

Abstract Book

2024 Conference of the Netherlands Society for Evolutionary Biology

Tuesday 23 April 2024

Akoesticum, Ede, The Netherlands



Sponsored by



Organizing committee

Vasilis Kokkoris, Anne Kupczok, Renske Onstein, Melissah Rowe, & Sijmen Schoustra

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Program April 23 2024

- 8:45** Arrival with coffee/tea
- 9:15** Welcome & Introduction, Auditorium
- 9:25** **Keynote 1: Liliana d'Alba** (Naturalis) *"In Living Color: Evolutionary Insights into the Ecology of Animal Chromatic Patterns"*, Auditorium
- 09:55** **Keynote 2: Tom Shimizu** (AMOLF) *"Traveling-wave strategy for plant-mycorrhizal trade"*, Auditorium
- 10:30** Coffee/tea break
- 11:00** Parallel sessions with contributed talks
I Auditorium
II Tuinzaal
- 12:15** Lunch with network opportunities
- 13:30** **Keynote 3: Rosemary Gillespie** (Berkeley) *"Biodiversity & Belonging: Eco-evolutionary Dynamics Across an Island Chronosequence"*, Auditorium
- 14:00** NL Evo Biology 2023 prize winner, Auditorium
- 14:20** Coffee/tea break
- 14:50** Parallel session with contributed talks
III Auditorium
IV Tuinzaal
- 15:50** General Assembly, Tuinzaal
- 16:30** Cultural Intermezzo - FRAME by 'DansBlok', Auditorium
- 17:10** Poster session, Tuinzaal
- 18:30** Poster Prize winner & Closing remarks, Tuinzaal
- 18:35** Dinner

Keynote speakers

Liliana d'Alba (Naturalis)

Liliana D'Alba is an integrative and evolutionary biologist studying the evolutionary drivers of phenotypic diversity and their mechanistic foundations in birds and reptiles. She integrates field and laboratory methods to understand why and how birds are so colorful and what explains the large diversity of egg forms in vertebrates.

TITLE: "In Living Color: Evolutionary Insights into the Ecology of Animal Chromatic Patterns"

Abstract: Coloration serves many essential functions in the lives and reproduction of animals, it mediates social interactions with conspecifics and the environment and, because it is easily quantifiable it has rapidly become a model system to understand the evolution of phenotypic diversity. Using birds as a model system, I first reveal what we know about color production mechanisms, its origins in bird evolution and its importance in facilitating species diversification. Then I examine some examples of interactions between integumentary coloration and environment that enable us to make predictions about environment-specific changes in animal phenotypes particularly in light of anthropogenic impact. Finally, I briefly discuss how the conceptual foundations of color production and evolution could extend beyond biology and potentially be applied to research on biotechnology and the design of new materials.

Tom Shimizu (AMOLF)

Thomas Shimizu is a Group Leader at AMOLF Institute and a Professor of Physics at the Vrije Universiteit Amsterdam. His lab studies the physics of biological behavior, broadly defined. For the last several years his AMOLF team has been building a robot for automated imaging of growth and transport processes in mycorrhizal mycelial networks. He is known for developing innovative experimental and theoretical approaches to the study of small-organism behavior, such as bacterial motility (for which he won an NWO VIDI Award in 2012, as well as an Allen Distinguished Investigator Award in 2013 from the Paul G. Allen Family Foundation), and nematode worm motility (for which in 2015-2021 he was the leader of a Netherlands-wide consortium to investigate physical origins of variability in organism-scale behavior funded by FOM/NWO). His work on fungal networks has grown through a long-term collaboration with Prof. Toby Kiers and Dr. Vasilis Kokkoris (both of Vrije Universiteit), together with whom he is excited to pioneer a new biophysics of fungi that connects cellular-level dynamics to ecology and evolutionary biology.

TITLE: "Traveling-wave strategy for plant-mycorrhizal trade"

Abstract: Mycorrhizal fungi construct complex mycelial networks to collect and trade nutrient resources with plant roots. Like human-built commercial networks, these fungi face conflicting trade-offs in building networks that balance low construction costs with high geographic coverage and long-distance transport. Yet, how they navigate supply-chain design challenges is unknown. To monitor the construction of a living trade network, we built a custom-designed

robot for high-throughput time-lapse imaging that could track >500,000 fungal nodes simultaneously. We then measured ~100,000 cytoplasmic flow trajectories inside networks, toward and away from roots. We found mycorrhizal fungi build networks as 'self-regulating' traveling waves: pulses of growing tips pull an expanding wave of nutrient-absorbing mycelium whose density is self-regulated by fusion. I will discuss the significance of this traveling-wave strategy within the context of symbiotic trade, and present the first evidence that these fungi, despite their diffuse and distributed anatomy, achieve network-level control of cytoplasmic flows to meet trade demands.

Rosemary Gillespie (University of California, Berkeley)

Rosemary Gillespie is a Professor and Schlinger Chair in the Department of Environmental Science, Policy, and Management at the University of California, Berkeley, and is currently a Visiting Research Fellow at Jesus College, Oxford, UK. She was born in Scotland, receiving her B.Sc. in Zoology from Edinburgh University in 1980, then her PhD at the University of Tennessee Knoxville in 1986, and starting work in Hawaii in 1987, initially as a postdoc, and then in 1992 as Assistant Professor in Zoology and Researcher in the Hawaiian Evolutionary Biology Program. She joined the faculty at the University of California in Berkeley in 1999, where she continues her research focus on archipelagoes in the Pacific, using islands of known age and isolation to assess the combined temporal and spatial dimension of biogeography and determine patterns of diversification, adaptive radiation, and associated community assembly and conservation challenges. Dr. Gillespie is a member of the American Academy of Arts and Sciences and has been President of the American Genetics Association, the International Biogeography Society, and the American Arachnological Society, and is currently President of the International Society of Arachnology.

TITLE: "Biodiversity & Belonging: Eco-evolutionary Dynamics Across an Island Chronosequence"

Abstract: Biodiversity is suffering catastrophic decline and tracking and understanding the factors affecting change is a major challenge and one we are currently not meeting, in particular on remote islands. Here, I examine insights we can gain into biodiversity dynamics using temporal snapshots of biodiversity through extended evolutionary time. I use the Hawaiian chronosequence of islands of different geological ages to infer ecological and evolutionary change through extended time. I will first examine the factors that have shaped species diversification among different lineages of spiders and consider circumstances that allow the parallel or convergent evolution of ecological forms on different islands. I will then discuss how we are using high throughput sequencing approaches to infer how whole communities of arthropods change through the time frame provided by the islands of different age. I will focus on patterns of increasing diversity and complexity of interaction networks across the chronosequence. By adopting various theoretical and modelling approaches, we hope to encapsulate the "status" of a biological community in terms of its integrity and potential resistance and resilience to change in the future.

NL Evo Biology 2023 prize winner

Shixiong Cheng, Chris G. C. Jacobs, Elisa A. Mogollón Pérez, Daipeng Chen, Joep T. van de Sanden, Kevin M. Bretscher, Femke Verweij, Jelle S. Bosman, Amke Hackmann, Roeland M. H. Merks, Joost van den Heuvel & Maurijn van der Zee

TITLE: A life-history allele of large effect shortens developmental time in a wild insect population

Abstract: Developmental time is a key life history trait with large effects on Darwinian fitness. In many insects, developmental time is currently under strong selection to minimize ecological mismatches in seasonal timing induced by climate change. The genetic basis of responses to such selection, however, is poorly understood. To address this problem, we set up a long-term evolve-and-resequence experiment in the beetle *Tribolium castaneum*, and selected replicate, outbred populations for fast or slow embryonic development. The response to this selection was substantial, and embryonic developmental timing of the selection lines started to diverge during dorsal closure. Pooled whole-genome resequencing, gene expression analysis, and an RNAi screen pinpoint a 222bp deletion containing binding sites for Broad and Tramtrack upstream of the ecdysone degrading enzyme Cyp18a1 as a main target of selection. Using CRISPR/Cas9 to reconstruct this allele in the homogenous genetic background of a laboratory strain, we unravel how this single deletion advances the embryonic ecdysone peak inducing dorsal closure, and show that this allele accelerates larval development, but causes a trade-off with fecundity. Our study uncovers a life-history allele of large effect and reveals the evolvability of developmental time in a natural insect population.

NLSEB

Program parallel sessions

Session I Auditorium, Macro - Evolution

- 11:00 **Carne Blanco Gavalda** Niche conservatism prevails in repeated long-distance colonization of Madagascar mountains by the genus *Helichrysum*
- 11:15 **Jeremy Miller** Global Patterns in Spider Occurrence Data: Monitoring Cryptic Fauna in an Era of Human Observations Networks and Computer Vision Models
- 11:30 **Dieder de Frens** The repeated evolution of dispersal syndromes during angiosperm evolution
- 11:45 **Niladri Mondal** Genome and body size diversity of the fishes using comparative phylogenetic methods
- 12:00 **Luiz Jardim de Queiroz** Fish species–area relationships in the ‘archipelago’ of perialpine lakes amidst species extinctions and introductions

Session II Tuinzaal, Modeling Evolution

- 11:00 **Duur Aanen** Applying Weissman’s germplasm theory to budding yeast
- 11:15 **Hanna ten Brink** Changing environmental conditions result in the sudden collapse of a recently formed species complex
- 11:30 **Marco Saltini** Complex life cycles, ecological context, and evolutionary diversification
- 11:45 **Jana Riederer** Sexual selection driven by direct benefits leads to the erosion of direct benefits
- 12:00 **Hilde Schneemann** A fitness landscape model captures the effects of ploidy on hybrid fitness

Session III Auditorium, Genetics (omics) & Evolution

- 14:50 **Hannah Dugdale** Single-generation fitness proxies as predictors of long-term genetic contributions in a cooperatively breeding bird
- 15:05 **Rachael Cargill** The Arbuscular Mycorrhizal Fungal Cell Atlas
- 15:20 **Severin Uebbing** Evolutionary innovation in conserved regulatory elements associated with developmental genes in mammals
- 15:35 **Toni Gossmann** Phylonomtomics uncovers diverse evolutionary trajectories of mitogenomic fossils buried in mammalian and avian genomes

Session IV Tuinzaal, Ecology & Evolution

- 14:50** **Alanna Leale** Shifts and rebound in microbial community function following repeated introduction of a novel species
- 15:05** **Thomas Blankers** Uncertainty in selective regimes more than drift limits the predictability of evolution
- 15:20** **Euan Angus Young** The consequences of parental age on offspring fitness in humans
- 15:35** **Elise MJ Laetz** The Deadly Trio. How warming, acidification & deoxygenation destabilize the animal / algae symbiosis



Cultural Intermezzo

“FRAME” by DansBlok

In nature, the law of the strongest often applies, and fighting for an important position within an area or community is common. Yet, there are also forms of harmonious coexistence between two different groups - such as animals and plants - in which both parties benefit from each other's presence. Can we learn something from this struggle for space and acceptance of coexistence? We will explore this in a dance duet

DansBlok is a young, professional dance collective based in Leiden. We draw inspiration from social themes that fascinate us. Recognizable feelings and situations that we as young adults experience in our society are translated into stylized and at the same time abrasive productions.



Abstracts contributed talks (presenting author underlined)

Session I – Auditorium / Theme: Macro-Evolution

Niche conservatism prevails in repeated long-distance colonization of Madagascar mountains by the genus *Helichrysum* (Compositae, Gnaphalieae)

C. Blanco-Gavaldà, C. Roquet, G. Puig-Surroca, S. Andrés-Sánchez, S.G. Razafimandimbison, L.D. Moreyra, A. Susanna, M. Galbany-Casals, et al.

Autonomous University of Barcelona

Madagascar is a major biodiversity hotspot with exceptional levels of species richness and endemism. Despite the island's prolonged geographic isolation, most of its endemic plant species are the result of recent dispersal from continental Africa. The genus *Helichrysum*, which represents one-fifth of the Compositae species of the island, is a relevant case to study the evolutionary and biogeographic history of Madagascar flora. We generated a phylogeny based on target-enrichment data from 350 *Helichrysum* species (with 60% of Madagascar endemics) and conducted ancestral range estimation analyses. Our results reveal at least six independent dispersals from Africa since the Pliocene. Madagascar was colonized at least twice by Tropical Afromontane ancestors, leading to major radiations in the mountains. The southern African montane grasslands have also played a key role in Madagascar's colonization, giving rise to at least three clades. *H. mahafaly*, endemic to the arid SW region of Madagascar, originated from an ancestor coming from the arid region of SW Africa. The similarity between source and colonized habitats suggests the prevalence of niche conservatism, a common phenomenon in allopatric speciation. Our results underscore the affinities between continental Africa and Madagascar's montane floras. The radiations of *Helichrysum* in Madagascar mountains occurred within the last 2 My, coinciding with a transition towards a cool, arid climate and the expansion of open habitats.

Global Patterns in Spider Occurrence Data: Monitoring Cryptic Fauna in an Era of Human Observations Networks and Computer Vision Models

Jeremy Miller

Naturalis Biodiversity Center

Records of which species have been observed where and when is increasingly critical to understanding our changing world. Monitoring cryptic and diverse groups of organisms is critical at a time when our environment is warming and urbanizing. GBIF, the Global Biodiversity Information Facility, is the largest aggregator of primary biodiversity records. Most records in GBIF come from two major source categories: human observations networks, which tend to produce huge numbers of records but for relatively few species, and museum collections databases, which provide a more modest number of records including many species not found in the human observations networks data or other sources. Analysis using trait data shows that for the 5.3 million global records of spiders, data from human observations networks have significantly larger body size than museum collections data, suggesting the former is dominated

by relatively conspicuous species. Semiautomated taxonomic tools such as DNA barcoding and machine learning applications now complement classical expert-based taxonomy. Computer vision models are a form of machine learning that are currently being applied to taxonomic determination. We investigate museum collections as source material for building image libraries to power computer vision models. A blend of classical and semiautomated high-throughput taxonomic determination methods holds promise for biodiversity monitoring that includes cryptic and diverse taxa.

The repeated evolution of dispersal syndromes during angiosperm evolution

Dieder de Frens (WUR), Renske Onstein (Naturalis), Freek Bakker (WUR)

Wageningen University and Research & Naturalis Biodiversity Center

Angiosperms have evolved a diverse range of seed-dispersal syndromes over their evolutionary history that have undoubtedly played a role in their rise to dominance. However, how ancient angiosperms were dispersed, how global climate impacted the emergence of dispersal syndromes, and the influence of shifts between these syndromes on the spread of angiosperms across major biomes, remains largely unknown. Here, we addressed these questions by examining a set of fruit traits for >1200 species representing all extant angiosperm families. The ancestral states of major angiosperm clades, trends in the evolution of dispersal syndromes, and evolutionary correlations of dispersal and biome transitions were modelled. Marginal ancestral state estimation illustrated that ancestral angiosperms were likely dispersed by animals (zoochory) and had fleshy, indehiscent fruits. Stochastic character mappings showed that over macroevolutionary time, relative increases in zoochory and wind-mediated dispersal (anemochory) were associated with decreases in global average temperatures, water-mediated dispersal (hydrochory) showed no such pattern. We also found that rates of biome transition were dependent on zoochory, suggesting that animals have mediated the repeated colonization of angiosperms across biomes. In conclusion, the evolution of seed-dispersal syndromes and zoochory in particular have played an influential role in angiosperm evolution by enabling shifts between key traits and biomes.

Genome and body size diversity of the fishes using comparative phylogenetic methods

Niladri Mondal, Ingrid Bunholi, Hugo F. Gante

KU Leuven

Genome size is one of the main factors shaping organismal traits by having a strong correlation with cell size and impacting metabolic and developmental rates. While it is expected that body size varies depending on the number of cells and cell size, and as cell size is dependent on genome size, how body size and genome size covariate have rarely been investigated. Fishes are the largest group of vertebrates and possess a wide range of genome size and body size variation across the macroevolutionary level. Those conditions make them suitable to investigate a possible correlation between genome size and body size. We collected genome size and body size data for 1169 ray-finned species across 61 orders and investigated a correlation between them using both phylogeny-dependent and phylogeny-independent regression analyses. Both positive and negative correlations were found at subclade levels (i.e., order level). We also

examined trends in genome size and body size along the phylogeny to determine, for example, how many times reduction or increase occurred. This includes modeling the rate of evolution for both body and genome size to investigate the pattern of size distribution throughout phylogeny. We argue that the biological size index, a novel size metric calculated by factoring both genome size and body size – is a more sensible metric when discussing the size of an organism.

Fish species–area relationships in the ‘archipelago’ of perialpine lakes amidst species extinctions and introductions

Luiz Jardim de Queiroz, Timothy J. Alexander, Martin Luger, Daniela Achleitner, Rampal Etienne, Luís Valente & Ole Seehausen

Naturalis Biodiversity Center & University of Groningen

The species–area relationship (SAR), by which the species number increases with area, is one of the most universal patterns in ecology. SARs’ development has been intrinsically linked with the equilibrium theory of island biogeography, which states that there is a balance between immigration and extinction, and that the processes determining species composition are stochastic and equivalent across taxa. Yet, ISARs (island SARs) often do not account for other effects such as evolution (speciation), ecology (competition and predation) or anthropogenic factors (e.g. human-driven extinctions and introductions). We address the role of the latter on the fish community of 49 postglacial perialpine lakes distributed across the Danube, Rhine, Rhone and Po. We compiled a historic list of fish species distribution, and contemporary extinctions and introductions. We show that richness is strongly correlated with lake area, but the degree of correlation is distinct among drainages. Further, we found that the form and shape of the ISARs has changed following extinctions and introductions, especially by changing the slope of the curves. The magnitude of the impact of these threats was also distinct among drainages. Ongoing assessment of the effect of other lake features (e.g., elevation, isolation and depth), and their interplay with extinctions and introductions, can provide better understanding of the Anthropocene’s impact on biodiversity dynamics, both presently and in the future.

Session II – Tuinzaal / Theme: Modeling Evolution

Applying Weissman's germplasm theory to budding yeast

Duur K. Aanen; Bhavya Sree Vadlamudi

Wageningen University

In multicellular organisms, only mutations in germline cells can directly affect future generations while mutations in somatic cells cannot. This germline-soma distinction does not make sense for unicellular organisms, since the cell is the organism. Or does it? I challenge the generality of this assumption by considering the lifecycle of baker's yeast (*Saccharomyces cerevisiae*). Even though fermentation yields fewer cells than respiration, under aerobic conditions yeast cells use fermentation of glucose to produce ethanol. Only when glucose is exhausted, cells switch to respiration of the produced ethanol. I hypothesize that only a fraction of the cells continue to divide and switch to respiration. A change from exponential to linear growth after this shift is consistent with asymmetrical cell division, with a senescing mother cell, producing a finite number of dormant rejuvenated daughter cells. I present simulations of various fractions of cells continuing to divide asymmetrically and compare my simulations with experimental growth curves. According to my hypothesis, most cells produced during fermentative growth are "somatic", i.e. do not produce any offspring, while the cells continuing to divide after the switch to respiration constitute the germline, as they exclusively produce offspring and no somatic cells. I will discuss potential adaptive explanations for germline-soma differentiation and implications for the two evolutionary explanations for aerobic fermentation.

Changing environmental conditions result in the sudden collapse of a recently formed species complex

Hanna ten Brink

Universiteit van Amsterdam

Adaptive radiations, where a lineage diversifies into multiple species exploiting a variety of niches, are responsible for much of the diversity of life. It is therefore important to understand the factors that drive such radiations and how changing environmental conditions affect their persistence. Using a size-structured model, I study how changing environmental conditions impact the persistence of a six-species complex. At birth, individuals are constrained to feed on a common resource. As they mature, individuals diversify into six specialized forms, each adapted to feed on specific resources. Increasing food availability for a focal species can lead to the collapse of the species complex, with the majority of species going extinct, sometimes including the focal species itself. A change in environmental conditions affecting one species can trigger a cascade effect, altering the size structure of the focal species and subsequently affecting resource availability for other species. Coexistence of all species is under these altered ecological conditions no longer possible. Importantly, once species are lost, they cannot easily re-establish even if environmental conditions return to their original state, resulting in irreversible biodiversity loss. These findings underscore the vulnerability of species complexes to environmental change and highlight the potential for unexpected outcomes in the face of shifting ecological conditions due to climate change.

Complex life cycles, ecological context, and evolutionary diversification

Marco Saltini, Paula Vasconcelos, Claus Rueffler

Wageningen University and Research

Most eukaryotic organisms have complex life cycles, with ecological interactions shifting between juvenile and adult stages. Our models explore the impact of complex life cycles on community assembly through trait-dependent evolutionary diversification under diverse ecological contexts: different resource availability and different genetic architectures. We show that community richness depends on ecological contexts: gradual evolution results in variable species richness depending on resource availability, while mutations of large phenotypic effect promote the assembly of communities of species with complex life cycles. This reveals that complex life cycles do not inherently broaden the scope for evolutionary diversification, as the latter strongly depend on ecological contexts. This underscores the need for consideration of ecological contexts in trait-dependent diversification studies and, more specifically, in eco-evolutionary models of diversification.

Sexual selection driven by direct benefits leads to the erosion of direct benefits

J.M. Riederer, G. Cordeschi, F.J. Weissing

University of Groningen

Most sexual selection models assume that the evolution of female choosiness is driven by indirect (genetic) benefits, such as the production of more viable offspring or more attractive sons. There is ample empirical evidence that female choosiness can also provide direct (non-genetic) benefits, including access to good territories or paternal care. Yet, theoretical models of direct-benefits sexual selection are scarce. Here, we explore such a model using individual-based evolutionary simulations. In the model, males differ in the amount of resources at their disposal. Males can allocate resources into parental care (a direct benefit) or into ornamentation. Females can choose mates based on their ornamentation. The simulations reveal that female choosiness for ornamented males readily evolves, which in turn drives males to allocate more resources to ornamentation. At the individual level, females benefit from choosiness, since ornamentation is positively related to the amount of paternal care received. However, at the population level, coevolution between male ornamentation and female preferences leads to (almost complete) erosion of direct benefits. We also discuss intricacies of the co-evolutionary dynamics, such as transient polymorphisms in both male and female strategies, reversals in the direction of evolution, and population extinction ('evolutionary suicide') driven by direct-benefit sexual selection.

A fitness landscape model captures the effects of ploidy on hybrid fitness

Hilde Schneemann, John J. Welch

Institute of Science and Technology Austria

When two genetically differentiated populations or species come into contact and interbreed, their hybrid offspring will contain a mosaic of the genetic variants characterizing the parental

lineages, re-arranged into novel combinations. The fitness of these hybrids is central to the evolution of reproductive isolation, but also plays an important role in crop and animal breeding. Ploidy plays an important role in hybrid fitness, yet its exact effects remain poorly understood. I will present a simple, yet flexible, fitness landscape model, that can predict the fitness of hybrids of any ploidy and between any number of parental lineages. I show that this model can account for a broad range of patterns of hybrid fitness observed consistently across taxa. I then re-analyze published data on diploid and synthetically induced tetraploid hybrid crosses in rye and maize. This analysis suggests a novel interpretation of these data, and demonstrates that the model effectively captures dosage effects in tetraploids that allow us to quantitatively predict the relative fitness of different types of hybrids.



Session III – Auditorium/ Theme: Genetics(omics) & Evolution

The consequences of parental age on offspring fitness in humans

Euan A Young, Hannah Dugdale, and Erik Postma

Rijksuniversiteit Groningen

The consequences that parental age at birth have on children's fitness is important for understanding the evolution of the human life history. However, examining the intergenerational effects of ageing in human observational studies is challenging because parental ages correlate with many factors such as wealth and family structure. We estimated the effects of parental age on children's lifespan and reproduction using Swiss genealogical records from 1700-1950. We used within-subject centring to distinguish between among- and within-individual effects, controlling for confounding factors such as socioeconomic status, birth order, and temporal variation. We found that as both mothers and fathers age, their offspring have reduced childhood survival. However, we find no consequences of parental age on the lifespan of children after childhood, or their reproductive success, where social factors appear more important. Our results illustrate the importance of accounting for confounders when examining parental age effects and that reproductive ageing may shape selection on human reproductive timing through reduced childhood survival of offspring

The Arbuscular Mycorrhizal Fungal Cell Atlas

Rachael I.M. Cargill, Loreto Oyarte Gálvez, Sander van Otterdijk, Corentin Bisot, Marije van Son, Thomas S. Shimizu, E. Toby Kiers, Vasilis Kokkoris

Amsterdam Institute of Life and Environment, Vrije Universiteit Amsterdam

Arbuscular mycorrhizal (AM) fungi form extensive underground networks of filamentous hyphae that connect plant roots with the soil matrix. Interestingly, the AM fungal mycelium is coenocytic, resembling an 'open pipe' system with no cross barriers. This means all cellular contents flow through the mycelium in a common cytoplasm. This unique cellular organisation raises questions about how cellular components are organised, and how internal flows influence this organisation. Image analyses of the hyphal cell components can be challenging due to their fast movements, and very little is known about the structure of AM fungal cells and the underlying mechanisms regulating cytoplasmic flow. We built a custom-designed fluorescence microscope which, combined with fluorescent probes, enabled us to image the extraradical mycelial cellular components spatiotemporally without disrupting the network. Together with other microscopy techniques in live and fixed cells, these methods allowed us to explore the organisation, relative abundance and volume of nuclei and lipids, the structure of the microtubule cytoskeleton and their relation to nuclei. These results begin to uncover fundamental aspects of AM hyphal structure and function and provide a foundation for exploring the mechanisms controlling cytoplasmic flow.

Evolutionary innovation in conserved regulatory elements associated with developmental genes in mammals

Severin Uebbing, Acadia A. Kocher, Marybeth Baumgartner, Yu Ji, and James P. Noonan

Universiteit Utrecht

Transcriptional enhancers regulate gene expression in a cell type- and time point-specific manner. Multiple enhancers each regulating expression in specific contexts render gene regulatory architecture modular. This modularity has invited theoretical predictions that enhancers should be less affected by pleiotropic constraints than a gene's promoter or protein-coding sequence are, and that enhancer evolution should be important for evolutionary change at constrained developmental patterning genes. To test these theories, and to investigate what types of genes most commonly associate with regulatory evolution, we identified signatures of accelerated evolution in conserved gene regulatory elements across mammals. Interestingly, we found that genes that experienced a lot of sequence acceleration across the phylogeny were enriched for functions in development and gene regulation. Transcription factor genes and genes in the Notch signaling pathway showed more acceleration within their associated gene regulatory elements than other genes. We studied one accelerated element in depth using a transgenic enhancer assay and found that the modified sequence version drives enhancer activity in a novel expression domain, possibly implicating it in digit reduction in hoofed mammals. Overall, our results provide evidence that enhancer evolution has contributed frequently to evolutionary change involving constrained developmental signaling genes in mammals.

Phylonumtomics uncovers diverse evolutionary trajectories of mitogenomic fossils buried in mammalian and avian genomes

Toni Gossmann

TU Dortmund University

Sporadically genetic material that originates from an organelle genome integrates into the nuclear genome. However it is unclear what processes maintain such an integration over longer evolutionary time. Recently it was shown that nuclear DNA of mitochondrial origin (NUMTs) may harbour genes with intact mitochondrial reading frames despite the fact that they are highly divergent to the host's mitochondrial genome. Two major hypotheses have been put forward to explain the existence of such mitocoding nuclear genes: (A) recent introgression from another species and (B) long-term selection. To address whether these intriguing possibilities we conducted a large-scale analysis which we phrase "phylonumtomics" of more than 1,000 avian and mammalian species. We indeed identified that the subclass of divergent NUMTs harbouring mitogenes with intact reading frames are widespread across mammals and birds. We can show that for these NUMTs signatures of cross-species introgression are widespread in birds, but not mammals with the exception of ungulates. We can also show that a substantial fraction of deeply divergent NUMTs are maintained by selection. For a small number of NUMT genes we identify an evolutionary signature that is consistent with adaptive evolution including one human NUMT that is shared among seven ape species. This highlights the intriguing possibility that NUMT insertions occasionally may contribute to adaptation.

Session IV- Tuinzaal / Ecology & Evolution

Shifts and rebound in microbial community function following repeated introduction of a novel species

Alanna M. Leale, Francisca Reyes Marquez, Bas Zwaan, Eddy J. Smid, Sijmen Schoustra

Wageningen University & Research

Natural microbial communities continually encounter novel species that may successfully establish or simply be transient, yet both outcomes can alter the resident community composition and function. Preserving natural microbial communities and innovating synthetic ones require insight on the immediate and long-term impact of species introductions to both composition and function. For instance, it remains unclear whether there are gradual and long-term effects from repeated invasions where the introduced species fails to establish (so-called failed invaders). To investigate the persistent impacts by failed invaders, we performed an experimental test of community stability over multiple generations against repeated novel species introduction. We propagated a natural microbial community from a traditional fermented milk beverage for approximately 100 generations, with or without, repeated introduction of *Escherichia coli* at each transfer. Community function was determined by metabolic profiling, in which we observed alterations immediately following *E. coli* introduction, followed by recovery once ceased. In contrast to this proxy of community function, changes in the bacterial community composition were never detected. Our results evidence that community composition and function do not necessarily respond in parallel to an introduced species, potentially due to genotypic changes below species level detection or metabolic plasticity. Our work shows an ability for functional recovery in microbial communities and contributes insight on long-term community stability to sustained disturbances.

Uncertainty in selective regimes more than drift limits the predictability of evolution

Thomas Blankers, Karen Bisschop, Meike T. Wortel, Ken Kraaijeveld, Martijn Egas, Jacintha Ellers, Astrid T. Groot, Marcel E. Visser

University of Amsterdam

The repeatability of evolution is fundamentally interesting in understanding the origin and diversification of life as well as in developing evolutionary forecasting tools. Evolutionary repeatability is limited by unrepeatably selective regimes or by random limits imposed through stochastic evolutionary processes. We performed a replicated evolution experiment exposing *Caenorhabditis elegans* to a novel dietary bacterium in five institutes. Replication across institutes led to variation in selective regimes: although institutes shared the main axis of selection – adapting to new food – there was variation through lab-specific conditions, including lab-specific microbiomes. Replication within institutes varied the potential for stochasticity (drift) by introducing demographic and population genetic treatments: a population bottleneck, different reproductive modes, population age synchronization, and gene flow. We found high variation in fitness evolution across these different conditions. The effect of uncertainty in selective regime generally outweighed within-lab between-treatment (drift potential) variance in shaping repeatability. However, this general finding holds only up until a certain reduction in

effective population size. Our findings provide insight into boundary conditions within which information about selective regimes will increase our ability to predict evolution and beyond which stochastic evolutionary forces introduce significant random limits.

Single-generation fitness proxies as predictors of long-term genetic contributions in a cooperatively breeding bird

*Chesterton, E., Young, E.A., Sparks, A.M., Burke, T., Komdeur, J., Richardson, D.S., Dugdale, H.L.
University of Groningen*

Single-generation fitness proxies are often used to estimate individual fitness. How well these proxies predict long-term genetic contributions to future populations, however, is poorly understood. Here, we use the long-term Seychelles warbler dataset to consider how the acquisition of a dominant breeding position, age at first breeding attempt, length of dominant breeding tenure, lifespan, and lifetime reproductive success predict individual genetic contributions to a population ~3 generations in the future, as well as the likelihood of lineage extinction. We found that the acquisition of a dominant breeding position and age at first breeding attempt had no effect on individual genetic contributions, or the likelihood of lineage extinction. The length of dominant breeding tenure had a positive effect on the individual genetic contributions of males, but not females. Longer lifespans and a higher lifetime reproductive success were positively associated with individual genetic contributions and a reduced likelihood of lineage extinction in both sexes. Lifetime reproductive success explained more of the variance in individual genetic contributions than any single-generation fitness metric. Future studies should carefully consider the relationship between life-history metrics and reproductive success, as the relationship between life-history measures and individual genetic contribution is likely contingent upon the relationship between life-history and reproductive success.

The Deadly Trio. How warming, acidification & deoxygenation destabilize the animal / algae symbiosis

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Anthropogenic climate change is causing a domino effect of warming temperatures, increased acidification, and hypoxia – the “deadly trio” of environmental stressors. These stressors have been implicated in every mass extinction, but technical complications have made studying all three difficult in laboratory settings. Using a novel method, we investigated how exposure to two weeks of the “deadly trio” stressors affect the sea anemone, *Exaiptasia diaphana* and its symbiotic algae, a model system for stony corals. Following two weeks of exposure (based on the IPCC’s worst case scenario), performance tests were conducted to determine metabolic rate, thermal tolerance, and thermal tolerance plasticity. Anemones exposed to the deadly trio showed metabolic depression, which is likely an energy conservation strategy, due to a correlation with increased thermal tolerance. Furthermore, combined exposure of ocean acidification and hypoxia led to enhanced thermal tolerance plasticity, possibly because increased carbon dioxide enhanced photosynthetic activity. Multiple other parameters related to animal/symbiont health and performance were also investigated, but they remained stable

across all treatments, indicating a healthy symbiosis and good prognosis for acute exposure to these stressors. Our findings highlight the importance of considering all of the deadly trio stressors in ecophysiological studies and provide a reliable method for examining these stressors in laboratory settings.



Poster Abstracts – Alphabetically arranged by presenting author (underlined)

Factors that influence the caste ratio in a bacterial division of labour

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In *Streptomyces*, spontaneous genomic deletions can lead to the emergence of a distinct population of mutant antibiotic superproducers. Little is known about how these mutants arise and their distribution through colonies. In this work, we explored the temporal, spatial and dynamics of phenotypical mutations in *Streptomyces coelicolor* by combining empirical and theoretical approaches to understand: how and where this division of labour arises in growing colonies, and how the frequency of mutants is determined in response to resources or stress. To elucidate changes in the proportion of mutants in *S. coelicolor* colonies (mutation frequency), we destructively sampled *S. coelicolor* colonies grown under different conditions. Temporally, mutation frequency increased as colonies aged and grew, suggesting rapid mutation accumulation. Spatially, mutants accumulated disproportionately towards the colony edge, with mutation frequency higher in the interior. Moreover, since antibiotic production is a competitive cue of *Streptomyces*, colonies were exposed to antibiotics revealing an increase of mutation frequency. Additionally, direct competition with antibiotic-producing *Streptomyces* increased mutation frequency and spore production. Our results give more insights into the mechanisms of division of labor in *Streptomyces* colonies and provide evidence of the complex interplay between spatial and ecological factors through time, that may shape mutation dynamics in bacterial colonies.

Life on the edge: a new informatic toolbox to predict population vulnerability to global change

Christopher D. Barratt, Renske E. Onstein, Malin Pinsky, Sebastian Steinfartz, Hjalmar Kühl, Brenna R. Forester, Orly Razgour

Naturalis Biodiversity Center

Environmental change, compounded by anthropogenic activities are introducing new selection pressures on biodiversity. Species abilities to cope with this depends on the magnitude of environmental change occurring and the adaptive capacity of their intraspecific populations. Despite many recent informatic developments, we lack standardised tools to predict population vulnerability across taxonomic groups and geographic areas. To this end we developed the 'Life on the edge' framework (https://cd-barratt.github.io/Life_on_the_edge.github.io/), which combines population genomics and spatial modelling to quantify predicted climate exposure, neutral and adaptive genetic diversity, landscape connectivity and population vulnerability under future global change scenarios. Our tool is highly flexible for different biological systems and addresses an important knowledge gap in population-level climate change vulnerability assessments, paving the way for multiple georeferenced genomic datasets to be repurposed to provide new insights for conservation.

Displaying altruism as a sexual signal in human mate choice is an adaptation – an interdisciplinary overview of the evidence

Dajo Boog, Martijn Egas, Annemie Ploeger

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Numerous studies in humans have shown that altruism may influence mate choice decisions, highlighting its potential role as a sexual signal. Whether using altruism as a signal is an adaptation, however, remains largely unresolved. Here, we aim to investigate the adaptive nature of altruism as a sexual signal by constructing a comprehensive nomological network of evidence. The nomological network draws upon interdisciplinary scientific modes of evidence (psychology, medicine, physiology, genetics, phylogenetics, hunter-gatherer studies, cross-cultural studies, and theoretical studies) and is a framework to evaluate this evidence. Our analysis reveals an extensive breadth of evidence across the various disciplines supporting the hypothesis that altruism is an adaptive sexual signal. However, only the psychological evidence demonstrates substantial depth, with the studies using diverse measurement approaches. Other fields either exhibit limited variation in research methods or have a lack of studies, limiting the strength of their respective contributions. Despite these limitations, there is still sufficient support for the nomological network. Based on the evidence of the various disciplines, we can conclude that altruism as a sexual signal is an adaptation.

Fusion dynamics in the slime mold *Physarum polycephalum*

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Somatic fusion is a common phenomenon among filamentous fungi, colonial marine invertebrates, and acellular slime moulds. Often fusion is limited to genetically identical individuals, but it can occur between distinct individuals. Possible benefits of fusion may relate to more efficient nutrient transport, functional, and genetic complementation, and size increases. However, fusion can also be costly when genetic infections are transferred or parasitic nuclei that exploit their 'social partner' emerge. Whereas the fusion dynamics between conspecifics have been examined in great detail in fungi, very few studies have examined these dynamics in the acellular slime moulds—a group of species possibly even more susceptible to parasitism and exploitation of public goods as a result of their syncytial lifestyle (i.e., a multinucleated cell with a common cytoplasmic environment). Here I will discuss fusion dynamics observed between plasmodial lines of the slime mould *Physarum polycephalum*. I found that stable fusion was limited to clones. Close relatives at times fused, but this was always temporal. Via fluorescent microscopy, I examined if and how the exchange of nuclei and or cytoplasmic elements is limited during this period of fusion. This study confirms that somatic fusion between conspecifics, even between very closely related individuals, is limited. These results suggest that the potential costs of fusion outweigh the potential benefits in syncytial organisms.

The impact of genetic diversity on gene drive efficiency in *Drosophila melanogaster*

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Wageningen University & Research

A major challenge for biodiversity conservation is controlling invasive species, for which genetic biocontrol could be a valuable tool. Gene drive technology is one such method, whereby genetically modified individuals carrying a gene drive are released into the invasive population. The gene drive increases in frequency over generations and imposes a fitness cost (such as female sterility) on homozygous carriers. This could lead to eradication of the invasive population. Before this technology is tested in the field, we should be sure this technology is safe and effective. Importantly, we do not yet understand how genetic diversity could impact drive performance. Most gene drives are only tested in laboratory strains, such as the white-eyed *Drosophila melanogaster* line w1118. In this study, we test a gene drive in genetically diverse lines of *D. melanogaster*, collected from all over Europe by the DrosEU Consortium.

Biomechanical adaptation to a human-commensal niche in the house sparrow (*Passer domesticus*)

Ruth Fawthrop, Glenn-Peter Sætre, George Pacheco, Andrey Gavrilov, Mark Ravinet and*
*Melissah Rowe**

Netherlands Institute of Ecology (NIOO-KNAW)

The house sparrow (*Passer domesticus*) is a classic example of a human-commensal species; a species that depends upon anthropogenic resources for population persistence. Human-commensalism in the house sparrow likely arose during the Neolithic, coinciding with the introduction of agriculture within human societies. Expansion into an anthropogenic niche in the house sparrow was therefore likely associated with a transition in feeding ecology, in particular an increased reliance upon cultivated cereal grains. We hypothesise that human-commensal house sparrows have a stronger bite force which facilitates processing of these large, tough agricultural grains. To test this, we took measurements of in vivo bite force at the tip and base of the beak in human-commensal house sparrows (*P. d. domesticus*) and compared these to measurements taken from a non-commensal subspecies (*P. d. bactrianus*). Consistent with our expectations, we find the human-commensal house sparrow has a greater maximal bite force, at the base of the beak, than the non-commensal subspecies. This suggests that biomechanical adaptation may play an important role in expansion into an anthropogenic niche and persistence as a human-commensal.

Beta-lactamase induced social dynamics of *E. Coli*

Rotem Gross, Muhittin Mungan, Suman G. Das, Tobias Bollenbach, Joachim Krug, and J. Arjan G.
M. de Visser

Wageningen University

Treating *Escherichia coli* with the antibiotic cefotaxime at sub-lethal concentration leads to a complex response: cells are filamenting, a known mechanism related to delayed lysis and

enhanced antibiotic tolerance. Moreover, near lethal concentrations, the population displays complex dynamics, with a crossover from filamented to normal-sized cells after about 14 hours of exposure. Our experiments show that the filamentation causes an active break-down of the antibiotic by a chromosomally encoded enzyme. In fact, freshly introduced bacteria grow in this spent medium and survive at antibiotic concentrations higher than twice the lethal dose. Combining experimental results with theoretical modeling, we explore the biological and chemical pathway through which the bacterial colony inactivates the antibiotic. We argue that this pathway is ancient and common across a wide range of bacteria and constitutes a first line of defense which is triggered even when it is not necessarily effective against the cause of stress.

High genetic differentiation and low genetic diversity in a peripheral population of great tits (*P. m. intermedius*) revealed by mitogenome analysis

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Contact zones are usually considered meeting areas of pairs of closely related species and represent major geographical discontinuities. The species complex *Parus major* is a small passerine, which is widely distributed across Eurasia. Traditionally, this complex species is classified into four subspecies groups: major, bokharensis, cinereus, and minor, each with independent evolutionary histories that have been in secondary contact since the Pleistocene glaciation. Northeastern Iran has long been considered as one of these secondary contact zones between major, bokharensis and cinereus subspecies groups. Also, *Parus major intermedius* which is known from this region has long been suggested to have a hybrid origin from hybridization between the yellow western (major) and the grey-colored eastern (bokharensis or cinereus) subspecies groups based on its intermediate plumage coloration. In this study, we sequenced and assessed the complete mitochondrial genome of 67 individuals to elucidate the evolutionary origin of *Parus major intermedius*. Our findings demonstrate a pattern of low mitochondrial diversity and high genetic differentiation in *P. m. intermedius* in comparison with other studied populations. Furthermore, two specimens from the assumed hybrid zone, northeastern Iran (Lotfabad), with a similar phenotype to that of *P. m. intermedius* had bokharensis mtDNA, suggesting potential introgression between bokharensis and major groups.

Genetics of reproductive isolation of pan-fungicide resistance in *Aspergillus fumigatus*

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Reproductive barriers can take multiple forms, but all lead to the reproductive isolation of a population. They are a fundamental part of speciation, yet their origins are often unclear. The consequences of these barriers are difficult to explore since they take time to become apparent, but genomics allows us to pinpoint their location, leading towards genetic mechanisms. *Aspergillus fumigatus* is a soil-inhabiting fungus. It easily distributes through the wind-borne dispersal of its conidia. These spores can infect people, leading to invasive aspergillosis (IA), which is best treated with clinical fungicides. However, fungicide resistance in *A. fumigatus* is increasingly found, making treatment challenging. Strains of *A. fumigatus* are resistant to

agricultural fungicides, seem to be genetically clustered. Resistance to a compound is usually associated with a fitness penalty that is often mitigated with compensatory mutations, but little is known about their existence in the wider context of multi-fungicide resistance in *A. fumigatus*. In the current project, we will investigate the divergence between resistant and sensitive isolates due to the potential reduced fitness of the sexual offspring. We hypothesize that the independent segregation of compensatory mutations from antifungal resistance genes reduces the fitness of hybrid offspring. This research can provide information on how fungicide use can create reproductive barriers, leading to divergence within this species.

Transparent soil: promising novel technique to revolutionize the cultivation of AM fungi

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Vrije Universiteit Amsterdam

Arbuscular mycorrhizal fungi (AMF) form symbioses with the majority of terrestrial plants and are key players in ecosystem services, plant health, and plant nutrient acquisition. While the interactions of plants and AMF are well-studied, the diversity of AMF mycelial life history traits (LHT) is under-represented. Mycelial network structure is related to reproductive and resource allocation strategies, and therefore is crucial for understanding a species' evolutionary success. Examining traits has been impossible till now, due to the omnipresent challenge in AMF research to culture these obligate biotrophs under controlled experimental conditions. Although co-culturing both partners in natural soils may be closest to reality, the observation and analysis of the mycelial development in this setup is impossible. To investigate mycelial traits, the preferred method is in vitro co-cultivation with (non-photosynthetic) root organ cultures. However, this is only possible for a small fraction of AMF species. By using a promising novel non-sterile technique, 'transparent soils' (Paré et al., 2022, Symbiosis), we aim to investigate the network LHT diversity of less frequently studied AMF species due to their incompatibility with conventional in vitro conditions. Transparent soils use a super-absorbent, yet fully transparent granular polymer that can mimic certain soil properties, so that this setup is compatible with whole plants.

Tropical to temperate transitions facilitated rapid climatic niche evolution and increased diversification rates in Cannabaceae

Yunxia Li

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The cooling and drying of Earth since the Oligocene may have restricted the distribution and diversification dynamics of tropical plant lineages. However, whether shifts to temperate climates lifted eco-evolutionary constraints of tropical lineages, leading to rapid niche evolution and diversification, remains unknown. Here, we test this hypothesis in Cannabaceae, a family consisting of ca. 117 species, with around 70 species restricted to the tropics, and 30 species occurring in temperate regions (here I defined temperate region as out of the boundry of 23.4 °N and 23.4°S). Remarkably, out of 10 genera, two genera (*Celtis* and *Trema*) account for near 90% of total species within this family. We integrated a time-calibrated phylogeny with

distribution data and applied phylogenetic comparative methods to show that Cannabaceae originated in the tropical region in the Late Cretaceous, and more than 70% disperse events occurred out of the tropics in the Eocene. These dispersal events were associated with increases in diversification rates, with rapid evolutionary radiations within *Celtis* and *Trema*. Shifts to temperate regions were associated with increased niche evolution, particularly in niche variables related to survival in cold temperatures. Although tropical to temperate transitions are rare, our results suggest that such transitions may have led to changes in evolutionary constraints on ecological niches, leading to evolutionary radiation.

New localities and lineages of the Atlas dwarf lizard *Atlantolacerta andreanskyi* identified using mitochondrial DNA markers

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Atlantolacerta andreanskyi (Werner, 1929) is an endemic lizard from the High Atlas Mountains region of Morocco. A previous molecular assessment of this species using mitochondrial and nuclear DNA markers uncovered extensive genetic diversity with seven lineages indicative of a species complex. A morphological assessment of six of these lineages did not establish simple diagnostic features, and proposed these should be considered as cryptic species, while highlighting the need for greater sampling across the range. In this study, we sampled 5 individuals from 4 previously unsampled localities and carried out genetic analyses to compare these populations to the known variation. Phylogenetic reconstruction based on mitochondrial markers (12S rRNA and ND4) corroborates the previously described lineages and identified a new one. Interestingly, the two samples that account for this newly identified lineage have been collected from distinct localities – M'goun and Toumliline– that form a sister taxon to the population of Jebel Azourki.

Metagenomic analysis of the *C. elegans* microbiome in an evolution experiment across institutes

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Evolutionary processes are omnipresent and their effects become especially tangible for pathogen adaptation to antibiotics and in the emergence of new diseases. Nevertheless, little is known about how repeatable and ultimately predictable evolutionary processes are. In this study, we performed a large scale evolution experiment in which *Caenorhabditis elegans* was exposed to the novel dietary bacterium *Bacillus megaterium* and evolved over 15 weeks (~ 20 generations). Experiments were carried out in parallel at six different research institutes and WGS data was obtained for all 19 replicates after week 1 and 15. Additionally, the nematode fitness was measured at both timepoints. Here, we use the sequencing data to investigate the genomic host evolution and identify candidate genes that potentially drive adaptation. Using the WGS reads that do not map to the host genome, we identify microbial species that are associated with the nematodes. Interestingly, different research institutes reveal specific microbial signatures and differ strongly in species diversity. As the microbiome is assumed to impact the

host's evolution, this finding reveals a general limitation in the repeatability of experimental conditions.

Finding the blind spots: Evolution of the eyes in spiders

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Naturalis Biodiversity Center

How many eyes do spiders have? The easy answer is that most spiders have eight of them. However, this is not always true. Many species have adapted to various environments modifying their eyes according to their needs. These changes go from the enlargement of some eyes to the size reduction and loss of pairs of eyes, with some species forfeiting these organs altogether. Spiders have two independent nerve pathways that bring the information from the eyes to the integration centres in the brain. To understand the drivers of the eye evolution and their subsequent impact on the brain, we first need to know where and how the basic morphology of the eyes has changed. We reviewed and categorized eye modifications across the whole Order Araneae, placing them in a phylogenetic context. This study is the first step toward understanding the coevolution of the eye-brain system in spiders.

Transposable elements on the move: horizontal transfer of transposable elements in Fungi

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Transposable elements (TEs) are mobile DNA sequences that are found in almost all living organisms. TEs can transpose within their host genomes, shaping host genomes and function. Recent evidence from non-fungal eukaryotes and recent fungal data suggests that TEs are frequently horizontally transferred between species, implying that transferred TEs at least partially shape fungal genomes and their evolution. In this study, we aim to systematically detect horizontal transfers of TEs in a set of over 1,000 publicly available fungal genomes representing diverse fungal taxa. Through a comprehensive bioinformatics approach, we will infer the minimal number of unique, independent horizontal transfer events. Preliminary results demonstrate that fungal genomes exhibited substantial variability in genome size, TE content and composition, lacking a clear phylogenetic pattern, suggesting frequent horizontal transfer of TEs occurs. Our bioinformatics approach yielded in total 16 million TEs, of which 2 million are sufficiently long and possess a TE-related protein domain for future analyses. We expect to find numerous horizontally transferred TEs, to date potential TE expansions within genomes and to elucidate prominent TE types or fungal species involved in horizontal transfer events. We anticipate that our efforts contribute to a better understanding of the mechanisms driving horizontal transfer of TEs and the role of horizontal transfer of TEs in fungal genome evolution.

Trabecular bone functional adaptation sheds new light on the important role of climbing in early hominin locomotion

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Humans are the only apes that do not rely on the arboreal locomotion that characterises the niches of all other living apes. Since, arboreal locomotion affords access food and safety from danger, abandoning the ability to climb must have presented early hominins with significant challenges in terms of food access and predator avoidance. However, despite its evolutionary importance, the nature and pacing of this shift remains contested. Alongside clear adaptations to bipedal locomotion, early hominins retained ‘ape-like’ anatomical features associated with arboreal locomotion in modern apes. These ape-like traits are interpreted in two ways: 1) like other African apes, early hominins relied on combinations of arboreal and terrestrial locomotion, or 2) the ape-like traits were unused retentions of an ancestral state. Falsifying these hypotheses requires developmentally plastic skeletal traits reflective of locomotion during life. A large body of work is showing that trabecular bone structure dynamically adapts to variation in loading conditions and therefore represents a functional record of habitual behaviour. Using microCT scanning I mapped variation in trabecular bone structure throughout the postcranium of South African fossil hominins (*Australopithecus africanus*, *A. sediba*, *Paranthropus robustus*, *Homo naledi*) and extant apes (gorillas, chimpanzees, orangutans, humans). Results provide support for the importance of climbing in hominins after the adoption of bipedalism.

Is arbuscular mycorrhizal fungi internalizing photosynthetic cyanobacteria?

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The symbiogenesis theory describes the birth of eukaryotic life as a result of endosymbiosis, where single cell organisms turn into the organelles of eukaryotic cells. Half a century later, questions like “how endosymbionts were acquired”, and “how they became permanent organelles” remain unanswered. Naturally occurring endosymbiotic systems can help explore these long-lasting questions but are hard to encounter. Despite their rarity, here we provide the first evidence of an uncharted endosymbiotic interaction between cyanobacteria and soil fungi. Specifically, upon co-culturing the cyanobacterium *Nostoc* with the model arbuscular mycorrhizal fungus (AMF) *Rhizophagus irregularis*, we show internalization of *Nostoc* cells in the fungal hyphae. To further explore this interaction, we use in vitro culturing techniques alongside confocal and electron microscopy as well as molecular analysis. Initial evidence suggest that the fungus incorporates large amounts of chlorophyll in its mycelia and spores. Furthermore, we observe cell wall structural alterations at the interface of the two organisms, possibly to facilitate internalization of *Nostoc* cell or cell components. We now aim to understand how stable and widespread this interaction is and what function it serves. Whether this is a mutualistic or predatory interaction remains to be determined. This novel system provides an opportunity to address evolutionary questions regarding the evolution of AMF and endosymbiotic processes.

The formation of a germline in budding yeast

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Unicellular organisms lack a distinction between germline and soma, since the cell is the individual. So how do unicellular organisms protect their genetic information over time? We hypothesize that during linear growth unicellular organisms form a "germline" lineage that exclusively produces offspring cells with few mutations. Consistent with this hypothesis, a quiescent cell fraction was isolated in budding yeast populations after glucose exhaustion at high density by Allen et al. (2006). However, it is unknown which factors, cell density, glucose exhaustion, or a combination of the two, trigger the switch from exponential to linear growth. In our study, we investigated the signals for the onset of linear growth in budding yeast (*Saccharomyces cerevisiae*). We generated growth curves at variable nutrient concentrations, starting densities, and addition of quorum-sensing (QS) molecules. We found that cells grow longer in the exponential phase with increasing glucose concentrations. In the presence of QS molecules, we observed a slow initial growth followed by an exponential growth pattern. However, the obtained results do not provide conclusive evidence for the presence of linear growth in budding yeast cells. It is crucial to study the growth curves for longer periods in larger culture volumes. Further research using labelling techniques and gene expression analysis is essential to provide clear insights into how unicellular organisms maintain their genetic integrity.

Analysing Spatial Gene expression in coenocytic mycorrhizal networks

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Arbuscular Mycorrhizal Fungi (AMF) constitute a group of ancient and widespread obligate plant symbionts. AMF form mycelial networks within plant roots and soil to collect and trade nutrients with hosts. This symbiosis is mutualistic, enhancing plant nutritional status and stress tolerance, thereby playing a pivotal role in the health and productivity of ecosystems. Interestingly, AMF mycelia are coenocytic, meaning the entire hyphal network constitutes a single cell. In this gigantic single cell, thousands of nuclei, nutrients and cytoplasm move similar to an open pipe system. Here we investigate how gene expression is regulated in this unique interconnected multinucleate environment. We first established a novel technique using microchips allowing us to obtain spatially undisturbed mycelia. Then, we studied spatial gene expression by designing a novel Fluorescent In-Situ Hybridization (FISH) protocol, in which fluorescently labelled probes hybridize and visualize RNA transcripts in fixed mycelium. We studied the expression of the FAD1 mRNA, involved in fatty-acid metabolism, and the ribosomal RNA, and observed differences in RNA density across the network and in nuclear transcription. Despite the seemingly chaotic AMF cell organization, we show that expression is spatially regulated. Because of this work, we can link gene expression to network traits to better understand how spatial gene expression contributes to morphological and physiologic differences in AMF networks.

Community-wide micro-evolutionary adaptation to anthropogenic stress: context dependency and ecological implications

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NIOO-KNAW / Wageningen University

Natural ecosystems are changing rapidly due to anthropogenic influences, causing physiological stress in organisms. Rapid micro-evolutionary adaptation is increasingly recognized as a mechanism that enables organisms to deal with increased stress levels. Most studies in the field of eco-evolutionary dynamics and rapid evolutionary adaptation have focused on single species, while natural communities consist of populations of different species that interact, potentially affecting each other's evolutionary trajectories, and may differ in their adaptation potential. Therefore, in this research we specifically adopt a community perspective by simultaneously addressing the evolutionary response of multiple species. We will test whether the community context affects evolutionary trajectories and vice versa. Aim is to quantify the degree to which rapid evolution mediates the response of freshwater communities (Cladocera) to salinization, a major anthropogenic stressor. By combining an evolution experiment in outdoor mesocosms with laboratory common garden experiments, the following hypothesis will be tested: evolution will contribute to a dampening of stressor effects on individual populations, compositional turnover, biodiversity and ecosystem functions. This poster presentation addresses the research proposal, providing insight in the research context, aims and the experimental set-up.

Plants and mycorrhizal fungi trading: when is a deal a deal? An explicit-resource model with variable trade investment

Laura van Schijndel, Hilje Doekes, Eric Siero

Wageningen University and Research

Mycorrhizal fungi, which can trade nutrients for plant carbon, are often called a promising alternative to solve the overuse of fertilisers in agriculture. However, we do not understand well under which conditions trade actually occurs when multiple actors are involved, and what the cost/benefit ratio to the crop is. Wyatt et al. (Evolution, 2014) modelled this for multiple plants and fungi trading, and found a network-wide exchange rate. However, their model requires each organism to give a fixed amount of resources in trade, and assumes every plant could trade with every fungus. Yet in a crop field, many plants and fungi are too far away to trade, leading to more fragmented trading networks. We want to know whether we still expect a global exchange rate in such a sparse network. Moreover, single-connected organisms would be exploited by their partners because of the fixed spending requirement . Hence, we ask if the global exchange rate result still holds when plants and fungi can also hoard resources instead of trade them. Therefore, we are developing a model where a plant and a fungus can freely choose the amount of resources they give in trade. Joint evolutionary optimisation of these amounts results in an optimal exchange rate for each pair of traders. In the future, we want to extend this model to multiple plants and fungi and test whether we find a global exchange rate, and whether this depends on the network structure.

Unraveling the evolutionary tale of allopolyploid *Arabidopsis kamchatica*

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The study of allopolyploid species like *Arabidopsis kamchatica* presents a fascinating avenue for exploring the dynamics of polyploid evolution. *A. kamchatica* poses a complex evolutionary history involving multiple hybridization events between *A. lyrata* and *A. halleri* in East Asia. In a previous study, we provided evidence that the Siberian selfing diploid *A. lyrata* is one of the progenitors of *A. kamchatica*. Using long-read sequencing technology, we have sequenced the genome of a *A. kamchatica* lineage that originated from this progenitor, aiming to generate a chromosome-level assembly. A high-quality reference genome is imperative for studying the evolution of the two subgenomes and investigating the sequences for signatures of homeologous exchanges. By combining population-level sequencing data of different geographical locations, we aim to describe the evolutionary history of *A. kamchatica*, while identifying the different origins that lead to the formation of the species. This project explores the evolutionary trajectory of the subgenomes within *A. kamchatica* and investigates how they interact since their fusion into the allopolyploid state, shedding light on the enduring impact of the mating system differences of their parental origins. Ultimately, the study of *A. kamchatica* will enhance our comprehension of polyploid genome evolution while also underscoring the necessity of a population-level analysis for resolving the complex evolutionary origins of allopolyploidization.

Tissue Genomics: Deconvolution of 5MC with Somatic Site Frequencies

Justin Jon Schader Wilcox, Quentin Foucault, and Toni Goßmann

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Tissue heterogeneities represent a fundamental evolutionary interface at the junction of phenotype and genotype. Such heterogeneities typically arise from epigenetic modifications to tissues during development, but evolutionary studies on epigenetic variation are hindered by their capacity to isolate pure tissues. The application of evolutionary methodologies to questions of tissue heterogeneity may however allow for the efficient deconvolution of mixed tissues across eukaryotes without restriction. Here, we apply somatic site frequency information to deconvolute 5MC methylation patterns. We first run simulations to demonstrate the efficacy of detection of somatic sites in normal tissues. We then test the methods on artificially mixed bisulfite reads taken from a great tit—a common focus of evolutionary studies with ubiquitous non-canonical 5MC methylation in non-CpG context. We accurately derive the mixtures of blood and brain reads using somatic sites. We then use this information to perform unbiased and accurate deconvolution of brain tissue methylations in CpG (CG) and non-CpG (CH) context, allowing for the recovery of 20-30% of differentially methylated sites and approximately 50% of CpG islands and gene bodies even in mixtures with contamination levels up to 90%. Ultimately, this approach highlights the utility of evolutionary theory across scales, and provides a new methodology for studies on mixed tissues with the potential for application beyond 5MC.