 28 flightless and 33 flighted species, representing nearly 50% of extant flightless birds. Genome size was estimated using GenomeScope2, and Phylogenetic Generalized Least Squares (PGLS) analyses were applied to identify predictors of genome size across the phylogeny. Genome size exhibited a strong phylogenetic signal ($\lambda = 0.715$) and showed no correlation with body mass. Flightless birds had genomes approximately 0.048 Mbp larger on average than flying birds, although this trend was marginally non-significant ($p = 0.052$) and largely driven by ratites. To further assess the effects of flight loss, we focused on Rallidae ($n = 17$; 10 flightless, 7 flighted), a clade with multiple independent transitions to flightlessness, where genome size variation was minimal. Comparisons between closely related flightless and flighted species revealed no significant differences, suggesting that substantial evolutionary time may be required for detectable genome size changes following flight loss. Finally, we found a weak correlation between genome size estimates and assembly size, indicating that these metrics are not directly interchangeable. Overall, our results suggest that loss of flight alone does not lead to rapid or consistent increases in genome size in birds.

18:30 – 18:45

Nancy Choudhary, *University of Bonn, Germany*

Poaceae and Cucurbitaceae: model non-model systems to investigate anthocyanin biosynthesis

Anthocyanin biosynthesis is one of the best-characterised and most extensively studied secondary metabolic pathways in plants, largely informed by work in classical model species such as maize, petunia, and snapdragon. Although often assumed to be conserved across angiosperms, the evolutionary dynamics of this pathway remain understudied across diverse plant lineages. Here, we use a comparative genomics approach to investigate anthocyanin biosynthesis in two large and ecologically distinct plant families: Cucurbitaceae and Poaceae. Using orthologs from established model systems, we surveyed anthocyanin biosynthesis genes and their regulatory networks across extensive genomic and transcriptomic datasets from both families. In Cucurbitaceae, we identified a systematic absence of core anthocyanin and proanthocyanidin biosynthesis genes, as well as their transcriptional regulators, suggesting an evolutionary loss of the pathway at the family level. In contrast, Poaceae species retain anthocyanin pigmentation but exhibit extensive evolutionary rewiring, in which non-orthologous genes have functionally replaced canonical pathway components. This represents a striking case of convergent evolution. These contrasting outcomes—complete pathway loss versus functional rewiring—highlight distinct mechanisms by which conserved metabolic traits can be modified over deep evolutionary time. We therefore propose Cucurbitaceae and Poaceae as complementary non-model systems for studying the regulation and evolution of anthocyanin biosynthesis in dicots and monocots, respectively. Our findings challenge the assumption of universal conservation of anthocyanin biosynthesis and provide a new framework for investigating its evolutionary loss, diversification, and innovation.

Session 6B – Plasticity, Life Histories and Integrative Evolution

17:15 – 17:30

Stefano Lapadula, *University of Milan, Italy*

Back in black: colonization out of extreme environments challenges the evolutionary dead-end paradigm

Life-history specialization is often hypothesized to constrain evolutionary reversibility, potentially leading to evolutionary dead ends. Subterranean organisms exemplify this idea due to extreme adaptations such as eye loss and depigmentation. However, ecotones such as springs—interfaces between caves and surface freshwater systems—may provide opportunities to test whether highly specialized lineages retain phenotypic plasticity. Following the discovery of spring populations of the freshwater isopod *Monolistra pavani*, previously considered strictly cave-dwelling, we conducted an integrative study combining population genomics, behavioural experiments, field surveys, spectroscopy, and demographic modelling. Spectroscopic analyses revealed eumelanin-related absorbance peaks in pigmented spring individuals, indicating environmentally induced pigmentation. Behaviourally, spring populations exhibited higher movement rates and evidence of diel activity variation compared to cave populations. However, light-response experiments showed no behavioural differences between cave individuals and pigmented or depigmented spring individuals. Genome-wide SNP analyses revealed strong genetic differentiation between cave and spring populations, with higher genetic diversity in spring populations. Approximate Bayesian Computation supported a historical divergence between cave and spring populations approximately 43,000 generations ago, rejecting scenarios of recent colonisation or strong founder effects. No loci under divergent selection were detected, suggesting limited adaptive genetic differentiation. These results indicate that extreme subterranean specialization does not preclude long-term exploitation of surface ecotones. Paleogeographic evidence suggests that caves may have served as glacial refugia, while spring habitats became available following ice retreat. Overall, our findings challenge the view of caves as evolutionary dead ends and highlight the potential for ecological flexibility in highly specialized lineages.

17:30 – 17:45

Safira Moog, *Johannes Gutenberg University Mainz, Germany*

Dormant immunity in bumblebees

This project investigates immune function in bumblebee queens during diapause, a dormant state that allows organisms to survive prolonged periods of unfavourable environmental conditions. Diapause is characterised by developmental arrest and reduced metabolic activity, making it a key life-history strategy for many insects, including bumblebees. Although diapause enhances survival, it also presents challenges such as limited resources and increased susceptibility to infection. Reduced metabolic activity may constrain immune function, yet maintaining immune defence is essential to resist parasite infection and colonisation. Because immune activation is metabolically costly, it remains unclear to what extent insects can mount or regulate immune responses during diapause. Temperature is likely to play a critical role in this balance, as lower temperatures further suppress metabolic processes.

To address these questions, we use proteomic approaches to quantify the expression of immune-related proteins, including antimicrobial peptides, in the haemolymph of immune-challenged bumblebee queens undergoing diapause at different temperatures. This allows us to assess the capacity for immune activation under varying thermal conditions. In addition, we measure survival during diapause and post-diapause colony productivity to evaluate the long-term consequences of immune challenges. Together, this study provides insights into how physiological constraints and environmental factors shape immune regulation during diapause, with implications for insect ecology, evolution, and resilience under changing climates.

17:45 – 18:00

Dheeraj Halali, *University of Cambridge, United Kingdom*

Phenotypic plasticity drives defence toxin variation in herbivorous insects

Plants and herbivores engage in a continuous evolutionary arms race: plants produce diverse chemical defences to deter herbivory, while herbivores evolve mechanisms to overcome them. Many herbivores can sequester plant toxins for their own defence. More rarely, some lineages exhibit biochemical plasticity—the ability to both sequester toxins and synthesise them de novo, and to switch between these strategies. Biochemical plasticity represents a key evolutionary innovation that may influence diet breadth. By reducing dependence on host plants for defensive compounds, it may enable herbivores to exploit a wider range of hosts. In contrast, specialists that rely solely on sequestration are often constrained to narrow host ranges. Here, we investigate how seasonal and spatial host shifts influence defence chemistry in biochemically plastic Heliconiini butterflies. We conducted field sampling of butterflies and their host plants (*Passiflora*) in Panama and Brazil across wet and dry seasons. Defensive compounds (cyanogenic glycosides) were identified using LC-MS. We found that toxin composition in biochemically plastic butterflies varied significantly across locations but not across seasons. This pattern likely reflects differences in plant community composition among locations, which remain relatively stable seasonally. As a result, butterflies utilise different host plants in different regions, leading to spatial variation in toxin profiles. In contrast, Heliconiini species that have lost biochemical plasticity and rely exclusively on either sequestration or biosynthesis exhibit stable toxin composition across both space and time. These findings highlight biochemical plasticity as an important evolutionary innovation that allows herbivores to adjust their defensive strategies in response to environmental variation, potentially facilitating broader ecological niches.

18:00 – 18:15

Lina Marie Raubold, *Richard Gilder Graduate School at the American Museum of Natural History, United States of America*

Generalists in hiding? Uncovering the hidden feeding habits of sea slugs (Gastropoda, Nudibranchia) through dietary metabarcoding

Dietary preferences are fundamental to an animal's ecology, and shifts in diet are often key drivers of diversification. Nudibranch sea slugs, like many invertebrates, are generally considered highly specialized predators, with some species thought to feed on a single prey species. Consequently, transitions among prey types have been proposed as a major force underlying their extensive radiation. However, comprehensive data on the feeding ecology of nudibranchs remain limited, as these small and often cryptic marine invertebrates are difficult to observe in situ. Here, we apply dietary metabarcoding to investigate the trophic ecology of nudibranchs and demonstrate its potential as a tool for studying the diets of elusive marine organisms. Contrary to expectations of strict specialization, our DNA metabarcoding analyses reveal more diverse and previously unrecognized dietary patterns across all sampled nudibranch taxa. Even species assumed to be specialized predators on cnidarians were found to consume a broader range of prey, including arthropods, bryozoans, poriferans, and diatoms. These findings suggest that generalist feeding strategies may be more widespread among nudibranchs than previously thought. A more comprehensive understanding of their dietary ecology provides important insights into their roles within complex marine food webs and raises new questions about the influence of diet on their evolutionary diversification.

18:15 – 18:30

Dean Hodapp, *Johannes Gutenberg University Mainz, Germany*

A cross-species population genomic analysis of solitary bees

Understanding the capacity of organisms to respond to ongoing and future environmental challenges is a central goal of evolutionary and conservation biology. Solitary bees are ecologically and economically important pollinators but are experiencing widespread declines. Although they comprise more than 75% of global bee diversity, they may be particularly vulnerable due to higher levels of floral specialization, prolonged dormancy periods, and the absence of colony-level buffering mechanisms that can mitigate environmental stress. Despite their importance, solitary bees remain understudied, and key aspects of their genetic variation, demographic history, and adaptive potential are largely unknown. To address this gap, we apply whole-genome resequencing and population genomic analyses to assess adaptive potential across representative species from three of the seven bee families. We investigate population structure and standing genetic variation to infer levels of gene flow among contemporary populations and to evaluate how these species respond to local environmental conditions. In parallel, we analyse recent selection signatures to identify genomic regions under selection. Detecting conserved targets of selection across species may reveal shared adaptive responses to common environmental pressures. This study represents one of the first comparative population genomic analyses of solitary bees. By improving our understanding of their evolutionary potential and responses to environmental change, it provides a foundation for developing effective conservation strategies for this diverse and vulnerable group of pollinators.

18:30 – 18:45

Tim Prezelj, *Slovenian Academy of Sciences and Arts, Slovenia*

Do maternal effects shape sex-specific growth in a size-dimorphic spider

Maternal effects—the influence of maternal genotype or phenotype on offspring phenotype—are an important source of transgenerational variation in life-history traits. These effects can be sex-specific, such that the maternal environment and/or genotype generates divergent phenotypic outcomes in sons versus daughters. Although empirical evidence remains limited, sex-specific maternal effects have long been proposed as a mechanism contributing to the evolution of sexual dimorphism. We recently showed that such effects can help resolve sexual conflict over body size in the highly sexually size-dimorphic (SSD) spider *Nephilingis cruentata*. However, the underlying mechanisms and pathways remain unclear. Maternal nutrition is a key pathway through which maternal effects may arise, influencing offspring growth, survival, and development via resource allocation to eggs or embryos. Here, we investigate how maternal feeding regime (low versus high food availability) shapes sex-specific growth trajectories in *N. cruentata*. Using longitudinal monitoring across two consecutive generations, we quantify carapace width (CW) growth rates, inter-moult intervals, and adult size in male and female offspring. This design allows us to test whether maternal effects differentially influence growth and development between the sexes. We predict that offspring of low-fed mothers will exhibit slower growth and reach smaller adult sizes compared to offspring of well-fed mothers, with effects strongest during early development. We further expect sons to be more sensitive to maternal nutrition than daughters, due to their shorter developmental period. Although maternal effects alone may not fully explain sexual size dimorphism, our study will provide insights into how sex-specific sensitivity to maternal nutrition contributes to variation in growth trajectories underlying SSD.

Session 7A – Microbiomes and Symbiosis

09:00 – 09:15

Li-Wen Chu, *University of Konstanz, Germany*

Exploring shifts in symbiotic interactions using *Paramecium bursaria* and *Chlorella* species

Endosymbiotic relationships between ciliates and algal symbionts have evolved independently multiple times. These interactions are often nutrient-based mutualisms, in which ciliates provide nitrogen to their symbionts while algae supply photosynthetically derived carbon, resulting in net benefits for both partners. However, the outcome of this interaction can shift along a continuum from mutualism to parasitism depending on environmental conditions, and the factors driving these shifts remain poorly understood. In this study, we investigate how environmental conditions influence the balance of costs and benefits for each partner in ciliate–algal symbioses. We use the ciliate *Paramecium bursaria* and examine its interactions with several closely related green algae of the genus *Chlorella*, many of which are capable of forming facultative endosymbiotic associations. By experimentally varying environmental factors—including light availability, nutrient levels, and host and symbiont densities—we quantify how these conditions affect the costs and benefits experienced by each partner. This approach allows us to assess the context dependence of the symbiosis and identify conditions under which the interaction shifts from beneficial to detrimental. Our results show that the relationship between *P. bursaria* and *Chlorella* species spans a continuum from mutualism to exploitation, depending on both environmental context and symbiont identity. These findings highlight the dynamic nature of endosymbiotic interactions and provide insights into the ecological and evolutionary factors that govern their stability and persistence over time.

09:15 – 09:30

Diana Rojas Guerrero, *Jagiellonian University, Poland*

Micro-allies during mega-crisis? The role of the microbiome in insect community responses to climate change

Symbiotic bacteria play a central role in host biology and evolution, often influencing traits that enable organisms to persist in heterogeneous and rapidly changing environments. In High Arctic ecosystems such as Greenland, climatic conditions fluctuate dramatically across seasons, raising questions about how insects cope with such extremes. Microbial symbionts, which can provide protection against stressors and supply limiting nutrients, may therefore be key drivers of local adaptation. Here, we investigate the drivers of microbial community composition and identify symbionts potentially involved in local adaptation across multiple insect systems. Focusing initially on *Ochlerotatus* mosquitoes, we detected a high diversity of associated microbes but found no evidence for stable symbiotic associations. Comparisons between aquatic larval stages and adults revealed a pronounced reduction in microbial abundance during metamorphosis. In contrast, other arthropods inhabiting the same aquatic environments maintained facultative symbionts, such as *Rickettsia*, throughout development and into adulthood. Expanding our analysis to the broader insect community, we found that the most prevalent bacterial associate across taxa was the endosymbiont *Wolbachia*. Notably, *Wolbachia* was highly prevalent and diverse in hoverflies (Diptera: Syrphidae), exhibiting host specificity and geographic structuring. Together, our results show that while some insects persist in High Arctic environments without stable symbiotic associations, others exhibit diverse and lineage-specific symbiotic strategies. Understanding the functional roles of these interactions will provide key insights into how insects adapt to and thrive in extreme Arctic ecosystems.

09:30 – 09:45

Veronika Andriienko, *Jagiellonian University, Poland*

Host biology and population structure shape microbiome variation in sap-feeding insects

Microbial symbionts play a central role in insect evolution by enabling hosts to exploit nutritionally challenging diets and adapt to diverse ecological conditions. In sap-feeding Auchenorrhyncha, ancient obligate symbioses are essential for host survival, while facultative microbes provide additional ecological flexibility. However, how host biology, population structure, and geography jointly shape microbiome variation across species remains poorly understood. Here, we analysed the microbiomes of over 5,000 adult individuals spanning more than 30 Auchenorrhyncha species, including planthoppers (Fulgoromorpha) and leafhoppers (Cicadomorpha), sampled from over 150 wild populations across mainland Northern Europe and Baltic Sea islands. Using 16S rRNA amplicon sequencing combined with host COI barcoding, we assessed how microbial community composition and abundance vary with host species identity, population structure, geographic location, and sex. Microbiome composition differed strongly among host species, reflecting deep evolutionary divergence in symbiotic systems dominated by obligate endosymbionts. At the population level, beta-diversity analyses revealed consistent effects of geographic location, indicating contributions of environmental context and population structure. Differences between males and females were primarily quantitative rather than qualitative: community composition was largely shared between sexes, whereas symbiont abundance was often higher in females, with effect sizes varying among species. Finally, we applied hierarchical modelling of species communities (HMSC) to disentangle the relative contributions of host biology, geography, and host genetic background to symbiont presence and abundance. Together, these results demonstrate that microbiome variation reflects the interplay between long-term evolutionary constraints and ecological context in widespread insect hosts.

Session 7B – Ecological Interactions

09:00 – 09:15

Davide Piazza, *University of Padua, Italy*

How are microbiomes transmitted across animals? An integrative approach to quantify the ecological factors driving microbiome transfer using guppies

Microorganisms play an essential role in animal health, yet the mechanisms governing their colonization and transmission remain poorly understood. Here, we investigated microbiome transmission using guppies (*Poecilia reticulata*), an established model in animal behavioural ecology. Aquatic systems provide a unique opportunity to disentangle environmental from host-driven processes of microbiome dispersal. We generated two cohorts of guppies with distinct microbial profiles and placed them in cohabitation setups either allowing direct contact or preventing it. Using an integrative framework combining genomic approaches (16S rRNA amplicon sequencing and metagenomics), behavioural tracking, fluorescence microscopy, and ecological modelling, we characterised microbiome dynamics across four host compartments (skin, gills, gut, and gonads). Our results reveal distinct transmission pathways for external versus internal microbiomes, as well as pronounced sex-specific and microbe-specific differences in transmission dynamics. Understanding how microbiomes are transmitted between hosts, and how these processes vary across tissues, is crucial for elucidating microbiome function. These insights also hold strong potential for improving microbiome-based interventions across a wide range of animal systems, including humans.

09:15 – 09:30

Bartłomiej Molasy, *Jagiellonian University, Poland*

Evolutionary stability of bumblebee–microbiota interactions in cold environments

The evolutionary stability of host–microbiota interactions is often assumed to underpin animal adaptation, yet their persistence under extreme environmental conditions remains poorly understood. Cold environments impose strong physiological and ecological constraints, including short growing seasons, limited resources, and thermal stress, making them ideal systems to investigate the resilience of symbiotic relationships. Bumblebees (*Bombus*) harbour a simple, host-specific gut microbiota composed of a small number of bacterial genera commonly referred to as a core microbiota. While this community is thought to contribute to host health and adaptation, its dynamics across harsh northern environments remain largely unexplored. To address this, we analysed the gut microbiome of 137 individuals representing 13 *Bombus* species collected from cold regions in Sweden and Greenland (Zackenberg Valley). Amplicon sequencing of bacterial 16S rRNA gene regions (V1–V2 and V4), combined with cytochrome oxidase subunit I (COI) barcoding, enabled microbiota profiling and host species identification. Complementary metagenomic analyses provided insights into microbial functional potential and strain-level diversity, while fluorescence in situ hybridisation (FISH) confirmed the presence, absence, and spatial localisation of key taxa. We observed the absence of *Gilliamella*, a key genus of the bumblebee core microbiota, in individuals from Greenland, challenging the assumption of a universally conserved core microbiota across *Bombus*. These findings suggest that extreme environmental conditions may destabilise host–microbe associations, either through direct ecological constraints or through the fitness costs associated with maintaining symbionts. Overall, this study highlights the context dependence of host–microbiota interactions and provides new insights into their role in adaptation to extreme and changing environments.

09:30 – 09:45

Michelle Borgers, *Martin-Luther-University Halle-Wittenberg, Germany*

Living in the shadows of fungi – the bacterial symbionts of bark beetles

To efficiently exploit plant sap, many phloem- and xylem-feeding insects have evolved intimate symbioses with microorganisms. These symbionts contribute to nutrient supplementation, digestion, and detoxification of plant defence compounds. The composition of these microbial communities can vary across species, populations, and individuals. Bark beetles are key components of forest ecosystems and harbour diverse bacterial and fungal microbiota that facilitate colonisation of host trees. While research has largely focused on ambrosia beetles and their fungal symbionts, comparatively little is known about their associated bacterial communities. In this study, we characterise the bacterial microbiome of bark beetles from the Leipzig floodplain forest. Using eight cross-vane traps, we collected 15,174 individuals between March and June 2025 at two-week intervals. Specimens were morphologically sorted, and a subset (n = 533) was identified using COI barcoding. We profiled bacterial communities using near full-length 16S rRNA metabarcoding with Oxford Nanopore sequencing. In total, approximately 2 million reads (mean length ~1,430 bp) were obtained from 494 individuals representing four ambrosia beetle species, with an average of 3,879 reads per sample. We analysed temporal variation in microbial communities both within and among species to characterise patterns of symbiont diversity and dynamics. This study provides new insights into the bacterial microbiomes of bark beetles and highlights their temporal variability, contributing to a more comprehensive understanding of insect–microbe interactions in forest ecosystems.