Abstract Book

2025 Conference of the Netherlands Society for Evolutionary Biology

Tuesday 8 April 2025
ReeHorst hotel, Ede, The Netherlands

Sponsored by

Organizing committee

Vasilis Kokkoris, Anne Kupczok, Renske Onstein, Melissah Rowe & Aileen Berasategui Lopez

Table of Contents

Program 3
Keynote speakers 4
Program parallel sessions 5
Cultural intermezzo 7
Abstracts contributed talks 8
Poster abstracts 20

8:40	Arrival with coffee/tea
9:15	Welcome & Introduction, Theatre Cerise
9:25	**Keynote 1: Dr. Inge Loes ten Kate** (Utrecht University) *“Planetary evolution and what is the role of life”* Theatre Cerise
09:55	**Keynote 2: Dr. Hassan Salem** (Max Planck Research Group on Mutualisms, MPI for Biology, Tübingen, Germany) *“Adaptation through symbiosis”* Theatre Cerise
10:30	Coffee/tea break
11:00	Parallel sessions with contributed talks I Theatre Cerise II Calluna
12:20	Lunch with network opportunities
13:30	NL Evo Biology 2023 prize winner, Theatre Cerise
14:00	Parallel session with contributed talks III Theatre Cerise IV Calluna
15:15	Coffee/tea break
15:50	General Assembly for NLSEB members, Calluna
16:30	Cultural Intermezzo - THE BLIND MUSICMAKER by Jorn ten Hoopen, Theatre Cerise
17:10	Poster session, Lou Lou
18:40	Poster Prize winner & Closing remarks, Lou Lou
18:45	Dinner, Roekel

Keynote speakers

Dr. Inge Loes ten Kate (Utrecht University)

TITLE: “Planetary evolution and what is the role of life”

Abstract: If we look around us in the Solar System, we see four Earth-like rocky planets, that were all formed around the same time from bits of the same reservoirs but are now 4.5 billion years later entirely different. The biggest outlier of all is the Earth as the carrier of life. The differences between these planets show that we clearly can talk about planetary evolution. What drives the evolution of planets and would the Earth have evolved as it has if there were no life? In this talk I will explain what we can learn from Earth to understand other planets, but more importantly what these planets can teach us about the Earth. I will conclude with a few answers, but probably considerably more questions.

Dr. Hassan Salem (Max Planck Research Group on Mutualisms, MPI for Biology, Tübingen, Germany)

TITLE: “Adaptation through symbiosis”

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

Program parallel sessions

Session I, Theatre Cerise

11:00	**Niek Barmentlo** *Immune gene diversity after a bottleneck; the evolutionary conundrum of optimizing population level disease resistance*
11:15	**Tao Feng** *Asteraceae genome evolution through a phylogenomic synteny lens*
11:30	**Kasper P. Hendriks** *Reaching for the sky: exploring massive convergent evolution towards woodiness in Brassicaceae*
11:45	**Martijn A. Schenkel** *Remote-control meiotic drive of sex chromosomes*
12:00	**Samin Farhangi** *A decade of virus evolution in wild insect populations: Genomic variations of Malacosoma californicum pluviale nucleopolyhedrovirus*

Session II, Calluna

11:00	**Aileen Berasategui** *Molecular evolution in a defensive symbiosis*
11:15	**Marjolein Bruijning** *The bacterial march to endosymbiosis: on-ramps and off-ramps*
11:30	**Julian Vosseberg** *Genome evolution of Asgard archaea: a window into eukaryogenesis?*
11:45	**Aditi Batra** *Resistance variation and bacterial interactions shape the adaptation of a genetically diverse bacterial population to antimicrobial treatment*
12:00	**Victoria Terry** *Are arbuscular mycorrhizal fungi internalizing photosynthetic cyanobacteria?*

Session III, Theatre Cerise

14:00	**Patrick Meirmans** *Whole genome duplication leads to significant but inconsistent changes in climatic niche*
14:15	**Alger Jorritsma** *The evolution of plasticity and evolvability in a simple gene regulatory network*
14:30	**Ryan F.A. Brewer** *Angiosperm evolution and biogeography across the floristically diverse Canary Islands archipelago*
14:45	**Spyros Kanellopoulos** *Impact of multi-fungicide resistance on the fitness of Aspergillus fumigatus*
15:00	**Liedewij Laan** *Global genetic rewiring during compensatory evolution in the yeast polarity network*

Session IV, Calluna

14:00	**James France** *Deciphering the evolution of an enigmatic balanced lethal system in newts*
14:15	**Isabel Rathmann** *Discovering repeatability in genetic evolution in a cross-laboratory evolution experiment with Caenorhabditis elegans*
14:30	**Marco Saltini** *Ecological contexts drive transitions in the sexual systems of mirror-image flowers*
14:45	**Ruth Fawthrop** *Dietary adaptation to human-modified environments in two anthrodependent bird species*
15:00	**Sultan Ahmed Nazir** *Evolution of phage-encoded bacterial virulence*

Cultural Intermezzo, Theatre Cerise

THE BLIND MUSICMAKER by Jorn ten Hoopen

Inspired by Richard Dawkins' "The Blind Watchmaker," this experimental software explores the evolution of music by treating musical elements as genes. Through random mutations and digital selection, the program generates an ever-changing soundscape in real time. Although still fully in development, The Blind Musicmaker invites you to witness how chance and subtle shifts can lead to unexpected and intricate musical expressions. Enjoy this live demonstration of evolutionary creativity—a playful intersection of art and science.

Abstracts contributed talks (presenting author underlined)

Session I – Theatre Cerise

Immune gene diversity after a bottleneck; the evolutionary conundrum of optimizing population level disease resistance

N.W.G. Barmentlo, J. Ellers, M. Bosse

Vrije Universiteit Amsterdam

It is increasingly appreciated that the genetic diversity of immune genes in wild animal populations strongly influences their disease susceptibility. Additionally, immune gene diversity is typically assumed to be higher than the average gene diversity as a result of balancing selection. As such, the question arises whether immune gene diversity is maintained in thriving populations that went through a bottleneck. The underlying assumption here being that lack in immune gene genetic diversity would result in non-viable populations through lack of disease resistance. To test this theory, we studied the genetic diversity of immune genes relevant for African Swine Fever virus survival in five wild boar populations varying in their general level of genetic diversity (n=60). This allowed us to assess diversity patterns of genes relevant for surviving an ongoing epidemic. We found that, while assessing all populations, immune genes varied strongly in their level of genetic diversity, indicating that likely not all immune genes are under balancing selection. The genes that were found to be more diverse than the average autosomal diversity in all five populations, were shown to often increase in relative diversity after increased inbreeding. From this we concluded that selection predominantly maintains diversity in immune genes already showing higher diversity without inbreeding.

Asteraceae genome evolution through a phylogenomic synteny lens

Tao Feng, Eric Schranz

Wageningen University

The Asteraceae is the largest flowering plant family, ubiquitous in most terrestrial communities, and morphologically hyper-diverse. An ancient whole genome triplication occurred at approximately the same time as the evolutionary innovation and adaptive radiation of the family during the middle Eocene. Despite its importance, the genomic contents arising from this triplication have yet to be tracked in context of the Asteraceae genome evolution. We applied a phylogenomic synteny analysis of 21 Asterales genomes and to study the paleo-hexaploidization. We identified 15 ancestral linkage groups that date back to the common diploid ancestor of all Asteraceae. Each of these groups was triplicated, resulting in 45 genomic blocks, which serve as the foundation for cross-family analyses. We found that modern genomes are genetic mosaics of the 45 genomic blocks. 157 genes retained three paleo-hexaploid derived syntenic paralogs across most Asteraceae species. Transcription factors and auxin-related genes are significantly overrepresented in the conserved triplets, and expression of the paleo-hexaploidy paralogs is spatiotemporally differentiated. These genes are involved in the development of floral capitulum, a remarkable morphological innovation. The discovery of conserved triplicated genes can direct further study to understand the evolutionary innovation, and the synteny-phylogenomic framework provides a comparative framework to characterize newly sequenced Asteraceae genomes.

Reaching for the sky: exploring massive convergent evolution towards woodiness in Brassicaceae

Kasper P. Hendriks

Naturalis Biodiversity Center

The earliest flowering plants, dating back ~130 million years, had a woody growth form. Over time, many evolved into herbaceous forms, yet an estimated 700 herbaceous lineages independently re-evolved woodiness. This widespread convergent evolution has puzzled scientists since Darwin, and the underlying reasons remain unresolved. Recent studies propose drought as a key driver, forming the basis of the 'drought hypothesis'. Given the increasing impact of climate change and prolonged droughts, understanding how plants adapt to water scarcity is crucial, necessitating a thorough evaluation of this hypothesis. I investigate woodiness shifts in the mustard family (Brassicaceae). Despite comprising only ~4,000 species, this family accounts for one in seven woodiness shifts among all flowering plants (~300,000 species), making it an ideal model system. A core component of my research is constructing a time-calibrated phylogeny for 3,500 species—the largest of its kind for any plant family of this size. This framework enables the precise identification of the family’s ~100 woodiness shifts and provides a robust statistical basis for testing evolutionary links between woodiness and environmental factors. Here, I present preliminary findings on the evolution of derived woodiness, demonstrating how this data enhances our understanding while revealing that the underlying eco-evolutionary processes are far more complex than previously thought.

Remote-control meiotic drive of sex chromosomes

Naomi L. Greenberg, Manus M. Patten, Martijn A. Schenkel

University of Groningen

Some selfish genetic elements drive at meiosis to achieve transmission distortion, breaking the rules of Mendelian segregation to enhance their own evolutionary success. It has been previously shown that enhancers of drive must act in cis in order to gain the selfish benefit of drive and that suppressors of drive will be selected at any unlinked loci. Here, we model the evolution of an autosomal trans-acting gene (Distorter) that causes the Y-chromosome (or even 0-chromosome) to drive, a phenomenon we call “remote-control meiotic drive”. We show that such a gene may spread in the population when linked to a second locus, Assister, whose alleles are transmitted at different frequencies through sperm as compared to eggs, for which we consider various scenarios, e.g. genes subject to sexually antagonistic selection or sex-limited drive. Depending on the mechanistic details of sex-chromosome drive, Distorter’s spread can additionally facilitate transitions between XY and X0 sex determination. We discuss these results in relation to sex allocation theory, and as proof of principle for a novel type of naturally occurring or synthetically useful sex-ratio-distorting selfish genetic element.

A decade of virus evolution in wild insect populations: Genomic variations of Malacosoma californicum pluviale nucleopolyhedrovirus

Samin Farhangi, Dieke Boezen*, Nick Somsen, Elisabeth A. van Strien, Baptiste Lehraud, Elisabeth A. Herniou, Jenny S. Cory, Mark P. Zwart*

NIOO KNAW

Virus populations evolve rapidly, as demonstrated extensively in humans and agro-ecosystems. In contrast, virus evolution in wild ecosystems—where viruses can act as both disease reservoirs and key ecological players—remains understudied due to challenges such as limited time-series data. Here, we analyzed 97 Malacosoma californicum pluviale nucleopolyhedrovirus (McplNPV) isolates collected from western tent caterpillar populations in British Columbia, Canada between 2002 and 2013. Two dominant haplotypes, Hap-I and Hap-II, and their recombinant derivatives, were identified. Hap-I initially predominated, followed by a phase in which mixed-haplotype infections occurred, followed by the predominance of recombinants. This temporal pattern was observed across two field sites, indicating a synchronous genotypic turnover in the virus meta-population. Unexpectedly, the invading Hap-II and recombinant variants had lower infectivity than the displaced Hap-I, suggesting that factors beyond infectivity drove the observed shift. These findings highlight the speed and ecological significance of virus evolution in wild ecosystems.

Session II – Calluna

Molecular evolution in a defensive symbiosis

Aileen Berasategui

Amsterdam Institute for Life and Environment, Vrije Universiteit Amsterdam

Many insects rely on microbial protection early in development, yet the role of microbes in safeguarding pupae remains understudied. Here, we describe a mutualistic relationship between the fungus Fusarium oxysporum and the leaf beetle Chelymorpha alternans. The symbiont rapidly proliferates during pupation, forming a conspicuous coating that protects the beetle against predation. Eliminating the fungus reduces pupal survival, highlighting its defensive role. In return, emerging beetles disperse Fusarium to host plants, where it retains its phytopathogenic traits, causing wilt disease. Despite harboring a reduced genome, Fusarium maintains key metabolic pathways for both plant colonization and insect defense, including virulence factors and mycotoxins. Comparative genomics of ten symbiont strains from Cassidinae beetles revealed high functional conservation relative to non-insect-associated Fusarium lineages. Defensive symbionts evolved smaller genomes with fewer protein-coding and tRNA genes, as well as fewer repeats, underscoring the link between genome reduction and symbiosis. Our findings shed light on a mutualism predicated on pupal protection of an herbivorous beetle in exchange for symbiont dissemination.

The bacterial march to endosymbiosis: on-ramps and off-ramps

Marjolein Bruijning, Andrew H. Moeller, Gavriela Carver, Mohamed S. Donia, Britt Koskella, Prerna Singh, C. Jessica E. Metcalf

University of Amsterdam

Host-associated bacteria are found across the tree of life and can have crucial influences on the performance of their hosts. Despite the clear importance of such intimate host-microbe associations for individual hosts, it remains a mystery how and when these associations establish, and how these may impact host evolution and adaptation. This knowledge gap is partly due to the lack of theoretical frameworks that capture the evolutionary dynamics of host-microbiome systems. I explore to what extent the foundation for such frameworks lies in existing evolutionary theory. For this talk, I merge insights from classical population genetics, quantitative genetics and evolutionary ecology to highlight three key drivers that shape the fate of a host-microbe association: Host life history, chance and ecological context. By seeking general principles emerging from broad features of host and microbe, and benefiting from the wealth of theory existing the field of evolutionary biology, this work paves the way for future empirical tests to unravel the origin, function and evolution of the vast ubuiquity of the host-microbe associations surrounding us.

Genome evolution of Asgard archaea: a window into eukaryogenesis?

Julian Vosseberg, Kassiani Panagiotou, Stephan Köstlbacher, Daniel Tamarit, Jolien J.E. van Hooff, Thijs J.G. Ettema

Wageningen University & Research

Asgard archaea are a group of archaea that represent the closest prokaryotic relatives of eukaryotes. The eukaryotic branch likely sprouted from within the Asgard archaeal class Heimdallarchaeia. Eukaryotes are considered far more complex than prokaryotes and their genomic repertoire vastly expanded due to numerous gene duplications, transfers, inventions and fusion events during the early stages of eukaryogenesis. The expanding repertoire of Asgard archaeal genomes, including several closed genomes and genomes from novel groups, is likely to improve our view on Asgard archaeal genome evolution, including how different genetic innovations have shaped the genome content of Asgard archaea and, potentially, that of earlly eukaryotes. In this study, we perform large-scale phylogenetic analyses and use gene tree-aware reconciliation methods to reconstruct ancestral genomes and illuminate the evolutionary genome dynamics of Asgard archaea. The first results of these analyses specifically hint at an increased rate of gene duplications in Asgard archaea compared to other archaea. This suggests that the mode of genome evolution of Asgard archaea is, to some extent, reminiscent of that of eukaryotes. With further analyses on gene inventions, duplications, fusions and transfers in Asgard archaea we expect to provide additional pieces of the enigmatic puzzle of the origin of eukaryotes.

Resistance variation and bacterial interactions shape the adaptation of a genetically diverse bacterial population to antimicrobial treatment

A Batra, L Tueffers, K Haas, T Loeblein, J Botelho, M Habig, D Schuetz, G Sakalyte, F Buchholz, E Berríos-Caro, H Uecker, D Unterweger, H Schulenburg

Wageningen University and Research

Many infections are polymicrobial in nature. In turn, microbial interactions, genetic variation, spatial structuring, and horizontal gene transfer can shape infection characteristics, including the evolution of antimicrobial resistance (AMR). Past work on AMR in polymicrobial infections relied on observational patient data, for which cause-effect relationships are difficult to infer, or focused on interactions between different bacterial species, ignoring the commonly encountered variation within species. To rectify the current knowledge gaps, our study used an experimental approach to assess the influence of within-species genetic variation and associated effects as well as spatial structuring on AMR evolution. We combined 12 genotypes of the pathogen P. aeruginosa that varied in AMR and their pairwise interactions. We found that standing genetic variation, microbial interactions, and spatial structure significantly impact population composition upon experimental evolution under antibiotic selection, thereby affecting bacterial survival and the spread of AMR. A second evolution experiment confirmed the importance of genetic variation and microbial interactions on population survival and adaptation. We conclude that ecological dynamics in genetically diverse pathogen populations are key for our understanding of infection characteristics and AMR evolution, and, therefore, deserve particular attention during development of novel antibiotic treatment strategies.

Are arbuscular mycorrhizal fungi internalizing photosynthetic cyanobacteria?

Victoria Terry; Julian Hage; Emre Akgün; Bianca Turcu; Tom Shimizu; Toby Kiers; Vasilis Kokkoris
Amsterdam Institute for Life and Environment, Vrije Universiteit Amsterdam

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 the 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. Here we provide the first evidence of an uncharted endosymbiotic interaction between cyanobacteria and soil filamentous fungi. Specifically, upon co-culturing the cyanobacterium Nostoc together with arbuscular mycorrhizal fungus (AMF), we show internalization of – or parts of – Nostoc cells in the fungal hyphae. To further explore this interaction, we use novel culturing techniques alongside confocal and electron microscopy as well as molecular analysis. Initial evidence suggests that the fungus incorporates large amounts of chlorophyll in its mycelia and spores. Furthermore, we observe cyanobacteria cells within the outer layers of the AMF cell wall, presumably the first stages of nostoc internalization. We now aim to understand how stable and widespread this interaction is and the function it serves. Whether this is a mutualistic or predatory interaction remains to be determined. Regardless, this novel system provides an exciting opportunity to address long-lasting evolutionary questions regarding the evolution of AMF and endosymbiotic processes in general.

Session III – Theatre Cerise

Whole genome duplication leads to significant but inconsistent changes in climatic niche

Patrick Meirmans & Filip Kolář

Universiteit van Amsterdam

Polyploidization is a widespread large-effect macro-mutation with far-reaching consequences on genomic, phenotypic, and evolutionary potential. It has frequently been suggested that polyploids generally have different niche preferences than their diploid relatives. Popular hypotheses state that polyploids prefer colder and more xeric conditions, and higher altitudes. Niche modeling studies in mixed-ploidy species provide opportunity to directly compare recently originated polyploids with their lower-ploidy ancestors. However, the available studies are typically limited to single species and use a wide variety of methodologies. Though these studies show constrasting results, the methodological diversity makes it difficult to make any broad generalizations. In this study, we use 25,857 georeferenced ploidy-verified occurrence data for 129 mixed-ploidy flowering plant species, to test the following questions: 1) How frequent is niche differentiation in mixed-ploidy species? 2) Is there consistency in the direction of the niche shifts following ploidy increase? Specifically, do polyploids typically shift or expand to colder conditions, more xeric conditions, or higher elevations? 3) Do polyploids exhibit broader niches and/or larger distribution ranges than their diploid relatives? 4) Are the ranges of polyploids (current, past and future) more dynamic than those of diploids?

The evolution of plasticity and evolvability in a simple gene regulatory network

Alger Jorritsma & Piet van den Berg

KU Leuven

Organisms adapt to environmental change by plastic phenotypic responses, genetic adaptation, or a combination of the two. Their genetic wiring determines the capacity for both these types of adaptation, respectively through shaping responses to environmental cues (plasticity) and through modulating the phenotypic effect of mutations (evolvability), but it is unclear how these capacities co-evolve. Here, we present a large-scale evolutionary simulation study in which a simple gene regulatory network must adapt to a wide range of environmental change regimes. We systematically investigate the evolution of plasticity and evolvability in this network, depending on the speed and predictability of environmental changes, and the reliability of environmental cues. We find that reliable cues lead to the highest adaptability in fast and erratically changing environments, mostly through plasticity. In contrast, less reliable cues lead to the highest adaptability under intermediate environmental variability, mostly through changes in the gene regulatory network that allow it to harness mutations more effectively (i.e., through evolvability). Additionally, we find that networks that mostly rely on evolvability gradually lose plastic capacity, whereas highly plastic networks evolve to become sensitive to mutations as well. More generally, our results show that the plasticity and evolvability of biological systems are tightly intertwined.

Angiosperm evolution and biogeography across the floristically diverse Canary Islands archipelago

Ryan F.A. Brewer, Ornela Dehayem Nanwou, Laura van Hoek, Rampal S. Etienne, Luis Valente, Frederic Lens

Naturalis Biodiversity Center

Islands offer unique opportunities to study the uneven distribution of biodiversity across the tree of life as their biotas are typically composed of lineages with different ages, diversities, and traits occurring in the same geographical arena. However, the causes of unevenness across the tree of life on islands remain unresolved. Here, we present the most complete time-calibrated phylogenomic tree of life for any archipelago flora, including 671 species of native Canary Islands flowering plants (~50 % of the native flora), and estimate colonisation times in 364 insular lineages for which 80% have been estimated for the first time, to address the causes of unevenness in the flora. We find that the Canary flowering plants are the result of 881 independent colonisations, over 50% more than previously estimated. Overall, the Canary Islands flora is characterized by remarkably high extinction and colonisation rates that maintain macroevolutionary equilibrium, without a correlation between lineage age and species diversity. Insular woodiness acts as a key innovation and comprises lineages with higher speciation, lower extinction rates relative to the rest of the flora, and a detectable diversity-dependence; in non-insular woody clades, diversity appears unbounded, limited by high turnover rates. Our results reveal that macroevolutionary assembly processes in the iconic Canary Islands flora strongly depend on varying diversification rates tied to insular floristic traits.

Impact of multi-fungicide resistance on the fitness of Aspergillus fumigatus

S. G. Kanellopoulos, E. Leeflang, T. Bayraktar, D. Aanen, E. Snelders, B. Auxier

Wageningen University and Research

Aspergillus fumigatus is a ubiquitous fungus that proliferates in plant-degrading material. It distributes through the dispersal of its asexual spores. These spores can infect people, leading to various diseases, which are best treated with clinical antifungal compounds. Increasingly, A. fumigatus strains are detected that exhibit multi-fungicide cross-resistance to clinical and agricultural antifungals, challenging treatment. Strains of A. fumigatus that are resistant to agricultural fungicides, seem to be genetically clustered, separate from susceptible strains. Resistance to a compound is usually associated with a fitness penalty that is often mitigated with compensatory mutations. In the current project, we investigate the divergence between resistant and sensitive isolates due to a 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. In the scope of this research, the mutations that are responsible for multi-fungicide resistance are experimentally characterized by introducing them into susceptible A. fumigatus with CRISPR/Cas9 knock-ins. Finally, the CRISPR/Cas9 mutants will be tested for their fitness and virulence with a competition model and Galleria mellonella as a host. The outcome of this research can provide information on how broad fungicide use can create reproductive barriers, leading to divergence within this species

Global genetic rewiring during compensatory evolution in the yeast polarity network

Enzo Kingma, Liedewij Laan

TU Delft

Functional defects resulting from deleterious mutations can often be restored during evolution by compensatory mutations elsewhere in the genome. Importantly, this process can generate the genetic diversity seen in networks regulating the same biological function in different species. How the options for compensatory evolution depend on the molecular interactions underlying these functions is currently unclear. In this study, we investigate how gene deletions compensating for a defect in the polarity pathway of Saccharomyces cerevisiae impact the fitness landscape. Using a transposon mutagenesis screen, we demonstrate that gene fitness has changed on a genome-wide scale in the compensated strain. An analysis of the functional associations between the affected genes reveals that compensation impacts cellular processes that have no clear connection to cell polarity. Moreover, genes belonging to the same process tend to show the same direction of gene fitness change, indicating that compensation rewires the fitness contribution of cellular processes rather than of individual genes. In conclusion, our results strongly suggest that functional overlap between modules and the interconnectedness of the molecular interaction network play major roles in mediating compensatory evolution.

Session IV- Calluna

Deciphering the evolution of an enigmatic balanced lethal system in newts

James France, Ben Wiesltra

Leiden University

All crested and marbled newts (the genus Triturus) suffer from an extreme genetic disorder known as a 'balanced lethal system' that results in the spontaneous death of half of their embryos. How can such a radically disadvantageous trait evolve and persist in the face of natural selection? It has long been known that Triturus' chromosome 1 occurs in two distinct variants that are both required for survival. However, the genomic architecture of chromosome 1 remained a mystery, preventing explaining the evolution of the balanced lethal system. We use target capture sequencing to construct a detailed genetic map of the Triturus genome. We find that each form of chromosome 1 has suffered from a single gigantic deletion, each removing approximately 1% of the genome. We also observe that each deletion is compensated for by an equivalent duplication of the same region on the other variant of chromosome 1. This pattern strongly supports the hypothesis that the entire balanced lethal system evolved instantly, in a single unequal exchange between two sister chromosomes. We then model the implications of this macromutation. Counterintuitively, because the two rearranged forms of chromosome 1 can compensate for each other's deficiencies better than their unrearranged ancestor can, the balanced lethal system causes populations to become reproductively isolated from the rest of the species, allowing the system to endure, despite the huge loss of offspring.

Discovering repeatability in genetic evolution in a cross-laboratory evolution experiment with Caenorhabditis elegans

Isabel Rathmann

University of Amsterdam

Repeated adaptation to similar environments is common, including in bacterial resistance evolution and the emergence of new diseases. Nevertheless, little is known about how repeatable and ultimately predictable evolutionary processes are in general. What are the factors that enable or diminish parallel evolution within and between treatments, laboratories, and biological replicates? In this study, we performed a large scale evolution experiment in which Caenorhabditis elegans evolved over 20 generations, exposed to the new bacterial food source Priestia megaterium. This experiment was carried out in parallel at five research institutes across the Netherlands. In individual labs, additional treatments were applied, influencing the population demography through bottlenecks, sexual reproduction modes and decreased gene flow. We obtain time-resolved whole genome pool-Seq data and detect global and local signatures of parallel genetic evolution between treatments and labs. We identify candidate genes and gene functions that potentially drive adaptation. With metagenomic analyses, we discover lab-specific microbial profiles that change throughout the course of the experiment. With this unique data set at hand, we identify the boundaries of repeatability in experimental evolution. Lab differences are inevitable and we ask how these decrease the repeatability in laboratory evolution. This sets a boundary for less controlled, natural systems and will inform evolutionary predictions.

Ecological contexts drive transitions in the sexual systems of mirror-image flowers

Marco Saltini, Spencer C.H. Barrett, Eva Deinum

Wageningen University and Research

Mirror-image flowers exhibit a form of sexual asymmetry where a flower's style deflects to either the left or right, with a pollinating anther orientated oppositely. It is a floral polymorphism known by Charles Darwin, it occurs in at least 11 unrelated angiosperm families, and is a striking example of adaptive convergence in form and function associated with insect-mediated cross-pollination. In several lineages, dimorphic enantiostyly (one stylar orientation per plant, both forms occurring within populations) has evolved from monomorphic enantiostyly, where all plants produce both style orientations. Using a modelling approach, we investigate the gradual evolution of dimorphic enantiostyly from a monomorphic, ancestral type. Unlike traditional theoretical models, which often use population genetics or sex allocation theory, for the first time we employ adaptive dynamics to explore how ecological forces drive this transition. Our results show that dimorphism can evolve from an ancestral monomorphic population depending on the interplay between inbreeding depression from geitonogamy, pollination efficiency, and plant density, and that the newly emergent dimorphic population is stable against invasion by monomorphic mutants.

Dietary adaptation to human-modified environments in two anthrodependent bird species

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

Netherlands Institute of Ecology (NIOO-KNAW)

Humans have been modifying environments for millennia, driving ecological and evolutionary change. Whilst anthropogenic selective pressures generally pose a huge threat to global biodiversity, a small number of populations have adapted to thrive in human-modified environments, evolving a dependence upon anthropogenic resources. The house sparrow (Passer domesticus) and tree sparrow (Passer montanus) represent two charismatic species in which human-commensalism has independently evolved. Both species likely first expanded into an anthropogenic niche during the Neolithic, tracking the spread of wheat- and rice-based agriculture, respectively. Thus, we expect increased human association led to a transition in feeding ecology, specifically an increased reliance on tough, domesticated cereal grains. To assess whether this transition to a hard seed diet is associated with adaptive changes in the structure and function of the feeding apparatus, we measured bite force, skull and beak morphology, and jaw musculature in human-commensal and non-commensal Passer sparrow populations. Consistent with expectations, we found some evidence of stronger bite forces in human-commensal populations, associated with changes in craniofacial morphology, including increased head width. Our findings highlight the role of dietary adaptation in the ability to thrive in human-modified environments and may provide insights into parallel adaptation to a human-commensal niche.

Evolution of phage-encoded bacterial virulence

Sultan Ahmed Nazir, *Bram van Dijk*
Utrecht University

Temperate bacteriophages are viruses capable of both horizontal transmission through virions particles (lytic cycle) and vertical transmission through integration into bacterial chromosomes (lysogenic cycle). By integrating, these phages can enable bacteria to express their cargo genes, including virulence factors often linked to bacterial pathogenicity. Despite the threat of lysis posed by phages and their selfish evolutionary nature, bacteria have evolved to depend on phage-encoded traits. This raises two key questions: Why have bacteria adapted to rely on phage-encoded pathogenicity, and why are phages more prone to carrying virulence genes compared to other Mobile Genetic Elements? Using a combination of ordinary differential equation (ODE) models and individual-based simulations, we identify potential phage-specific mechanisms that explain how a weakly beneficial chromosomal gene can transition to being phage-encoded. Specifically, we explore two key factors: (1) the co-regulation of prophage induction and gene expression, and (2) virion dispersal in spatially structured populations. These mechanisms provide insights into the evolutionary processes driving the association of virulence genes with phages and the broader implications for bacterial-phage interactions.

Poster Abstracts – Alphabetically (last name) arranged by presenting author (underlined)

Experimental evolution of multicellularity in *Streptomyces venezuelae*

Luis Alfredo Avitia-Domínguez, Ruth Viveros, David Norte, Natalia Tschowri, Roeland Merks, Daniel Rozen

Leiden University

The transition to multicellularity is one of Earth's most significant evolutionary innovations, enabling greater size, resource efficiency, dispersal, and other benefits to individuals. While transitions between uni- and multicellularity are better understood in eukaryotes, they remain poorly explored in bacteria. Specifically, we know little of how changes to multicellular size affect the architecture and fitness of bacterial colonies. To address this, we created an experimental evolution approach to explore multicellular transitions in Streptomyces venezuelae, a filamentous bacterium with multicellular development. In liquid culture, S. venezuelae forms multicellular pellets that fragment into hyphal clusters or spores. To select for changes in the pellet size of populations, we used size-selective filters to serially transfer either only the Smallest or Largest pellets. After experimental evolution, we observed heritable changes in multicellular morphology, notably a near-complete reversion to unicellularity in Small populations and an increase in Large ones. Multicellular size changes were accompanied by variations in hyphal fragmentation, sporulation loss, branching, and growth rate. Ongoing genomic analysis has revealed the genetic basis of the observed phenotypic shifts. Our findings shed light in causes and consequences of Streptomyces multicellularity, offering a framework to study its role in nutrient transport, division of labor, and intercellular cooperation.

Monitoring and conservation of aquatic genetic resources in the Netherlands

Chris Barratt, Annemieke Rattink, Wout Abbink

Wageningen University and Research

At the request of the FAO Global plan of Action for the conservation and sustainable use of aquatic genetic resources (FAO GPA for AqGR), and on the instructions of the Dutch Ministry of Agriculture, the Centre for Genetic Resources of Wageningen University and Research (WUR) instigated a statutory research project focused on monitoring genetic resources in the Netherlands in 2022. Here we report on our first results using population genomic data for Mussel (Mytilus edulis), Turbot (Scophthalmus maximus), Zander (Sander lucioperca) and European eel (Anguilla anguilla). With reference-genome aligned SNPs (2796-41893 per species) for large numbers of individuals (152-550 per species) and sampled populations (4-38 per species) we summarise population structure, differentiation and genetic diversity, forming a basis for future monitoring. Our work assists the improvement of national policies, legislation, research and education concerning the conservation, sustainable use and development of aquatic genetic resources, and contributes to raising public awareness about the importance of genetic resources and aquaculture.

Beyond the Highlands: Climate Drives Evolutionary Connections Between Ancient Neotropical Mountains and Lowland Biomes

Yago Barros-Souza, Monique Maianne, Rafael F. L. Barduzzi, Leonardo M. Borges

Naturalis Biodiversity Center

The assembly of montane plant communities through time is shaped by historical contingencies and environmental gradients. However, the extent to which the diversity of lowlands influences lineage composition in ancient highland ecosystems remains unclear. Here, we investigate evolutionary connections between the campos rupestres, a hyperdiverse montane vegetation complex in eastern South America, and surrounding lowland biomes—savannas, rainforests, and seasonally dry tropical forests (SDTFs). Using phylogenetic beta diversity analyses for 13 angiosperm clades, we assess lineage dissimilarity between campos rupestres subregions and adjacent biomes. We also apply generalized dissimilarity modeling (GDM) to evaluate the influence of climate, soil, and geographic distance on phylogenetic composition. Our results reveal high lineage permeability between the campos rupestres and lowlands, with montane subregions often sharing more lineages with adjacent biomes than among themselves. Climate is the strongest driver of phylogenetic dissimilarity, while soil and geographic distance play comparatively minor roles. By showing that lineage movements across biome boundaries have been common over time and spatial scales, our study challenges the idea that ancient Neotropical mountains are isolated sky-islands. Instead, we emphasize the dynamic nature of montane plant diversity and the pivotal role of climate in shaping evolutionary connections between highlands and lowlands.

Evaluating the adaptive role of phenotypic plasticity to temperature to cope with climate change in Lemna minor

Blanco-Sánchez, M. & Verhoeven, K.J.F.

Netherlands Institute of Ecology (NIOO-KNAW)

Climate change is altering the temperature and precipitation patterns worldwide, compromising the persistence of plant populations. In a climate change scenario, phenotypic plasticity may be a crucial mechanism to cope with the higher climatic variability and unpredictability. However, understanding whether plasticity can mitigate the negative effects of climate change is far from resolved. Using the clonal duckweed species Lemna minor, our research project will use a multidisciplinary approach to shed light on the adaptive value of phenotypic plasticity under climate change conditions. First, we will characterize differences in performance of ~60 L. minor clonal lines under four contrasting temperature regimes, providing relevant knowledge about genetic differentiation and plasticity patterns in this species. Then, we will quantify plasticity to temperature in gene expression and traits, in 20 lines with the highest and lowest overall performance, to assess if plasticity in gene expression and traits is associated with differences in performance. To empirically confirm whether plasticity is adaptive, we will use experimental evolution assays in which populations with high and low plastic lines will evolve under ecologically-meaningful temperature regimes, expecting a higher abundance of high-plasticity lines under heterogeneous conditions. Our project will enhance our knowledge on the role of plasticity to cope with the increased temperature heterogeneity of climate change.

ERGA: The European Reference Genome Atlas in The Netherlands

Mirte Bosse

Vrije Universiteit Amsterdam

ERGA stands for the European Reference Genome Atlas. This is an European consortium committed to cataloguing European eukaryotic biodiversity through the generation of high-quality reference genomes. Erga is a bottom-up initiative encompassing hundreds of European researchers, with the mission to generate reference genome assemblies of European eukaryotic species across the tree of life, including threatened, endemic, and keystone species, as well as species important to agriculture, fisheries, pests, and to ecosystem function and stability. The ERGA community also want to provide information about the use of genomic resources and build a distributed genomic infrastructure across the continent that addresses imbalances in resource availability and country representation. ERGA would like to connect to more researchers in The Netherlands, so if you are interested, dont hesitate to come for a chat!

Mechanisms of Hyphal Healing in Arbuscular Mycorrhizal Fungi: Insights into Fungal Adaptation.

Rachael Cargill, Loreto Oyarte Gálvez, Andrew Vanderleek, Corentin Bisot, Marije van Son, Thomas S. Shimizu, E. Toby Kiers, Vasilis Kokkoris.

Vrije Universiteit Amsterdam

Arbuscular mycorrhizal (AM) fungi are ancient symbionts that associate with most terrestrial plants and play a key role in ecosystem functioning by supporting plant growth, contributing to nutrient cycling and mediating ecosystem diversity. Underground, AM fungi form intricate networks of filamentous hyphae that extend through the soil and facilitate nutrient transport to the plant. At the cellular level, AM fungal hyphae are aseptate; their hyphae form one continuous cell where all contents flow freely. Despite their ecological significance, the response of these aseptate hyphae to physical disturbance remains underexplored. Here, we investigate the mechanisms of hyphal wound healing in AM fungi by inducing damage in symbiotic mycelia and comparing the response between two strains. We show that the onset of wounding elicits rapid cytoplasmic efflux, which is subsequently mitigated by a cytoplasmic ‘gelation’ response. We highlight the resilience of AM fungal hyphae to physical damage, revealing strain-specific variation in healing mechanisms, including differences in hyphal architecture and ‘gelation’ timing. While previous research demonstrated diverse healing responses between AM fungal families, our findings show that significant variation can also occur between strains of the same species. Our results underscore the adaptive capacity of AM fungi to repair physical damage, which is particularly relevant given their prevalence in ecosystems prone to soil disturbance.

Phylogenetic Insights into the Relationship Between Chrysanthemum L. and Ajania Poljakov

Elvira Castillo-Almansa, Miyang Liu

Wageningen University and Research

Chrysanthemum spp. has long been an important crop in China, but its classification and its relationship with other genera remain topics of ongoing debate. The classification of

Chrysanthemum spp. has undergone several revisions, with recent discussions questioning whether Chrysanthemum spp. and Ajania spp. should be recognized as distinct genera. This study investigates the phylogenetic relationships between Chrysanthemum spp. and Ajania spp. by analyzing various molecular markers (matK, rbcL, ITS, ETS, and CDS) and employing phylogenetic reconstruction methods such as Maximum Likelihood, Bayesian Inference and coalescent approaches, as well as a Median Network analysis. Although this study includes a broader range of Chrysanthemum species compared to other similar research, the results from multiple analyses show no clear distinction between the two genera. However, a noticeable pattern emerges, where certain species of Chrysanthemum and Ajania tend to cluster together in the phylogenetic trees. Specifically, Ajania species that do not form clades with other Ajania species often share clades or form sister groups with C. arcticum, C. glabriusculum, C. lavandulifolium, C. indicum and C. zawadskii. Regarding the markers selected, rbcL and CDS ones appear to be the most reliable for phylogenetic analysis for these taxa. Among phylogenetic methods, the ML approach performed better for Chrysanthemum spp. than Bayesian inference, as it produced fewer polytomies.

Developing efficient ABMS of many-agent foraging using Abmax

Siddharth Chaturvedi, Steven Kocken, Ahmed El-Gazzar, Yuzhen Qin, Marcel van Gerven

Radboud University

Firstly, we introduce Abmax. It is an agent-based modeling (ABM) framework developed in Jax. It provides tools for efficient agent manipulations like adding, removing, searching, sorting, and updating an arbitrary number of agents on a hardware accelerator like GPUs/TPUs. Secondly, we show its efficiency in simulating large ABMs in parallel. Then, we present some of its future applications in developing computational models of ecological systems. For instance, modelling continuous non-episodic evolution in a many-agent foraging scenario and controlling the population dynamics by using reinforcement learning for spawning resources. Such examples highlight the importance of environment enrichment and characteristics in shaping the evolved embodied intelligence.

Behavioural innovation promotes population expansion in great tits: behavioural and epigenetic mechanisms

Xiaomei Chi, Alice R. Pereira, Barbara M. Tomotani, and Kees van Oers

The Netherlands Institute of Ecology (NIOO-KNAW)

Anthropogenic changes, such as human settlement expansion and climate change, rapidly alter environments. This causes shifts in species distribution, such as range expansion. Adapting to new environments offers challenges to organisms, and certain traits may aid range expansion, yet what are the key traits remains unclear. Additionally, epigenetic mechanisms like DNA methylation and histone modifications, could reveal how environments shape gene expression and traits. We are conducting a common garden experiment to assess the genetic and environmental background of behavioural and epigenetic differences between populations. By integrating these approaches, we aim to uncover mechanisms driving population expansion in great tits.

Multiscale modeling of antimicrobial resistance evolution in microbial communities

Burak Demirbas, Meike Wortel
University of Amsterdam

Predicting evolutionary trajectories of antimicrobial resistance (AMR) is crucial in tackling challenges posed by resistant microbes. AMR incurs both costs and benefits to organisms, which depend on extracellular conditions, such as interspecies interactions in microbial communities. How interactions in communities consisting of many species affect the predictability of AMR evolution has so far been understudied, especially in fungi. To address this question, we developed a multiscale model integrating cell growth, metabolism, and resistance mechanisms in Candida species exposed to the antifungal drug fluconazole. Our resource allocation model captures the kinetics of key metabolic pathways, and is parameterized using experimental and literature data. We propose that alterations in fungal metabolism are central in the development of different modes of antifungal resistance. Indeed, our results show that the optimal resistance strategy depends on the metabolic mode, i.e. respiration or fermentation. We extend this model to include multiple species and run computational simulations where we track AMR evolution in diverse microbial communities. In this way we generate testable hypotheses on how community interactions such as nutrient competition and cross-feeding influence the evolution of fluconazole resistance. Our findings have potential applications in designing robust antifungal strategies and improving our understanding of AMR emergence in natural and clinical settings.

Does genetic diversity impact gene drive efficiency in Drosophila melanogaster?

Nicky R. Faber, Jackson Champer, Bart A. Pannebakker, Bas J. Zwaan, and Joost van den Heuvel
Wageningen University

Gene drive technology could be a valuable tool for addressing several contemporary challenges, including combating disease vectors, conserving biodiversity, and controlling agricultural pests. A gene drive can be designed to modify a population by spreading a beneficial or neutral trait, or to drive a deleterious effect into it with the goal of suppression or eradication. However, although gene drives have been shown to work in several species, there is the potential for resistance to evolve against it. Importantly, we do not yet know how standing genetic diversity in the genome could impact drive performance. Most gene drives are only tested in laboratory strains, such as the white-eyed Drosophila melanogaster strain 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. We find that the gene drive shows considerable variability in efficiency, but that only 0.3% of this variability can be ascribed to heritable genetic effects. Selection against the gene drive is possible in this context, but will likely be inefficient and imprecise, potentially giving a gene drive enough time to fixate in the population. Furthermore, we find several types of mutations at the gRNA target sites, indicating that resistance could likely to evolve against this gene drive in a non-polygenic way.

Investigating the Maintenance of Alternative Reproductive Tactics in Tetranychus urticae males

Koen Freerks, Martijn Egas

Groningen Institute for Evolutionary Life Sciences (GELIFES)

Rapid environmental change necessitates predictive models of ecological and evolutionary responses, which can be effectively tested in species that display polymorphisms. Our project investigates the eco-evolutionary dynamics of male two-spotted spider mites (Tetranychus urticae), which exhibit alternative reproductive tactics (ARTs): fighter and sneaker tactics. Unlike other species where ARTs are linked to morphological differences, these tactics are behaviourally distinct yet morphologically identical. To understand how these tactics are maintained, we are establishing selection lines of fighters and sneakers. By employing advanced behaviour quantification tools, we can determine the behavioural phenotypes of individual males, enabling artificial selection for fighter and sneaker traits. Using these selection lines, we aim to manipulate and observe eco-evolutionary feedback loops, examining the influence of operational sex ratio, maternal effects, and genetics on ART dynamics.

Ecological effects on diversity and repeatability during antibiotic resistance evolution

Pietro Gadaleta, Meike Wortel

Universiteit van Amsterdam

The trajectory and outcome of evolution can be represented by a fitness landscape, which defines the relationship between genotype and fitness . While most studies focus on static or externally driven fluctuating landscapes, little attention has been given to dynamic landscapes shaped by interactions within the population. Understanding these dynamics is crucial, as ecological interactions can fundamentally alter evolutionary trajectories, affecting diversity, repeatability, and adaptability in ways traditional models fail to capture. To address this gap, we introduce a fitness model incorporating ecological interactions through environmental feedback. We simulate E. coli evolution in the presence of cefotaxime, a β-lactam antibiotic, through a serial transfer experiment. Experimental data show that resistance mutations improve survival but reduce growth without the antibiotic. Additionally, resistant bacteria degrade the antibiotic faster, benefiting sensitive but faster-growing strains, leading to ecological interactions between genotypes. Our algorithm includes genetic drift, selection, and environmental changes driven externally or by the genotypes within the population and shows how these factors shape evolutionary outcomes, repeatability, and population diversity. Finally, we compare our results with a deterministic model to evaluate the predictive power of our approach in fluctuating environments.

Collective β-lactam resistance in Escherichia coli due to β-lactamase release upon cell death

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

Wageningen University and Research

Collective antibiotic resistance occurs when populations of bacteria survive antibiotic treatments that are lethal to individual bacteria, which affects the efficacy of drug therapies. Several mechanisms may lead to collective resistance, including the production of drug-degrading enzymes. Here, we integrate experiments with mathematical modeling to understand the collective survival of Escherichia coli challenged with cefotaxime. We observe complex dynamics, involving initial biomass growth due to filamentation, followed by decline and subsequently growth recovery. We show that production of AmpC, a chromosomal β-lactamase, is responsible for cefotaxime degradation, allowing the resumption of cell division in surviving filaments. Our model suggests that the release of AmpC via cell lysis accelerates antibiotic clearance, and does so particularly in strains with low cell-wall permeability that privatize periplasmic cefotaxime hydrolysis. Our findings support the hypothesis of enhanced survival of β-lactamase-producing bacterial populations via altruistic cell death.

Recent and rapid assembly of an island species–area relationship in postglacial lakes

Luiz Jardim de Queiroz, Rampal S. Etienne, Luis Valente, Ole Seehausen

Naturalis Biodiversity Center & University of Groningen

The island species–area relationship (ISAR) is a fundamental ecological pattern. While most ISAR studies focus on ancient systems, it remains unclear whether classic ISARs can form over short evolutionary timescales. Focusing on a new fish community dataset of the Alps' postglacial lakes, we report an ISAR with a classical shape formed in less than 15,000 years. Despite their young age, these lakes exhibit an ISAR that mirrors older systems, with key classic ecological patterns such as the small-island-effect and an asymptotic shape. Mixed models suggest that immigration responds primarily to surface area and saturates, likely due to a limited regional species pool. Conversely, speciation is primarily driven by depth and remains unconstrained by the geographical space. We show that ISARs can develop rapidly after habitat formation, offering new insights into how lakes function as island systems.

Evolution of an extrinsic synthetic community under the pressure of interactions with manure native microbiota

Jun Liu, Xia Li, Yanliang Xu, Shuqi Zou, Mingxiong He, Jing He, Dick de Ridder, Anne Kupczok

Wageningen University & Research

Introduction: Selection pressures are driving forces of evolution. Selection pressures commonly include physical and chemical stresses, such as temperature and antibiotics. In microbial ecosystems, interactions between species considerably influence the succession and dynamics of microbial communities. Species interactions also drive evolution and could alter the evolutionary trajectory of members of communities. However, how interactions influence the evolution of microbes in communities needs to be uncovered. Study Design and Results: Here, we study the interactions between the manure microbiota generating ammonia emissions and a synthetic community containing lactic acid bacteria (LAB SynCom) that mitigates ammonia emissions. Recently, we found that the LAB SynCom significantly inhibited the manure ammonia-producing bacteria by antagonism. Therefore, we employed the negative interactions as the selection pressure to conduct experimental evolution of the LAB SynCom in manure. We found that the pH value of manure containing LAB SynCom decreased gradually during the experimental evolution with more than 400 generations. Metagenomics including the variant calling and annotation was applied to explore the evolution of the LAB SynCom. Preliminary results show that we detected 3309 variants in the LAB SynCom. The evolutionary profiles of the LAB SynCom will be revealed by evolutionary metagenomics in the near future.

Do mountains share a common diversification history?

Saijing Liu, Wen-Na Ding, Frederic Lens, Renske E. Onstein

Naturalis Biodiversity Center

Mountains harbor disproportionate biodiversity, making them ideal natural laboratories for studying the process driving species radiation. However, how closely related species diversify across separate mountain systems remains poorly understood. In this study, we hypothesize that mountains share a common diversification history, with montane lineages sharing similar diversification rates across different mountain systems. However, we expect diversification rates to be higher in montane than lowland lineages, suggesting that montane environments provide ecological opportunities for species radiations. We used four plant genera (Draba, Hypericum, Gentiana, Primula), with more than 1600 species across at least three mountain systems (Andes, Himalayas, Rockies, Alps), often representing dominant elements. Then, by integrating phylogenetic and distribution data, we used diversification rates models to test our hypotheses. The results show that diversification rates are taxon-specific and vary across mountain systems but are higher for montane than lowland taxa. Shifts in diversification rates coincided with major geological and climatic events suggesting that differences in geological history, climatic conditions, and ecological opportunities across mountain systems, rather than similarities, explain variation in montane radiations. Our study provides novel insights into the mechanisms underlying plant diversification in mountain systems.

Accelerating Streptomyces Development Through Experimental Evolution

David M. Norte, Niels Molkenboer, Luis A. Avitia-Dominguez, Ruth P. Viveros, Natalia Tschowri, Daniel Rozen

Leiden University

Streptomyces are a group of filamentous bacteria notable for their complex life cycle, prolific production of secondary metabolites, and well-orchestrated multicellular development. Understanding the timing and regulation of their development is crucial for comprehending how they transitioned from single cells to complex multicellular structures. Regulatory genes and signaling pathways ensure developmental transitions occur at appropriate times, such shifting from vegetative growth to reproduction and secondary metabolism. However, the timing of these transitions varies between species, raising questions about how life cycles evolve and how it impacts fitness. Here, we develop an experimental evolution approach to study the evolution of Streptomyces venezuelae life cycle by establishing conditions that favor rapid development. We used serial transfer conditions that promoted survival and proliferation of early-produced spores while killing all other cells. We observed several significant heritable shifts in development and life-cycle after 25 cycles: 1) evolved lineages developed ~4 hours faster than the ancestor, representing a 25% reduction in life-cycle timing and a ~100-fold increase in early sporulation 2) final total spore number in evolved populations increased ~4-fold. Overall, our results uncover the evolutionary lability of developmental life cycles in Streptomyces and confirm the value of an experimental evolution approach for studying bacterial multicellularity.

Role of beta-lactamase release in collective resistance against beta-lactam antibiotics

Abraham Ochoa-Guerrero, Joost Hollander and J. Arjan G. M de Visser

Wageningen University and Research

Bacteria resistant to β-lactam antibiotics pose a particular health concern due to the global importance of these drugs. In Gram-negative bacteria, the main resistance mechanism involves β-lactam degradation through intracellular β-lactamase enzymes. Release of these enzymes in the environment via cell lysis may accelerate drug degradation and enhance the survival of bacterial populations, but the factors driving such "collective resistance" remain unclear. This project aims to understand the potential effect of bacterial cell lysis on survival and evolution of high-level β-lactam resistance, providing valuable insights into how bacteria may collaborate to collectively resist β-lactam treatment.

Antibiotic resistance evolution in spatially structured environments compared to unstructured, well-mixed environments.

Josia Pool, Arjan de Visser & Hilje Doekes

Wageningen University & Research

Antibiotic resistance is designated by the World Health Organization as a top threat to global public health, as antibiotic resistance makes antibiotic drugs and treatments less effective. Experimental evolution can be used to 'simulate' the evolution of antibiotic resistance, by culturing bacterial populations under antibiotic selection pressure for many generations. However, most studies perform these experiments in a well-mixed, unstructured environment while outside of the laboratory bacteria often live in a spatially structured environment. Local dynamics in such environments may pose different selection pressures on the bacteria, thus potentially altering the evolutionary pathways to resistance. In this work we performed a systemic literature search aiming to characterize the effects of spatial structure on antibiotic resistance evolution. We selected studies which performed experimental evolution under antibiotic selection pressure in both well-mixed and spatially structured conditions and re-analyzed their data. Parallel-mutated genes were classified into four main mechanisms of antibiotic resistance and quantified the occurrence in both conditions. Preliminary results are inconclusive, because many mutated genes lack information about their implication in antibiotic resistance, of their function altogether. This illustrates current gaps in knowledge of the function of re-occurring mutations in antibiotic resistance.

Arabidopsis lyrata and its response to extreme weather events

Maarten Postuma, Elmar van der Wijk, Rashmi Sasidharan, Victoria Mironova, Philippine Vergeer,

Wageningen University

Under climate change, species inhabiting northern mountainous areas are predicted to decline. Here we investigate the relation between life history traits, population growth rates and environmental change by comparing the life history traits of eight Norwegian Arabidopsis lyrata populations in the period 2005-2007 to 2022-2024. We find that extreme, and local weather events such as flooding, and drought are the main drivers in changes in life history resulting in changes in population growth rates and in turn population size. Next to this, we show that there are differences between populations in their ability to cope with these stressors, and shed light on the genetic and epigenetic mechanisms that underly differences in adaptability. This emphasizes the need of including these mechanisms in models predicted the response of species to climate change.

Elucidating the role of transposable elements and satellite repeats in tomato centromeric architecture

Elias Primetis, Yazhong Wang, Roven Rommel Fuentes, Willem van Rengs and Charles Underwood

Radboud University

Centromeres are crucial chromosomal regions for forming kinetochore complexes that connect to spindle microtubules and segregate chromosomes during cell division in eukaryotes. Despite the variations in centromere size, structure, and repetitive sequences within and between species, their function remains conserved. High-copy satellite repeats and specific transposable element (TE) families are the main components of centromeric repeats, while their functional region can be defined by loading a histone H3 variant (CENH3). CENH3 nucleates the kinetochore and displays dynamic regulation. High-quality genome assemblies of the cultivated tomato (Solanum lycopersicum) and wild relatives have revealed that not all tomato chromosomes contain long tandem arrays of satellite repeats as is the case in Arabidopsis thaliana and human centromeres. The high abundance and diversity of TEs and satellite repeats mean that tomato chromosomes are dynamic and heterogeneous in nature and make the localisation of centromeres in tomato even harder. Therefore, the identification of tomato centromeres requires robust CENH3 ChIP-seq data. The detailed TE and satellite repeat annotation of tomato and wild relative genomes will be presented. Decoding the detailed composition and organisation of the centromeres in tomato will enlighten their evolutionary dynamics and functional roles in plant genetics.

Evolutionary Consequences of Mycelial Fragmentation in the Leafcutter Ant Fungus, Leucoagaricus gongylophorus

Asta Rødsgaard-Jørgensen, Caio Leal-Dutra, Vasilis Kokkoris, Jonathan Zvi Shik
Vrije Universiteit Amsterdam

Leafcutter ants cultivate the multinucleate fungal symbiont, Leucoagaricus gongylophorus, in underground nests. Each fungal cell contains up to 17 nuclei, which seem to be genetically different, with an unresolved ploidy. Previous studies have shown that regrowth from small hyphal fragments can lead to allele loss and even the failure to produce staphylae - the nutrient-rich reward structure, essential for ant nutrition. However, fragmentation is a natural aspect of colony life, as mature colonies can contain hundreds of physically isolated fungus chambers, all initiated from small fungal fragments. This study investigates the consequences of mycelial fragmentation on the fungal cultivar's allelic profile. Six fungal morphotypes were isolated through serial transfer to new media, and allelic changes at 10 microsatellite loci were analyzed to assess changes in allelic profiles and their relation to staphylae production. To test whether the same phenomenon occurs in the presence of the ants, six fungus chambers of ten mature Panamanian leafcutter colonies were analyzed for the same microsatellite loci and compared based on their physical distance from each other within the colony. This poster will present the preliminary findings of the genetic changes caused by fragmentations, along with the ants' role and the fungal mechanisms, respectively, in ensuring an even distribution of nucleotypes across the colony.

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

J. Romeijn, I. Bañales, M.F. Seidl
Utrecht University

Transposable elements (TEs) are mobile DNA sequences that are found in almost all living organisms. TEs can transpose within their host, shaping host genomes and functions. Recent findings suggest that TEs are frequently horizontally transferred between species, including fungi. Our preliminary data in a set of over 1,000 publicly available fungal genomes from diverse taxa revealed significant variation in TE composition and genome size, which is strongly correlated with TE content. Since we did not observe a strong phylogenetic signal underlying these patterns, we interpret these as signals of frequent horizontal transfer of TEs, suggesting that transferred TEs shape fungal genomes and their evolution. Here, we aim to systematically detect horizontal transfers through a bioinformatics approach which yielded 16 million TEs in total, with 2 million encoding TE-related protein domains. Among these, 1.3 million TE pairs between species exhibit higher sequence similarity than expected for vertical inheritance and are likely horizontally transferred. From these TE pairs, we are currently in the process to detect unique and independent horizontal transfer events. Moreover, we will elucidate the prominent TE types or fungal species involved in horizontal transfer events. We anticipate that our efforts will 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.

Spatial analysis of gene-expression in Arbuscular Mycorrhizal Fungi' mycelium

Sander van Otterdijk, Jonathan Shklarek, Brian van de Kieft, Jurr Liefting, Philipp Savakis, Vasilis Kokkoris, Evelina Tutucci

Vrije Universiteit van Amsterdam

Arbuscular Mycorrhizal Fungi (AMF) are ancient and widespread obligate symbionts that establish mutualistic associations with plants, significantly enhancing plant health and development. Given their pivotal role in both natural ecosystems and agriculture, understanding their unique cellular and molecular biology is essential. A distinctive feature of AMF is their coenocytic mycelium, where living hyphae lack septa, resulting in a multinucleate cytoplasmic network. However, how gene expression is regulated within this syncytial environment remains poorly understood. Here, we investigated the spatial regulation of gene expression in the model AMF species Rhizophagus irregularis using Fluorescent In-Situ Hybridization (FISH). This approach enabled us to visualize RNA transcripts within fixed fungal mycelium using fluorescently labelled probes. By integrating spatial gene expression data with network growth patterns, we aim to understand how localized gene expression contributes to the morphology and physiology of early developmental networks. Specifically, we analyzed the expression of FAD1 mRNA, involved in fatty acid metabolism, and ribosomal RNA (rRNA), revealing variations in RNA density across the mycelial network and differences in nuclear transcriptional activity. Our findings suggest that gene expression in AMF is spatially regulated, shedding new light on the complex intracellular dynamics of these ubiquitous symbiotic fungi.

Co-evolution of host and endosymbiont genomes during Eukaryogenesis: the role of sexual reproduction

Alkmini Zania, Paulien Hogeweg, Samuel von der Dunk

Utrecht University

Sexual reproduction is a trait shared in all eukaryotes, and was present in the last eukaryotic common ancestor. Current eukaryotes mostly inherit mitochondria from one parent, but the mechanisms that ensure this vary hugely in different species, and the ancestral trait is unknown. It is unknown when sex appeared in relation to the acquirement of mitochondria and its role in the evolution of endosymbiosis. In this project, a multilevel, individual based model of endosymbiosis is used to study the role sex in the co-evolution of host and symbiont genomes. Evolutionary simulations were performed on populations of cells that live on a 2D grid, each cell consisting of one host and one or more symbionts, the latter inherited by one parent (asexual reproduction) or two parents (sexual reproduction). Our results indicate that sex poses threats, due to the emergence of selfish symbionts that can drive populations to extinction. However, resolution of this conflict is possible, and can drive the evolution of signalling, allowing the host to control the symbiont's cell cycle. In fact, in many cases the populations that survive sexual reproduction outperform the asexual populations that evolve under the same conditions. In addition, when evolved on a nutrient gradient, populations can speciate and adapt to different conditions. This protects the total population from complete annihilation by selfish symbionts.

Macroevolutionary impact of anthropogenic extinctions on mammalian island faunas worldwide

Pepijn Helleman & Luis Valente

Naturalis Biodiversity Center

Islands harbour a rich biodiversity, resulting from high levels of endemicity, ancient lineages, and unique adaptations. We investigated the extent to which mammalian island faunas are threatened from a taxonomic and evolutionary perspective. We hypothesize that global geographical hotspots of threatened species diversity (TSR) and threatened phylogenetic diversity (TPD) are decoupled and respond differently to physical island features. By including these two distinct facets of biodiversity, we aim to identify islands of particular concern for conservation and examine whether island features (area and isolation) are good predictors of threatened diversity. We developed a new computational pipeline to aggregate and map biodiversity data on insular mammals and to compute TSR and TPD for 302 islands worldwide. Our results show an unequal global distribution of threatened diversity of insular mammals. Hotspots of TSR and TPD are found in the western Malay archipelago and Madagascar, mostly in large islands with high current diversity of mammals. In terms of the fraction of threatened mammals, the highest proportions of TSR and TPD are found in the Gulf of California, Madagascar, and the Philippines. While absolute TPD is positively correlated with area, the proportion of TPD shows a more intricate pattern. Our findings suggest that simply evaluating the number of threatened species in conservation may miss out on important centres of threatened unique insular biodiversity.