

Abstract Book

2023 Conference of the Netherlands Society for Evolutionary Biology

Tuesday 16 May 2023

Akoesticum, Ede, The Netherlands



Sponsors



ISME

Organizing committee

Renske Onstein, Vasilis Kokkoris, Anne Kupczok, Sijmen Schoustra, Marjon de Vos

Program May 16 2023

- 8:45** Arrival with coffee/tea
- 9:15** Welcome & Introduction, Auditorium
- 9:25** **Keynote: Felicity Jones** (University of Tübingen), TITLE: “A stickleback's guide to adaptation: upcycling, non-coding hacks and epigenomic bling”, Auditorium
- 10:00** **NL Evo Biology 2022 prize winner**, Auditorium
- 10:30** Coffee/tea break
- 11:00** **Parallel sessions** with contributed talks
I Auditorium, Theme Ecology & Evolution
II Tuinzaal, Modeling Evolution
- 12:15** Lunch with network opportunities
- 13:30** **Keynote: Franjo Weissing** (University of Groningen) TITLE: “Sexual Selection: New Insights From an Old Theory”, Auditorium
- 14:05** **Parallel session** with contributed talks
III Auditorium, Genomics & Evolution
IV Tuinzaal, Macro-Evolution
- 15:20** Coffee/tea break
- 15:45** General Assembly Tuinzaal
- 16:30** **Cultural Intermezzo - WHAT IF**, Auditorium
- 17:10** Poster session, Tuinzaal
- 18:30** Poster Prize winner & Closing remarks, Tuinzaal
- 18:35** Dinner, with optional **round table** discussions

Keynote speakers

Felicity Jones (Friedrich Miescher Lab, Tübingen)

Felicity Jones studies how variation in genome function in natural populations facilitates adaptation to different environments and the evolution of new species. She combine diverse functional genomic and population genomic techniques to study adaptive divergence in epigenomics and gene regulation, recombination, and adaptation from standing genetic variation. Her work leverages divergent natural populations and their hybrid zones in a powerful evolutionary model system: threespine stickleback fish. Compared to traditional model organisms, sticklebacks provide a powerful system to understand genome function in the context of natural populations and the environment.

TITLE: “A stickleback's guide to adaptation: upcycling, non-coding hacks and epigenomic bling”

Abstract: As organisms face unprecedented rates of climate change, a major focus in our field is to understand what facilitates and/or constrains the rate at which species can adapt. With their recent adaptive radiation from marine into freshwater habitats, stickleback fish provide an excellent system to dissect the heritable molecular basis of adaptation and factors that facilitate and constrain this evolutionary process. I'll present some of the major insights we've learnt from sticklebacks including the importance of standing genetic variation, the critical role of the non-coding genome and the epigenome in adaptation to new environments. In addition to helping us understand the evolutionary process, this work provides important insight into how the genome functions in a natural, genetically diverse species evolving in diverse environmental conditions, and under divergent selection pressures.

Franjo Weissing (U Groningen)

Franjo Weissing is a theoretical biologist with a strong interdisciplinary profile, applying ‘evolutionary thinking’ not only to biological systems, but also in psychology, sociology, economics, and the political sciences. His research centres on the causes and consequences of ‘adaptive diversity’ (diversity shaped by competition or natural selection). To this end, he studies selection-induced differences between cells, individuals, and populations, the emergence of new species, and the structure and patterning of ecological communities. By a combined theoretical and empirical approach, he also investigates whether adaptive evolution is predictable and to what extent ‘evolvability’ (the ability to adapt to environmental change) is shaped by natural selection.

TITLE: “Sexual Selection: New Insights From an Old Theory”

Abstract: Not surprisingly, it was Charles Darwin who (in 1871) laid the foundations of sexual selection theory. After a century of stagnation, the theory got off the ground in the 1980s. Although sexual selection is still an immensely popular research field, theory formation has again stagnated in the last two decades. Many researchers think that the theory has now been firmly established. In my talk, I will argue that, on the contrary, many fundamental issues have not yet been resolved and that even the standard models of sexual selection may yield surprising results. I will illustrate this with several examples from the research of my group.

NL Evo Biology 2022 prize winner

The spread of the first introns in proto-eukaryotic paralogs illuminates the origin of the nucleus.

Julian Vosseberg *Michelle Schinkel, Sjoerd Gremmen & Berend Snel*

Spliceosomal introns are a unique feature of eukaryotic genes. Previous studies have established that many introns were present in the protein-coding genes of the last eukaryotic common ancestor (LECA). Intron positions shared between genes that duplicated before LECA could in principle provide insight into the emergence of the first introns. In this study we use ancestral intron position reconstructions in two large sets of duplicated families to systematically identify these ancient paralogous intron positions. We found that 20–35% of introns inferred to have been present in LECA were shared between paralogs. These shared introns, which likely preceded ancient duplications, were wide spread across different functions, with the notable exception of nuclear transport. Since we observed a clear signal of pervasive intron loss prior to LECA, it is likely that substantially more introns were shared at the time of duplication than we can detect in LECA. The large extent of shared introns indicates an early origin of introns during eukaryogenesis and suggests an early origin of a nuclear structure, before most of the other complex eukaryotic features were established.

Program parallel sessions

Session I Auditorium, Ecology & Evolution

- 11:00 **Joana Sabino Pinto** (*GELIFES*) The role of MHC-mediated sexual selection in the evolution of amphibian disease resistance
- 11:15 **Yannick Woudstra** (*NIOO-KNAW & Naturalis Biodiversity Center*) Some like it hot: urban-rural divergence in growth and phenology response to the urban heat island in common dandelion.
- 11:30 **Monique de Jager** (*UU*) Critical transitions and evolutionary hysteresis in movement: Habitat fragmentation can cause abrupt shifts in dispersal that are difficult to revert
- 11:45 **Shepherd Nehanda** (*TDC & WUR*) Substrate variation shapes community structure and functionality in natural microbial communities - a field and laboratory experiment
- 12:00 **Matti Gralka** (*VU*) Fundamental metabolic strategies of heterotrophic bacteria

Session II Tuinzaal, Modeling Evolution

- 11:00 **Sam von der Dunk** (*UU*) Regulatory interference drives the evolution of host--symbiont signaling during eukaryogenesis
- 11:15 **Magdalena Kozielska** (*RUG*) A Neural Network Model for the Evolution of Social Learning
- 11:30 **Joost van den Heuvel** (*WUR*) The evolution and genetics of ageing
- 11:45 **Julia Höglund** (*WUR*) Characterisation of deleterious genetic variants in non-model organisms: from present to extinct species

12:00 **Chris Barratt** (*NATURALIS*) Life on the edge: a new informatic toolbox to predict population vulnerability to global change

Session III Auditorium, Genomics & Evolution

14:05 **Daniel Tamarit** (*UU*) Inference and reconstruction of the heimdallarchaeial ancestry of eukaryotes

14:20 **Jacintha Ellers** (*VU*) Pleiotropy promotes preservation of genes when a phenotypic trait is lost: Evidence from RNAi knockdown experiments

14:35 **Bram van Dijk** (*MAX PLANCK*) Identifying and tracking mobile elements in evolving compost communities yields insights into the nanobiome

14:50 **Brigida Gallone** (*NATURALIS*) Fungarium collections in the genomic era: the *Mycena* genus

15:05 **Yumi Nakadera** (*VU*) Identifying seminal fluid proteins via transcriptomics in a simultaneously hermaphroditic snail species

Session IV Tuinzaal, Macro-Evolution

14:05 **Alexander Kotrschal** (*WUR*) Artificial selection for predation survival shapes life-history traits and collective motion in guppies (*Poecilia reticulata*)

14:20 **Qin Tian** (*NATURALIS*) Rapid in-situ diversification rates in the cosmopolitan plant family Rhamnaceae explain the origin of temperate biodiversity hotspots

14:35 **Alexandra van der Geer** (*NATURALIS*) The biogeography of island elephants: when does Jumbo shrink?

14:50 **Gerrit Potkamp** (*RUG*) Rapid light-induced changes in visual gene expression in African cichlids do not covary with ecology or diversification rate

15:05 **Thomas Blankers** (*UVA*) Non-adaptive and allopatric radiations provide complementary insight into universal mechanisms and outcomes of speciation

Cultural Intermezzo

WHAT IF?

Natural selection has led to the appearance (phenotype) of all species today: But what about the phenotypes that never existed? What if the circumstances were different? In this documentary-theatre performance by dramaturg **Wessel Padberg**, we dive into the world of forbidden phenotypes; phenotypes that are possible but - as yet - have not happened. Drawing on artists from different times and disciplines, we will look at their views on these phenotypes, covering humans, plants, animals and fungi. Let this art invite you to look at your profession in a fresh new perspective and get inspired by all these creatures you thought could not exist.

Wessel Padberg (he/him) is a dramaturg with broad cultural interests. Currently he is finishing his master's degree in Dramaturgy at the University of Amsterdam. He has a great love for theatre, visual arts, sensory experiences, social issues and Dutch literature.

Round table discussions

Time: 18:35 during dinner. No registration required.

Table 1: Data archiving and management (Chair: Sebastian Lequime (RUG))

Table 2: Drafting a successful research proposal in the field of evolutionary biology (Chair: Jacintha Eller (VU Amsterdam) & Bas Zwaan (WUR))

Table 3: Education in evolutionary biology (Chair: Jelle Zandveld (UU))



Abstracts contributed talks

Session I – Auditorium / Theme: Ecology & Evolution

The role of MHC-mediated sexual selection in the evolution of amphibian disease resistance

Joana Sabino Pinto, Ido Pen, Martine Maan

GELIFES, University of Groningen

Sexual selection is a strong evolutionary force that can promote or inhibit adaptation to environmental challenges. In the face of novel pathogens, sexual selection can influence population persistence by impacting the spread of resistance alleles (i.e., the major histocompatibility complex (MHC)). The MHC encodes proteins that recognize pathogens and activate the immune system, allowing the organism to fight pathogenic invasions. Many vertebrates preferentially mate with partners carrying beneficial MHC alleles, conferring higher resistance to the offspring. It is unknown whether this mechanism also operates in amphibians. Many amphibian species are currently under threat, with a major role for an invasive lethal pathogen. Hence, it is important to establish the possible role of MHC-mediated sexual selection in amphibian resistance evolution. Given that the amphibian immune system differs from that of other vertebrates, we cannot extrapolate insights from other vertebrate studies. We combine theoretical simulations with field screenings and experimental trials to determine whether sexual selection and MHC are linked in amphibians, and to explore whether this interaction can lead to more resilient populations.

Some like it hot: urban-rural divergence in growth and phenology response to the urban heat island in common dandelion.

Yannick Woudstra, Roy Erkens, Heidrun Huber, Barbara Gravendeel, Koen JF Verhoeven

Terrestrial Ecology, Netherlands Institute of Ecology (NIOO-KNAW) & Naturalis Biodiversity Center

The urban heat island effect (UHIE) is a globally consistent pressure on species living in and closely around cities. Rapid adaptation to the UHIE is expected in urban wild flora, but experimental evidence is lacking. Here, we report the first evidence of genetic differentiation in a plant species in response to the UHIE. We sampled clonal seeds from common dandelion (*Taraxacum officinale*) individuals along an urban-rural gradient in the city of Amsterdam (The Netherlands). In common-environment greenhouse experiments, we assessed the effect of elevated temperatures on plant growth and the effect of vernalisation treatments on flowering phenology. We found that urban plants accumulate more biomass at higher temperatures and require shorter vernalisation to induce flowering compared to rural plants. Differentiation was also observed between different intra-urban subhabitats, with park plants displaying a higher vernalisation requirement than street plants. Our results show strong differentiation between urban and rural dandelions in temperature-dependent growth and phenology, consistent with adaptive divergence in response to the UHIE. Rapid adaptation to the UHIE may be a potential explanation for the widespread success of dandelions in urban environments.

Critical transitions and evolutionary hysteresis in movement: Habitat fragmentation can cause abrupt shifts in dispersal that are difficult to revert

Monique de Jaeger & M. B. Soons

Department of Biology, Utrecht University

Under habitat fragmentation, plant species' survival hinges on the ability of individuals to disperse from one habitat patch to another. While there is evidence that severe habitat fragmentation leads to evolution of reduced dispersal ability and that such decreased mobility is generally detrimental for species' survival, it is unknown whether species adapt via a gradual loss in dispersal ability or via a sudden shift from frequent to infrequent dispersal between patches (i.e., a critical transition). Using both a spatially explicit deterministic and individual-based stochastic model of hydrochorous seed dispersal, we show that a small increase in inter-patch distance can generate an abrupt shift in plant seed dispersal strategy from long to short distances. Most importantly, we found that a substantial increase in connectivity between habitat fragments is required to reverse this loss of long-distance dispersal, due to an evolutionary hysteresis effect. Our theory prompts for re-consideration of the eco-evolutionary consequences of habitat fragmentation as restoring habitat connectivity may require restoration of much higher connectivity levels than currently assumed

Substrate variation shapes community structure and functionality in natural microbial communities - a field and laboratory experiment

Shepherd Nehanda, Anna Alekseeva, Justine Chileshe, Bas Zwaan, Eddy Smid and Sijmen Schoustra.

Microbial ecology and Laboratory of Genetics, Tropical Diseases Research Centre Zambia and Wageningen University

Microbial communities co-exist and interact in natural ecological habitats while performing ecosystem functions. However, mechanistic understanding on how community composition and functioning respond to environmental perturbation is limited. In the short term, the ecological process of species sorting will lead to changes in relative abundance of microbial species; in the longer term evolutionary changes involving fixation of novel mutations may lead to adaptation in specific species present. Here we propagated natural microbial communities from mabisi, a Zambian traditional fermented milk, in both field (10 propagations) and laboratory experiments (30 propagations) in 5 different types with 3 replicates each. We sampled at various propagations for microbial 16S rDNA, pH, consistency and volatile metabolic compound analysis. We found reproducible patterns of species sorting depending on selective treatment (milk type). Genera belonging to lactic acid bacterial types increased in abundance in raw cow, UHT low fat and full cream milk treatments. In contrast, F100 and S26 milk treatments were dominated by non-lactic acid bacteria. There was a unique pattern of the volatile metabolic compounds per milk type. Results provide experimental evidence how environmental perturbation shapes how key microbial communities assemble, adapt and persist in niches while executing the ecosystem functionality.

Fundamental metabolic strategies of heterotrophic bacteria

Gralka, Matti; Pollak, Shaul; Cordero, Otto X.

Amsterdam Institute of Life and Environment, Vrije Universiteit Amsterdam

The enormous diversity of heterotrophic bacteria in the environment begs the question to what degree their metabolic niches can be understood in terms of a small number of simplified functional categories. Here, we show that, despite high variability at all levels of taxonomy, the carbon catabolic niches of heterotrophic bacteria can be summarized along a single axis, representing the preference for either glycolytic (sugars) or gluconeogenic (amino and organic acids) carbon sources. This preference is encoded in the abundance of metabolic pathways and associated with genomic GC content, which we hypothesize results from the difference in C and N supply associated with typical sugar and acid substrates. Thus, our work reveals that bacterial genomes are structured by a fundamental constraint on microbial evolution rooted in metabolism.



Session II – Tuinzaal / Theme: Modeling Evolution

Regulatory interference drives the evolution of host-symbiont signaling during eukaryogenesis

Samuel H. A. von der Dunk, Paulien Hogeweg, Berend Snel
Theoretical Biology & Bioinformatics, Utrecht University

How the complex eukaryotic cell arose from its simpler prokaryotic ancestors remains an evolutionary enigma. Here we study the impact of the mitochondrial endosymbiosis in the context of gene regulatory networks, complementing energetic perspectives. The endosymbiotic state introduced several unique challenges to cells such as coordination of host and symbiont cell-cycles, and leakage between host and symbionts of transcription factors (regulatory interference) and stretches of DNA (resulting in gene transfer). These challenges likely impacted genome and network evolution in proto-eukaryotes and may explain various eukaryotic characteristics. We study a computational model where we force two simple cells that regulate their own cell-cycle into an obligate endosymbiosis. In most evolutionary replicates, the host and symbiont manage to adapt to the endosymbiotic setting by evolving some form of cell-cycle coordination. Strikingly, we find that regulatory interference, which is inherently harmful, drives the evolution of signaling between host and symbiont. In one replicate, through signaling, the host almost takes complete control of the symbiont cell-cycle, resulting in high fitness. Moreover, host control resembles the regulatory dominance of the nucleus over mitochondria that emerged during eukaryogenesis. In sum, this study reveals the informational challenges of endosymbiosis and how they are overcome by evolution, with important implications for eukaryogenesis.

A Neural Network Model for the Evolution of Social Learning

Maqdalena Kozielska, Jacob Chisausky, Franjo Weissing
GELIFES, University of Groningen

The evolution of learning reflects the interplay between three main adaptive strategies – innate determination of preferences, individual learning, and social learning. Theoretical work suggests that innate determination, individual learning, and social learning will evolve in stable, unstable, and intermediate environments, respectively. However, existing models usually assume a very simple learning process. We studied the evolution of social learning in changing environments using a neural-network approach. This approach allows for studying more complex phenotypes in more complex environments. By means of individual-based simulations, we investigated under which conditions different types of learning will evolve. We found that the evolution of learning is indeed dependent on the extent of environmental changes. Stimulus enhancement, a type of social learning ignored by most models on the topic, evolved in intermediate environments, as predicted by simpler models. Imitative social learning evolved much less readily and only if social learning was followed by individual learning. Contrary to the expectations of earlier models, the evolution of social learning was neither boosted by a low cost nor by choosing successful teachers. This study highlights the utility of a neural-network approach to uncovering new principles underlying the evolution of (social) learning. It also

demonstrates that the conclusions of simple learning models may cease to hold in more complex settings.

The evolution and genetics of ageing

Joost van den Heuvel, Jelle Zandveld, Thomas Flatt, Tom van Dooren, Bas Zwaanere

Laboratory of Genetics, Wageningen University and Research

The classical evolutionary theories of ageing have been formulated decades ago, but which of these theories best fits life history data remains unknown. The theories of mutation accumulation (MA), antagonistic pleiotropy (AP) and disposable soma (DS) have similar evolutionary predictions, but they differ in their mechanistic assumptions. An integrative approach of evolutionary theory and population genetics is needed to find out which theory has most empirical support. The subtle mechanistic differences in assumptions between AP and DS have large consequences for the life histories they predict. The predicted life tables of DS fit data much better when compared to AP. Conveniently, this only leaves MA and DS, which can be contrasted by identifying the degree to which genetic trade-offs are at the basis of lifespan variation in natural populations. To do this, experiments are needed. We used experimental evolution to produce long- and short-lived flies and identified regions in the genome that are significantly different between these populations. Additional individual genotyping identified that some of these loci associate with lifespan. Lastly, variation of these lifespan loci was found to associate with other life history traits indicating trade-offs are operating. The finding of genetic trade-offs supports DS (and AP) when compared to MA. We show that our unique combination of evolutionary theory and population genetics allows for testing the classical theories of ageing.

Characterization of deleterious genetic variants in non-model organisms: from present to extinct species

Julia Höglund, Seyan Hu, Martijn F.L. Derks, Love Dalén, Mirte Bosse

Dept. of Animal Breeding and Genomics (ABG), Wageningen University and Research

Animals have always been exposed to extinctions. Now, during what can be seen as the sixth mass extinction, human activity has been one main reason for dramatic decline. When a population becomes smaller, threats affecting its genome become larger. It becomes more prone to inbreeding, genetic variation will be lost, and deleterious variation will increase in frequency. This leads to a worse ability to adapt to changing environments, due to lowered fitness and could lead to extinction. Hence, there is a crucial need to characterise and quantify damaging variation and its contribution to decline, for conservational purposes and understanding drivers of extinction. Such characterisation can be based on predicted deleteriousness. These types of scores are often species specific, and currently still largely unreliable, especially for non-model organisms. Thus, there is a need to expand accurate prediction of deleterious genetic variation beyond model species. Here, we used domesticated pig genomes to develop such a tool to score deleterious variants from sequence data. Substitution rates were estimated from the last common ancestor of pig and cow. The scoring model will then be trained within domesticated pig, validated with in wild boar and lastly tested in endangered pig species. In contrast to previous models, this model extends across similar

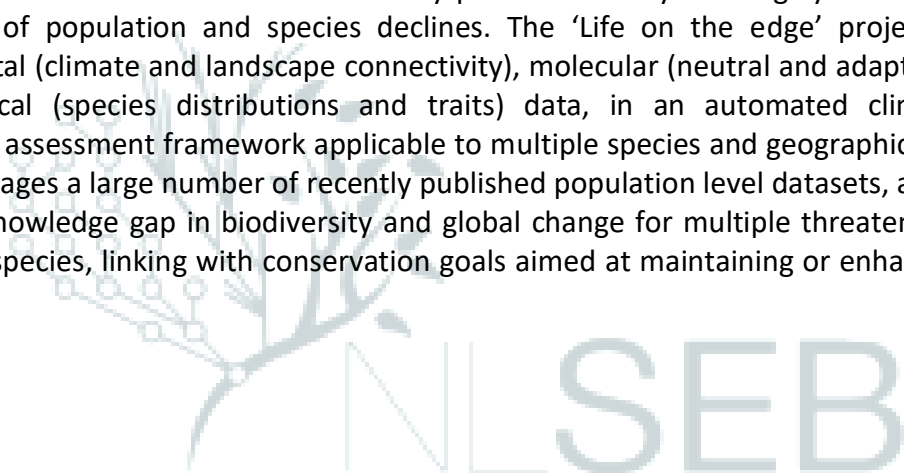
species already in the initial estimation, with the long-term goal of estimating how much genetic variation contributes to extinction.

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

Barratt CD, Onstein RE, Pinsky M, Steinfartz S, Kuehl H, Forester BR, Razgour O

Biodiversity and Society, Naturalis Biodiversity Center

Global change is affecting biodiversity in unprecedented ways, with environmental changes compounded by anthropogenic activities to introduce new selection pressures. Species responses to these pressures depend not only on the magnitude of change occurring, but also on the adaptive capacity of individuals and populations. To date, most climate change vulnerability assessments have focused at species level, lacking insights into population vulnerability, though this is beginning to change with the growing availability of large population level datasets. Assessing the adaptive capacity of populations and quantifying their vulnerability under future global change has therefore been a neglected area of biodiversity research. These insights are essential for conservation as they provide an early warning system to detect the initial signs of population and species declines. The 'Life on the edge' project integrates environmental (climate and landscape connectivity), molecular (neutral and adaptive diversity) and ecological (species distributions and traits) data, in an automated climate change vulnerability assessment framework applicable to multiple species and geographic regions. The project leverages a large number of recently published population level datasets, addressing an important knowledge gap in biodiversity and global change for multiple threatened and non-threatened species, linking with conservation goals aimed at maintaining or enhancing genetic diversity.



Session III – Auditorium/ Theme: Genomics & Evolution

Inference and reconstruction of the heimdallarchaeal ancestry of eukaryotes

Tamarit, D., Eme, L., Caceres, E.F., Stairs, C.W., De Anda, V., Baker, B. J., Ettema, T.J.G.

Theoretical Biology and Bioinformatics, Utrecht University

Eukaryotes, organisms with complex cells such as animals, plants and fungi, originated through the symbiosis of a bacterium and an archaeon. Recent advances in sequencing and computational methods indicate that the archaeal partner was related to Asgard archaea, but their identity and characteristics remain mysterious. Here, we analyze distinct gene marker datasets of an expanded genomic sampling of Asgard archaea and evaluate competing evolutionary scenarios using state-of-the-art phylogenomic approaches of unprecedented dimensions. Our results show, with high confidence, that eukaryotes are well-nested clade within Asgard archaea, as a sister lineage to Hodarchaeales, a newly proposed group within Heimdallarchaeia. Using sophisticated gene tree/species tree reconciliation approaches, we show that, similar to the evolution of eukaryotic genomes, Asgard archaeal genome evolution involved significantly more gene duplication and fewer gene loss events than other archaea. Finally, we infer that the last common ancestor of Asgard archaea likely was a thermophilic chemolithotroph, and that the lineage from which eukaryotes evolved adapted to mesophilic conditions and acquired the genetic potential to support a heterotrophic lifestyle. Our work provides key insights into the prokaryote-to-eukaryote transition and the platform for the emergence of cellular complexity in eukaryotic cells.

Pleiotropy promotes preservation of genes when a phenotypic trait is lost: Evidence from RNAi knockdown experiments

Jacintha Ellers, Janine Mariën, Niek Barmantlo, Sofia Chibante, Jesper Wolters & Katja Hoedjes

Amsterdam Institute of Life and Environment, Vrije Universiteit Amsterdam

Loss of metabolic functions is a hallmark of symbiosis, often caused by decay of the underlying genes. Insect parasitoids have repeatedly lost the ability for adult lipid accumulation, yet the genetic machinery encoding fatty acid synthesis is still intact. Previously, it has been suggested that the preservation of fatty acid synthesis genes is due to pleiotropic effects on other functions than lipid accumulation, such as neurogenesis, pheromone production and cuticular hydrocarbon production. Here we use the parasitoid wasp *Nasonia vitripennis* to test the hypothesis that loss of fatty acid synthesis genes would compromise these other functions. First, we found differences in fatty acid synthase (*fas1*, *fas2*, *fas3*) expression among the tissues where the other lipid functions are localized (head, male reproductive glands, and oenocytes, resp.), supporting tissue-specific functionalities of the three paralogs. We then performed RNAi knockdown of *fas1*, which caused a large increase of *fas2* expression in the oenocytes, possibly compensating for the decreased *fas1* expression. Subsequently, we knocked down all three paralogs and measured phenotypic functions. Lipid content and starvation resistance were not affected, but desiccation resistance and mating behaviour were strongly decreased, consistent with the observed changes in *fas2* expression in the oenocytes. Our results provide evidence for a role of pleiotropy in the conservation of gene networks when phenotypic traits are lost.

Identifying and tracking mobile elements in evolving compost communities yields insights into the nanobiome

Bram van Dijk

Microbial population biology, Max Planck Institute

Microbial evolution is driven by rapid changes in gene content mediated by horizontal gene transfer (HGT). While mobile genetic elements (MGEs) are important drivers of gene flux, the nanobiome – the zoo of Darwinian replicators that depend on microbial hosts – remains poorly characterised. New experimental approaches and analyses are necessary to advance our understanding beyond simple pairwise MGE-host interactions. To detect horizontal transfer, a bioinformatic pipeline (xenoseq) was developed to cross-compare metagenomic samples, which was then applied to metagenomic data from evolving compost communities. These communities were routinely exposed to an “MGE cocktail” derived from allopatric communities. We show that this results in the horizontal transfer of a multitude of previously undetected MGEs, including bacteriophages, phage-plasmids, megaplasmids, and even nanobacteria. Sequences that spread from one community to another are shown to disproportionately carry characteristics of phages and insertion-sequences, i.e., traits of canonically parasitic MGEs. We also show that one particularly prolific mobile element - a 313 kb plasmid – correlates substantially with rates of ammonia production, which under nitrogen limitation is likely beneficial. Taken together, our data show that new experimental strategies combined with bioinformatic analyses of metagenomic data stand to provide insight into the drivers of microbial community evolution.

Fungarium collections in the genomic era: the *Mycena* genus

Gallone Brigida, Maartje Cathelyn, Jorinde Nuytinck

Understanding Evolution, Naturalis Biodiversity Center

Understanding the taxonomic relationships among organisms and their evolutionary history is a critical step in establishing biodiversity conservation goals. Fungi are one of the most diverse group of eukaryotes, supporting the health of all ecosystems. Nevertheless, only 8% of fungal diversity has been currently described. Sampling and identification are often hampered by their elusive nature together with complex lifecycles. Over the past centuries fungal diversity has been preserved world-wide in Fungarium collections. The genomic revolution offers the opportunity to unlock this huge genetic repository to refine phylogenetic relationships, reconsider taxonomic assignments and describe new species. *Mycena* is a large, yet under sampled, genus of small mushroom-forming fungi that lacks a robust phylogenetic framework. It exhibits high variability in morphology, broad ecological versatility and striking phenotypic diversity, with several bioluminescent members. In this project we are developing the first genome-based classification of *Mycena*, that integrates contemporary and museum (type-)specimens, bridging taxonomy and evolution. We assessed the feasibility of generating whole-genome sequencing data from dried specimens and the efficiency of long-read high throughput barcoding for taxonomic identification of hundreds fungal specimens. Overall, the time has come to consistently integrate genomics in the study of fungal diversity and go beyond single-barcode approaches.

Identifying seminal fluid proteins via transcriptomics in a simultaneously hermaphroditic snail species

Yumi Nakadera, Miao Chen, Joris M. Koene

Ecology and Evolution, Amsterdam Institute of Life and Environment (A-LIFE), Vrije Universiteit Amsterdam

Seminal fluid proteins (SFPs) play significant roles in reproduction, and their genes are often observed to evolve rapidly. The current status of SFP research is not able to fully resolve the patterns of SFP evolution, as the prevalent model systems are almost exclusively separate-sexed species. We consider the great pond snail *Lymnaea stagnalis* as a fruitful model system to investigate SFP evolution, since they are simultaneous hermaphrodites and their reproductive biology is well documented. To establish a hermaphroditic model system that allows for in-depth SFP studies, we screened transcriptomes of *L. stagnalis* for SFPs. First, in order to obtain a male accessory gland-specific transcriptome we compared the transcriptome of a male and female reproductive gland: the prostate, which produces the majority of SFPs, and albumen gland, which produces the material the eggs are provisioned with. Second, we examined differential expression in prostate gland transcriptomes of snails reared in different social conditions – isolation, pairs and quintets. Using these approaches, we found candidate SFP genes highly expressed in prostate glands as well as SFPs that are differentially expressed between isolated and paired and/or grouped treatments. We will discuss the criteria for candidate SFP genes and their implications.



Session IV- Tuinzaal / Theme Macro-Evolution

Artificial selection for predation survival shapes life-history traits and collective motion in guppies (*Poecilia reticulata*)

*Hannah De Waele, Regina Vega-Trejo, Kevin Chou, Jori Noordenbos, Alexander Kotrschal
Animal Sciences, Behavioural Ecology, Wageningen University*

Predation exerts strong selection pressure on many traits. For instance, it is likely a major driver of the evolution of life-history traits and behaviour. A wealth of empirical evidence corroborates this idea. However, such data is often derived by comparing natural populations with associated confounding factors inherent to ecological comparisons. Experimental evidence on how predation impacts vertebrate evolution is surprisingly scarce. Here, we experimentally tested how predation impacts the evolution of life-history traits, collective behaviour, and cognition in guppies (*Poecilia reticulata*). We used three replicate lines of guppies artificially selected for adult predation survival for three generations and compared them to three control lines. We found that predation selected fish had larger, and more offspring, particular early in life, than controls, while several other traits were remarkably unaffected by selection. Additionally, we found that the offspring of survivors showed several differences in schooling characteristics and cognitive landscape, compared to fish from control lines. Our results demonstrate which aspects of life-history are shaped by predation and show that collective motion and cognition rapidly evolves under strong predation selection.

Rapid in-situ diversification rates in the cosmopolitan plant family Rhamnaceae explain the origin of temperate biodiversity hotspots

Qin Tian

*The Germplasm Bank of Wild Species in Southwest China, Kunming Institute of Botany, CAS;
Naturalis Biodiversity Center*

The underlying macroevolutionary processes that have shaped temperate biodiversity biomes remain poorly understood. We hypothesize that evolutionary dynamics related to dispersal rates, diversification rates, colonization time, coupled with Cenozoic climate change, shaped species richness across these biomes. We conducted environmental ordination, diversification and biogeographical analyses on a new Rhamnaceae phylogeny (574 species, ~52.2% of extant diversity), to evaluate macroevolutionary processes contributing to high species diversity in hotspots. Seven hotspots have extraordinary Rhamnaceae species richness: California, Mexico to Central America, Mediterranean Basin, Cape, Southwest Australia, Southeast Australia, and East China. Overlap in environmental occupancy across these regions and a colonization followed by high in-situ diversification rates almost contemporaneously were inferred for all regions except East China. We found higher immigration rates in Mexico to Central America and an earlier colonization time of East China than in other hotspots. The establishment and expansion of seasonal environments during the Oligocene may have provided the ecological opportunity for rapid in-situ diversification rates of Rhamnaceae in Mediterranean-type ecosystem biomes, whereas older (East China) or well-connected (Mexico to Central America) systems may have accumulated diversity through time and dispersal, respectively.

The biogeography of island elephants: when does Jumbo shrink?

A.A.E. van der Geer, G.A. Lyras, A. Athanassiou, G.D. van den Bergh, U.W. Prasetyo, E. Setiyabudi
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Before humans colonised the islands, many islands worldwide harboured at least one species of proboscidean, endemic to their island. Several genera are represented, including elephants, mammoths and stegodonts. Several of these island proboscideans evolved spectacular dwarfism to less than 10% of their ancestral size. In general, proboscideans exhibited far more extreme cases of dwarfism than extant insular mammals, which is consistent with the substantially more extended period of deep geological time that the selective pressures could act on these insular populations. We investigated the factors that influence the direction, degree and speed of body size evolution in fossil insular proboscideans worldwide. We assembled data on the geographical characteristics (latitude, island area, isolation), dispersal time and body size evolution of palaeo-insular species for 28 insular species of fossil elephants across 19 islands. Island area and body size are positively correlated, contrary to the trend in large mammals in general. We found a threshold of about 6-10 km distance between the island and the mainland, below which no dwarfism evolved. Presumably, this is due to continuation of genetic contact with the mainland population. Time in isolation is correlated to the degree of dwarfism exhibited. The presence of hominids as predator does not predict the occurrence and degree of dwarfism, contrary to earlier predictions.

Rapid light-induced changes in visual gene expression in African cichlids do not covary with ecology or diversification rate

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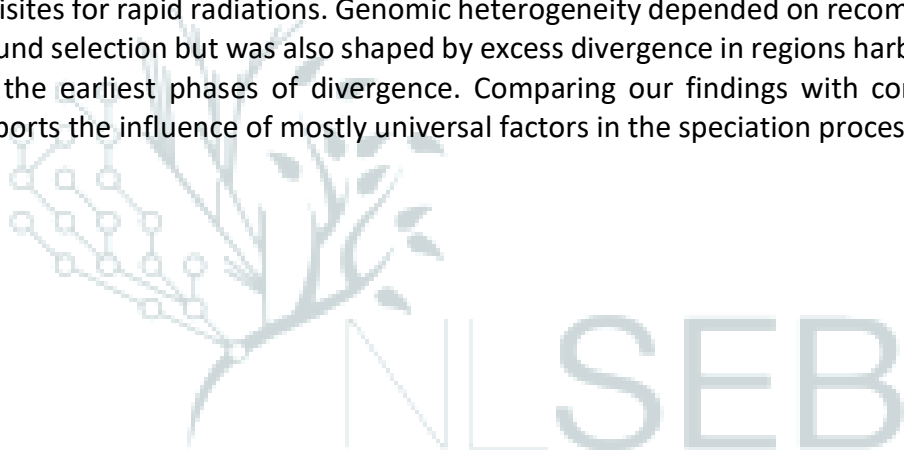
Phenotypic plasticity allows individuals to respond to environmental variation without genotypic change. This has led to the hypothesis that variable environments favour the evolution of higher levels of plasticity. In addition, the buffering effects of plasticity may affect lineage diversification rates, by either hampering or facilitating adaptive divergence. The visual system of cichlid fish is a suitable model for evaluating these hypotheses because of the diversity in cichlid visual habitats, visual system properties and species richness across lineages. Here, we expose 11 species of cichlids to different light treatments. These species represent a range of ecological niche widths and clade-diversification rates. After exposure to different light treatments, we quantify plasticity in the expression of several genes involved in visual perception: opsin genes, encoding the protein part of visual pigments, and *cyp27c1*, as a proxy for chromophore usage in the Vitamin A part of the pigments. We found substantial interspecific variation in both the degree and the direction of plastic change in visual gene expression. We found no support for the hypothesis that species inhabiting wider ecological niches are more plastic, or that visual plasticity covaries with clade diversification rates. However, the distinct changes in gene expression, together with the substantial species differences in these plastic responses, call for further investigation.

Non-adaptive and allopatric radiations provide complementary insight into universal mechanisms and outcomes of speciation

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The mechanisms involved in speciation are often thought to vary across the tree of life and across environments. For example, well-studied adaptive radiations are thought to be fueled by divergent selection in ecologically variable environments, but additionally are influenced heavily by biogeographic, genomic, and demographic factors. Non-adaptive radiations, producing ecologically cryptic and often allopatric taxa, are less well-studied but should likewise be influenced by these latter factors. Comparing among biogeographic contexts can help pinpoint universal mechanisms and outcomes. We investigated the contributions of biogeographic and evolutionary processes to population divergence along a speciation continuum in the non-adaptive radiation of the Hawaiian sword-tail cricket *Laupala*. We show progressive colonization of increasingly younger habitats by younger populations and striking intraspecific genetic structure at small spatio-temporal scales. The rapid differentiation among populations and species of *Laupala* shows that neither a specific geographic context nor ecological opportunity are pre-requisites for rapid radiations. Genomic heterogeneity depended on recombination rate and background selection but was also shaped by excess divergence in regions harboring mating song loci in the earliest phases of divergence. Comparing our findings with complementary systems supports the influence of mostly universal factors in the speciation process.



Poster Abstracts – Alphabetically arranged by presenting author (underlined)

The role of a long-term co-existence and environment in the ecosystem stability

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Natural ecosystems vary greatly in the diversity of species and their interactions, which are thought to define ecosystem stability and functionality. Ecological theory predicts that the stability of an ecosystem relies on balanced interspecies cross-talk and how these species interact with the environment. We study a popular Zambian fermented milk product, mabisi, as a model system to understand the mechanisms driving community stability. Using systemic approach and experimental evolution, we aim to clarify the role of initial microbe composition, environment and a long-term co-existence in the ecosystem stability and resilience. We challenged mabisi microbial community with different milk types and long-term propagation. Although the functional output (i.e. aroma profile) of mabisi converged upon propagation, there was variation in transcriptional profiles which could have led to aroma convergence. There was little difference in mabisi aroma between cow milk types, while composition was different according to plating results. However, goat milk significantly affected the functional profile of mabisi. These findings suggest that various members of mabisi community may perform similar functions. This can stabilize the functional output of the community until the environment change becomes more severe. We endorse mabisi as a tractable model to test evolutionary predictions and ecological stability/resilience of bacterial communities.

Drivers of body-size in ectotherms, the case of Chilean fishes

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Global change transformations are having substantial effects on biodiversity. Organisms' development and growth are affected by changes in temperature, and there is evidence that during past periods of global warming, marine and terrestrial organisms became smaller. Body-size reduction is the third universal response to global warming. Several hypotheses, mainly tested on endotherms, have been proposed to understand the dynamics that drive body-size, but body-size allometry in ectotherms has received less attention. The objectives of this research were aimed at: i) disentangle the role of ecological and evolutionary hypotheses in driving fish body-size comparing native and exotic species; ii) understand the role of island's biogeography in regulating body-size allometry; iii) understand the role of dispersion and migration propensity in driving body-size patterns, comparing migratory and sedentary strategies. Chilean fishes offer good opportunities to test different hypotheses of body-size allometry in ectotherms as we analyzed an extensive dataset composed of 75,198 records which included 25 species from 12 different families between latitudes -28.80 to -51.42 using linear mixed model methods analyses to discern which are the best environmental variables contributing to decreasing body-size, as well as incorporating factors related to dispersal capabilities, biogeographic isolation and levels

of exotic/native interactions. Freshwater fish body-size increases with increasing

Repeated evolution for allelic diversity in a conserved nonself recognition module across *Aspergillus* species

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The distinction between self and nonself is a fundamental requirement for multicellular life. In fungi, this distinction is provided by het genes, genes where allelic differences lead to cell death when brought together in the cytoplasm. Recently, in *Aspergillus fumigatus* we identified 5 loci whose alleles trigger nonself recognition, hetA-E. Here, we show that the hetE region of *A. fumigatus* is in fact homologous to hetA of *A. nidulans*. This complex locus is composed of three proteins; a NACHT+Ankyrin type NLR, a homolog of a yeast vesicle transporter *boi1*, and *rosA*, a repressor of sexuality. All three of these genes are under balancing selection, with divergent alleles found within populations. As these two *Aspergilli* are estimated to have diverged ~87 million years ago, the sharing of this complex locus is clearly unexpected. While the evolutionary pressures maintaining variation at the NLR and *boi1*-homolog may be similar to other het genes – the maintenance of the individual – the selective force maintaining variation for *rosA* is unclear. Despite the finding of allelic diversity at this locus across *Aspergillus* species, and even related genera, the alleles themselves are not conserved. Instead, it appears that alleles are arising *de novo* repeatedly on the order several millions of years. This work helps to understand the drivers of long-term balancing selection, as well as the maintenance of this diversity.

Exploring Natural Variation in Wild Boar Immunity and Susceptibility to African Swine Fever Virus

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Due to the influences of climate change and globalization, epizootic diseases are becoming more prevalent. Climate change for instance influences host abundances while globalisation allows for increased host-hopping of pathogens. African Swine Fever (ASF) is one such epizootic disease that started to affect different continents in the previous and present century, with detrimental consequences for pig breeders and wild boar populations. The current project aims to discover factors influencing susceptibility of wild boar to African Swine Fever in order to add to the list of genetic and physiological factors affecting epidemic occurrence. My goals are to assess the life-history drivers and evolutionary forces affecting wild boar immune function and be able to predict susceptibility to ASF of naïve populations. To accomplish this, I will use a combination of genomics, transcriptomics, microbiome assessments, body conditional measuring and immunoassay-based tools to feed a predictive model. This data will be collected from wild boar in countries with and without ASF to generate baseline data in order to make predictions for naïve populations. I expect to find populational differences in innate inflammation responses relevant for ASF survival, in part, due to the strong life-history plasticity of wild boar. Here, I present the experimental outline of the project and the first results from a pilot study in the field to test the proposed state-of-the-art ecological immunology tools.

Impact prediction of genetic variants to understand the genetic basis of life-history adaptation in *Drosophila melanogaster*

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Through genome sequencing, it has become possible to link single nucleotide polymorphisms (SNPs) to complex phenotypes, improving our understanding of their underlying mechanisms. However, linkage between hitchhiking loci and causative loci makes identification of causal SNPs for a complex phenotype a great challenge. This project aims to link genetic variation in the genome of *Drosophila melanogaster* to patterns of life-history adaptation by identifying causative variants affecting life-history traits amongst the numerous neutral variants. To predict impact of variants, we will develop a bioinformatics tool that scores the functional impact of variants for each position in the genome of *D. melanogaster* based on sequencing data. Variant impact predictions can give insights in the genetic health of populations. We present plans to associate genetic health with fitness adaptation in natural European *D. melanogaster* populations. The predictions will be validated *in vivo* by applying CRISPR-Cas9 precise genome-editing to study the effect of single nucleotide variants on fitness. By combining bioinformatics tools and genome editing, characterization of functional impact of nucleotide variants on fitness in the fruit fly can be achieved. This approach can potentially be used for the study of complex genotype-phenotype connections. Altogether, this project aims to uncover the genetic mechanisms of adaptation in the fruit fly by studying high-impact SNPs with impact on life-history.

A novel theory to explain sexual selection for costly male ornaments – no signal for male quality or mating benefit required

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In various species, females choose mates based on a threshold preference function where they only accept males with a signal above an internal standard. Based on empirical evidence, some species have a fixed standard yet others an adjustable standard: a female then changes her standard throughout her life based on the signals of encountered males. Here, we simulate the effects of an evolving standard, fixed or adjustable, on the evolution of a costly signal in a model of a haploid male and female population with genes for both a signal and standard. For the fixed standard, selection for no standard occurs when we assume costs associated with rejecting a male. Females thus mate randomly and consequently males produce no signal. However, if the female's standard is adjustable, there is selection for costly signals. This selection is driven by females adjusting their standard upwards after accepting males that passed their standard. Furthermore, this adjustment of the standard caused selection for exaggerated signals. Our findings suggest that for species with a fixed standard, maintaining this standard is not evolutionarily stable except in the unlikely case when there is no rejection cost. In contrast, if females can adjust their standard, their mate choice will select for exaggerated male signals. Such male ornaments can also evolve under the handicap principle, but our theory offers an alternative explanation where the ornament does not signal male quality or mating benefit.

Lipids On the Move: Exploring Lipid Dynamics in Arbuscular Mycorrhizal Networks

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Arbuscular mycorrhizal fungi (AMF) form ubiquitous, mutualistic associations with terrestrial plants. This symbiosis is fundamental to ecosystem functioning and is defined by the bidirectional exchange of nutrient resources; AMF transport mineral nutrients to their hosts and receive photosynthetically fixed carbon in return. Carbon is transferred from the plant host and exported from the intraradical mycelium (IRM) to the extraradical mycelium (ERM) by the fungus. Importantly, lipids are involved in transporting and storing plant-derived carbon across the hyphal network. Previous labelling experiments have shown bidirectional translocation of lipid droplets across AMF fungal colonies. However, we lack a quantification of lipid translocation in AMF hyphal networks across space and time. Here, we used fluorescence microscopy techniques to observe the movement of lipid bodies through *Rhizophagus irregularis* colonies. By staining the AMF strain C2 with Nile Red, we were able to visualise the intracellular movements of lipid particles across colonies at different stages of development. Further, we quantified lipid velocities to develop velocity profiles. We report a rich diversity of lipid morphologies that, to the best of our knowledge, have not been reported in AMF. In agreement with previous findings, we observed individual lipid droplets moving bidirectionally across the fungal colonies. In addition, we observed larger aggregations of lipid particles that exhibit biomolecular condensate-like properties. Time-lapse imaging revealed that lipids streamed within the cytoplasm on average from 7 - 10 $\mu\text{m/s}$ but can exhibit velocities higher than this range. Our observations suggest that lipid density increases as the ERM develops over time, and we observe a greater complexity of lipid physical properties. In future, it will be crucial to determine the relative viscosity and surface tension properties of these lipid aggregates, and the possible developmental triggers for their formation. This would improve understanding of the intracellular physical properties of AMF hyphal networks.

A natural allele shortens developmental time and facilitates rapid life history evolution in insect populations

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Developmental time (DT) is a key life history trait, and is currently under strong selection in insects to minimize ecological mismatches in seasonal timing caused by climate change. The genetic basis of responses to such selection, however, is poorly understood. Here, we show that ecdysone signaling is the main target of long-term artificial selection for fast or slow embryonic development in replicate, outbred populations of the beetle *Tribolium castaneum*. Pooled genomic resequencing, expression analysis, and RNAi screening pinpoint a 222bp deletion containing binding sites for Broad and Tramtrack, that regulates expression of the ecdysone degrading cytochrome CYP18A1. Using CRISPR/Cas9 to reconstruct this fast allele in an inbred laboratory strain, we demonstrate that this single deletion advances an embryonic ecdysone peak inducing dorsal closure, accelerates larval development, but trades off with fecundity. Our

study unravels the evolvability of DT, and reveals the presence of large-effect life history alleles in natural populations.

The endosymbionts of aphids in the Netherlands

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Bacterial endosymbionts can affect aphids in a multitude of ways. For example, they can change the colour of the aphids, protect them against their natural enemies, or help them adapt to different host plants. However, it is unknown how often these endosymbionts occur in natural populations in the Netherlands. In this study, we have gathered aphids from Dutch nature areas, parks, and gardens, and tested over 100 species of aphids for the eight most common facultative endosymbiont species. We found that most aphid species carry at least one of these facultative endosymbionts, and that this is correlated with the host plant range of the aphid species.

Mapping the evolution of the deadly Triturus genome

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All newts of the genus *Triturus* are afflicted by a genetic syndrome which causes the spontaneous death of exactly 50% of all embryos. The persistence of such a blatantly maladaptive trait is explained by a 'balanced lethal system' on *Triturus* chromosome 1. Here, recombination is suppressed and heterozygosity is essential for viability. Explaining the evolution of such a lethal genomic architecture has resulted in the proposal of several hypotheses, all of which involve significant rearrangement of the genome. Previously, empirical data has been difficult to obtain due to the vast size of the *Triturus* genome (c.a. 30 Gb). We use target enrichment to construct detailed linkage maps of the genome of *Triturus* and its closest relative *Lissotriton* (which is unaffected by the balanced lethal system). This allows the identification of genes associated with the balanced lethal system and enables us to model the rearrangement of chromosome 1. Our data show that the components of the balanced lethal system likely evolved as a result of a small number catastrophic rearrangements and deletions. We also show that the non-recombining region of chromosome 1 was initially small and grew to its current gigantic size later, likely via the accumulation of repetitive sequences. Further analysis allows us to determine the likelihood of various evolutionary scenarios and refine our model of the conditions that drove the evolution of the balanced lethal system in *Triturus*.

The relationship between environmental persistence and virulence - an experimental test

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The evolution of parasites virulence has attracted a significant amount attention from both theoretical as well as experimental biologists. Our current understanding of how virulence evolves is largely based on the trade-off hypothesis, which predicts the evolution of intermediate

virulence; however, there are many examples of evolutionarily stable high virulence. One extension of the trade-off hypothesis proposed to explain some of these cases is the “curse of the pharaoh” - also widely known as sit and wait hypothesis. This hypothesis revolves around the relationship between parasite virulence and durability in the external environment. A positive correlation between parasite virulence and durability in the external environment would support the Curse of the Pharaoh hypothesis whereas a negative correlation would indicate a trade-off between environmental persistence and virulence. At present, published data show mixed results. We hope to provide insights in to sit and wait hypothesis in parasite-host system using four strains of *Metarhizium* spp as parasites and red flour beetle *Tribolium castaneum* population (Cro1) as a host. Together with our phenotypic results, this will provide a significant step forward in understanding the dynamics and trajectories of virulence evolution.

How do insects avoid phototoxicity of chlorophyll?

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Evolution & Population Biology, IBED / UvA

Chlorophyll is a Janus-faced molecule of life and death. From light captured in photosynthesis, high-energy electrons emitted by chlorophyll travel down electron transport chains to generate the energy for carbon fixation. But electrons from chlorophyll can also kill cells via reactive oxygen species. Herbivorous insects ingest lots of chlorophyll, and have evolved mechanisms to protect themselves from its phototoxicity. Because these adaptations are so successful, they are largely unknown to science, and have been ignored in the coevolutionary arms race between plants and herbivorous insects. We have discovered that two special proteins protect the cotton leafworm from death by phototoxicity. When these proteins are knocked out, caterpillars feeding on green leaves die in the light, but not in the dark. Artificial diet with chlorophyll is likewise lethal to the knockout larvae when consumed in the light, but not in the dark. This finding holds the key to the first and most basic chewing insect adaptation to feeding on green plants.

Genome-scale phylogeny and comparative genomics of the fungal order Sordariales

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Within the fungal kingdom, the order Sordariales is of large biochemical and ecological importance. For example, the Chaetomiaceae family contains the widest known variety of thermophilic fungi, a polyphyletic trait with many biotechnological applications. To identify the key factors underlying genome evolution in the order, a robust framework of phylogenetic relationships within the order is essential. In our project, we utilized whole genome data from 106 genomes to infer a robust genome-wide phylogenetic framework of the order. We have now used this phylogeny as a basis for comparative genomics across the Sordariales. The comparative genomic analysis showed that the three largest families in the dataset (Chaetomiaceae, Podosporaceae and Sordariaceae) differ in the analyzed genomic traits. All genomic traits showed phylogenetic signal, and ancestral state reconstruction further revealed that the variation of the properties stems primarily from within-family evolution. Together, the results provide a framework for understanding genomic diversity in the fungal order Sordariales and

provide a basis for our ongoing studies on the influence of thermophilia on genome evolution. Additionally, the phylogeny and order-wide overview of genomic properties will be helpful for researchers studying other biochemical, ecological, genetic and evolutionary questions in this important group of fungi and beyond.

Spatial variation in temporal patterns of selection on reproductive timing in wild great and blue tits.

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Blue and great tits need to time their reproduction such that the highest food demands of nestlings coincide with the narrow peak abundance of caterpillars. To time their phenology, birds and caterpillars rely on temperatures in different periods of spring and, with non-uniform temperature changes in these periods due to climate change, they shift their phenology at different rates. The resulting phenological mismatch leads to directional selection on the birds' reproductive timing. We assessed whether there is spatial variation in the temporal patterns of selection on egg laying dates across 4 Dutch populations and whether these changes can be explained by spatial variation in phenological shifts of birds and caterpillars. For this, we analysed 66 years of breeding data and found that selection mainly acts through reproduction rather than survival, but that, despite overall selection for earlier laying, patterns over time show distinct local variation. The underlying relationships between temperature, bird and caterpillar phenology are the same, despite spatial variation for the periods for which temperature is important, and explain the selection patterns in each population. Hence, the spatial variation in temporal patterns of selection is caused by differential changes of spring temperatures and in habitat characteristics. Our findings underline that climate change is not necessarily acting on populations of the same species in the same way, even on a small spatial scale.

Better alone or together? : Intraspecific interaction affects the response of AMF to strigolactones.

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Arbuscular mycorrhizal fungi (AMF) form a nutrient based symbiosis with most land plants. The fungi forage the soil effectively for scarce nutrients, especially phosphorus, which then trade for photosynthetically derived carbon. Under phosphorus limitation, plants exude genus- specific phytohormones, known as strigolactones. Strigolactones have been seen to trigger physicochemical changes on AMF, such as: increased spore germination, pre-symbiotic hyphal branching and boost in metabolism. Past studies have examined this phenomenon in limited in-vitro settings where only one AMF strain is treated with a single strigolactone. But to draw ecologically relevant conclusions, it is essential to also investigate the potential of intraspecific competition to strigolactone signaling. Here we hypothesize that focal strain identity, strigolactone type, and partner strain can have strong effects on germination and pre-symbiotic hyphal architecture. We present an in vitro assay that examines how intraspecific competition affects the response of various AMF life history traits to strigolactones. Specifically, spores of the *Rhizophagus irregularis* strains C2 and A5, were germinated in presence of GR24 or 5-deoxystrigol. We used a semi-

automated high-resolution imaging system to document time of germination and to quantify multiple hyphal traits. Our results show that both strigolactones increased germination success for A5, but in the presence of C2 spores this positive effect was reduced. We further observed that GR24 positively affected the total hyphal length of A5, and that both strigolactones increased the quantity of hyphae of both strains. We conclude that intraspecific interactions are important drivers during AM germination in presence of strigolactones. Consequently, these factors may require consideration when assessing AM fungal responses to these phytohormones in the future.

Can hybridization promote persistence in a changing world?

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Agriculture, industry and climate change modify habitats, create novel environments and redistribute species. All of these processes require populations to adapt in order to persist in the changing world. Adaptation can be accelerated by hybridization and gene flow. However it is unclear under which conditions hybridization leads to positive fitness consequences in natural populations instead of negative ones. Wood ants offer a good system to understand the outcome and fitness consequences of hybridization in natural populations because they allow for replicated studies in nature and collection of long-term data. Our studies reveal that hybridization is prevalent between multiple wood ant species and that hybrids persist and occupy different microclimatic niche compared to the parental species. Furthermore, we reveal predictability of hybridization outcomes at the genomic level and the interplay of several different selective pressures shaping outcomes of hybridization.

Co-transfer of functionally interdependent genes contributes to genome mosaicism in lambdoid phages

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Lambdoid (or Lambda-like) phages are a group of related temperate phages that can infect *Escherichia coli* and other gut bacteria. A key characteristic of these phages is their mosaic genome structure which served as basis for the “modular genome hypothesis”. Accordingly, lambdoid phages evolve by transferring genomic regions, each of which constitutes a functional unit. Still, it is unknown which genes are preferentially transferred together and what drives such co-transfer events. Here we aim to characterize genome modularity by studying co-transfer of genes among 95 distantly related lambdoid (pro-)phages. Based on gene content, we observed that the genomes cluster into 12 groups, characterized by a highly similar gene content within the groups and highly divergent gene content across groups. Highly similar proteins can occur in genomes of different groups, indicating that they have been transferred. About 26% of homologous protein clusters in the four known operons engage in gene transfer, which affects all operons to a similar extent. We identified pairs of genes that are frequently co-transferred and observed that these pairs tend to be near to one another on the genome. We find that frequently co-transferred genes are involved in related functions and highlight several examples. In conclusion, epistatic effects, where the functioning of one protein depends on the presence of another, play an important role in the evolution of the modular structure of these genomes.

Does local eco-evolutionary selection shape community structure in natural yeast communities?

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Genetics, WUR,

Microorganisms such as Bacteria, Fungi, and Archaea, are widely spread and co-exist in microbial communities. These communities are shaped by eco-evolutionary selective forces such as the inflow of species, the availability of feedstock and external factors such as temperature, humidity and radiation. As the abiotic environment is expected to exert selective pressure, the organisation of microbial communities is expected to be dependent on geographical location driven by a process known as species sorting. Here, we use winemaking as a model to study species sorting in yeast communities. We analysed the fungal community in fermented grapes from eleven vineyards in and around the Netherlands using the internal transcribed spacer (ITS) and next-generation amplicon sequencing (NGS). Six vineyards are in a homogenous environment (former sea soil in Flevoland) and the others are from different environments. We expect the yeast communities from Flevoland to be similar to each other compared to the yeast communities found at other locations. Our results form a starting point for research into eco-evolutionary dynamics within fungal communities and have implications for our understanding of environmental selection shaping the structure of species communities.

Mine Fungi - Describing the microbial community in a novel environment for bioremediation purposes

Depa Petter Birger Madsen, Maliheh Mehrshad, Ayco Tack, Anna Rosling, Hanna Johannesson

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The microbes in the Kiruna underground mine are not only surviving and living in an extreme environment, polluted with heavy metals and high salt concentrations, but also able to utilize oil pollutants as a carbon source. From samples taken from the Kiruna mine, several different fungal strains have been isolated. Pure cultures have been shown to be able to grow on whole synthetic engine oils. Some of the isolated species are *F.oxysporum*, *T.harzianum*, *L. cadophora*, which have been previously described as opportunistic plant and/or fungal pathogens, here shown to be capable of oil degradation. The Kiruna underground mine is a novel environment to be studied. It is approximately 1700 meters deep, containing very few naturally occurring carbon sources with an influx of ground water entering the system. In addition to this, it is heavily impacted by human activity resulting in pollutants such as petrol, diesel, and engine oils, as well as heavy metals and high concentrations of nutrients and salts. All of which make it an extreme environment. To study and understand how these microbes survive such an environment and how they've adapted to it, both by phenotypic and genomic changes, is of great interest both from a basic science perspective but also for application purposes which aim at using these microbes for bioremediation purposes. The aim of the project is to describe microbial diversity present in the Kiruna underground mine, as well as their genomic properties and activity.

Host-microbe co-evolution in *C. elegans*

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Cooperation between hosts and their associated microbial gut communities enables an immediate plastic response in changing environments, facilitating host adaptive response. Research into host-microbe interactions has mostly focused on immediate responses with a single selection pressure. The aim of this project is to understand how interactions between biotic and abiotic factors shape host plasticity, fitness evolution and gut microbial composition. We used *Caenorhabditis elegans* as the host, along with naturally co-occurring microbes and the pathogen *Bacillus thuringiensis* (Bt), osmotic, and pH stress as biotic/abiotic environmental factors. We ask whether interactions with both pathogenic and non-pathogenic bacteria influence survival of *C. elegans* in changing abiotic environments and whether host and microbes co-evolve to facilitate host adaptation. Exposure to different salt levels was dose dependent but showed no significant effect on development and fertility of *C. elegans*, except for the highest level, which led to their premature death. Exposure to different pH levels revealed only weak effects on worm survival. However, *C. elegans* associated with different microbes at varying pH levels. Finally, nematocidal Bt affected fertility and development of *C. elegans* significantly compared to non-nematocidal Bt. We are currently co-evolving worms and microbes at different pH and salt levels, further exploring the effects of naturally co-occurring microbes on host survival.

An exploration of factors associated with gut microbiota in children of low-income setting

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Bacterial community composition in the first 36 months of human life is explained by factors that may be abiotic and biotic in nature. Multiple factors are reported to drive gut microbiota composition and diversity. Knowledge of factors that influence bacterial community composition and diversity is crucial for the health and well-being of individuals. Studies focusing on the composition and diversity of gut microbiota have mainly been conducted in high-income settings. This study is no different, however, it focuses on a population from low-income settings, a population affected by a different set of factors. Through a survey study model, we gathered unique information on factors affecting children in a remote district in Zambia. Among factors studied, Age, breastfeeding, consumption of indigenous fermented dairy food and use of antibiotics were strongly associated with alpha diversity indices of children's gut microbiota. Age, the consistency of stool and short stature (stunting) explained the beta diversity of gut microbiota composition. Our findings contribute to the knowledge of factors that may influence gut microbiota composition and diversity in children of low-income settings. Younger children (infants) were associated with a high relative abundance of *Bifidobacterium* and *Lactobacillus*. Stunting was associated with the presence of *Faecalibacterium*, *Blautia*, *Agathobacter* and *Fusicateribacter* among others.

Transitions from monomorphic to dimorphic enantiostyly: insights from adaptive dynamics

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Enantiostyly is a type of floral asymmetry in which the styles of flower are either deflected to the left or right side of the floral axis (mirror-image flowers). Phylogenetic evidence indicates that in several monocotyledonous lineages, dimorphic enantiostyly (all flowers of a plant have the same style orientation) has evolved from monomorphic enantiostyly (flowers within a plant have both stilar orientations). Here, we use a modelling approach based on adaptive dynamics to study the emergence of dimorphism in a population of plants with monomorphic enantiostyly under gradual evolution. Our results indicate that, depending on the balance between inbreeding depression following geitonogamy, pollination efficiency, and plant density, dimorphism can evolve from an initial, monomorphic population. In general, the newly-emergent dimorphic population is stable against invasion of a monomorphic mutant. However, our model predicts that under certain environmental conditions e.g., a decline of pollinators or scarcity of resources, a dimorphic population can revert back to its ancestral monomorphic phenotype.

Conditions for the evolution of anticipatory maternal effects: an experimental evolution study

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Phenotypic plasticity is found throughout all of biology and helps organisms fine tune their phenotypes to the environments they encounter. Traditionally, it is understood that these fine adjustments are based on the information collected by the developing organism. However, this information can also be collected beforehand, and be transmitted to the offspring by the mother. Theoretical studies have suggested that the evolution of anticipatory maternal effects requires specific environmental and informational conditions to be met. Here we share some results of experimental evolution with *Drosophila melanogaster* in which we varied the predictability and stability of environmental conditions between generations to explore how, and when, anticipatory maternal effects can evolve. We found the evolution of anticipatory maternal effects to be extremely sensitive to the specific combination of population history and current environmental predictability and stability, and that “silver spoon” effects are much more prevalent.

A beneficial role for gene expression noise in evolving populations

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Since most genetic mutations are deleterious, evolving populations will sometimes need to traverse unfavorable regions of the fitness landscape in order to move from one local fitness maximum to another. How can mutant populations survive these fitness valleys? We propose that in some cases, gene expression noise can benefit such populations. Inspired by mutations in the cell polarization mechanism of budding yeast (*Saccharomyces cerevisiae*), we are developing a stochastic model to simulate populations of a unicellular organism with noisy

protein expression, in order to investigate the effects of expression noise and epigenetic protein inheritance on the survival of maladapted populations. In our scenario, the cells produce random bursts of a cell cycle protein while growing exponentially in volume, and will divide when they have reached a sufficient size and protein concentration. Cells that grow too large without reaching the concentration threshold are killed. When, due to genetic mutations, the average expression is too low for reaching the concentration threshold, the population will decline. Our initial results show that moderate expression noise can increase the time until extinction of declining populations, thereby extending the window of opportunity for subsequent, beneficial mutations to occur.

What makes a good hybrid? The role of dominance, epistasis and ploidy in the outcome of secondary contact.

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The fitness of hybrids is an important component of reproductive isolation that shapes the opportunity for species persistence. Hybrids can solidify species boundaries through reinforcement selection if their fitness is low, but they can also facilitate introgression or form new lineages set on their own path of speciation. Which of these outcomes occurs depends largely on the environmental history and selective pressures under which the parental lineages accumulated their genetic differences, and on the interactions between their divergent genomes. The aim of my PhD is to integrate observations of hybridization across a wide range of systems and use simple fitness landscape models to identify the principal properties of genomic interaction that can account for the patterns observed. Investigating the effects of dominance, epistasis and ploidy on hybrid fitness, we find that their effects typically depend on genomic composition. Moreover, we can compare our predictions to genomic datasets to explore how genomic background affects the direction and consistency of selection on alleles segregating in a hybrid population. These results may help understand and predict the outcomes of secondary contact, and to interpret the often complex genomic signatures left by the build-up of reproductive isolation.

Traditional fermented foods to promote food and nutrition security in Africa

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Microbial ecology and evolution is central to traditional fermentation where microbial communities are repeatedly propagated to fresh raw materials to convert these into processed foods. Processes such as ecological species sorting and adaptive change due to fixation of novel mutation in individual bacterial lineages are important in shaping microbial communities and their functionality. Our study has societal impact that we highlight in this contribution: the promotion of food and nutrition security in Africa by ameliorating the quality and use of traditional fermented foods by strengthening the connected local value chains through fostering

women entrepreneurship. The choice for fermented foods is justified by the fact that transformation of raw materials by microorganisms makes foods generally safe, highly nutritious and sensory attractive with an increased shelf-life, while creating entrepreneurship opportunities for local women. So far efforts to combat hunger and malnutrition have largely overlooked the potential of the improvement of local food processing and optimization of the concerned value chains. Hence, making upgraded fermented foods the subject of efforts to stimulate (women) entrepreneurship is expected to have a direct effect on food and nutrition security by making improved fermented foods more available as well as an indirect effect through income generation to support livelihoods.

Testing the suitability of museum samples to explore the genetic basis of colour polymorphism in *Apamea*

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The diversity and evolution of butterfly wing pattern and colouration have fascinated biologists for a long time, as these traits are subject to a variety of ever-changing selective pressures. A famous example of this phenomenon is the colour polymorphism of the peppered moth (*Biston bitularia*). However, many more species in Lepidoptera have evolved (colour)polymorphic phenotypes, although it remains a puzzle why this is the case. Delineating the molecular mechanisms of wing colour variation in moth species may provide valuable insights into the adaptation potential and constraints within this Lepidoptera. Here, we aimed to identify the genomic differences between two colour morphs (dark versus light) in two moth species of the genus *Apamea*: *A. crenata* and *A. monopglypha*. Using historical material from the collection of Naturalis in Leiden, we collected 50 legs for each morph per species, isolated and pooled DNA per morph per species. After sequencing these pools, we were able to detect differences between colour morphs using GLM. In both species, we were able to identify genomic regions that differ between the two colour morphs. Further investigation showed that these regions are located close to the cortex gene region, which has been associated with dark/melanic colour polymorphisms in other Lepidoptera species. Our findings support the standing hypothesis that this mechanism is conserved in Lepidoptera and highlight the suitability of museum specimens in genetic research.

Are city birds genetically less sensitive to artificial light at night compared to forest birds?

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Most individuals on earth have established 24-hour rhythms in their behavior and physiology which are adjusted to their habitat primarily through the light/dark cycle experienced in their environment. In the past decades the natural light regime has been disrupted by artificial light at night (ALAN). This has caused many animal groups, including avian species, to change their patterns of behavior and physiology by altering their daily activity patterns and seasonal time of breeding. Previous studies on wild bird species have indicated that the effect of ALAN on activity

patterns differ between forest and city populations, whether this is an environmental or genetic effect is largely unknown. Here we present preliminary results from our common garden study, using the Great tit (*Parus major*) as a model. Birds from genetically forest and city origins were put into breeding pairs in climate-controlled aviaries, exposing half of the birds from each origin to ALAN and half to dark nights as control. The daily activity was monitored through infrared sensors, and individual feeding activity through RFID sensors. Our initial results indicate that city birds are less sensitive to light when compared to their forest counterparts, suggesting that city and forest populations are sufficiently isolated to be genetically different from each other. We hypothesize that rapid micro-evolution has caused city birds to be less sensitive to light to counter the detrimental effects of ALAN.

Multicontinental genomic analysis of a barley pathogen reveals patterns of local adaptation and association with modern human trades

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Human history is characterized by extensive migration. Human populations and their associated crops and livestock have been moved to foreign environments. Crop-associated microorganisms, including plant pathogens, have also been introduced to novel environments due to human migration. In a globalized world, the pace of organism movement has greatly increased during the past millennium. Today, the global trade of agricultural products is considered one of the key drivers of plant pathogen dissemination. The fungus *Pyrenophora teres* f. *teres* causes Net form net blotch (NFNB), a severe disease of barley. We have used 104 *P. teres* f. *teres* genomes from four continents to explore the population structure and history of pathogen dispersal. In general, *Pyrenophora teres* f. *teres* demographic history reflects the known history of its host, barley highlighting the importance of human migration and trading in the dispersal of the pathogen. Furthermore, our selective sweep analysis reveals many unique, rather than sheared, genomic regions under selection for each *P. teres* f. *teres* population, suggesting a rapid adaptation to local hosts and environmental conditions.

***Nostoc punctiforme* in symbiosis with arbuscular mycorrhizal fungi.**

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An endosymbiotic mutualistic relationship between cyanobacteria and fungi has exclusively been observed between the fungus *Geosiphon pyriformis* and the cyanobacterium *Nostoc punctiforme*. *Geosiphon* engulfs the cyanobacteria by invagination, forming siphonal bladders, where the *Nostoc* is protected from the external environment. In return, *Nostoc* provides the fungus with photosynthetically fixed carbon. Recent work has found large phylogenetic similarities between *Geosiphon* and arbuscular mycorrhizal fungi (AMF), an ancient group of widespread obligate plant symbionts, that require carbon input from their plant host to survive. Upon co-culturing of AMF and *Nostoc*, we find the first evidence of a previously undescribed interaction between cyanobacteria and AMF. We use in vitro culturing techniques and advanced microscopy to examine the nature of this unexplored symbiosis.

The influence of the environment on recombination landscapes

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Meiotic recombination occurs at different frequencies across positions within eukaryote genomes, generating a recombination landscape with hot and cold spots. Previous studies use sequencing of individual progeny or ChIPseq of DSBs, among other techniques, to analyze recombination landscapes. Recombination hotspots are associated with several epigenetic markers, including histone H3K4 methylations deposited by RNA polymerase. Little has been done to explore the effect of environment on recombination landscapes. Here, we studied how environmental effects on transcription affect the recombination landscape of heterozygote diploid *Saccharomyces paradoxus* in different environments. Genetically identical populations were grown in media containing either glucose or galactose as a carbon source, or grown at 30°C or 25°C on glucose before inducing meiosis. Differential transcription was confirmed by RNA sequencing. Haploid meiotic progeny were genetically sequenced at 1,000x depth. Reads were individually categorized as recombinant or parental based on variant positions, and normalized by sequencing depth. Using this measure, we generated recombination landscapes in different environments. Genome-wide recombination landscapes at a resolution of 10Kb presented stronger correlations between samples within treatments than would be expected with random effects. Changes in recombination rates may modify linkage between contiguous genes, affecting the genetic composition of the progeny.

Investigating the (a)sexual scandal in Arbuscular Mycorrhizal Fungi (AMF)

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Arbuscular Mycorrhizal Fungi (AMF) are a group of ancient fungi that form an obligate symbiosis with the roots of most plants. The symbiosis is mutualistic with both partners gaining multiple benefits, such as improved nutrition, increased growth and protection from stressors and pathogens. For that reason AMF are used widely as biofertilizers in agriculture and horticulture¹. But due to the obscure genetics of AMF only a few strains are exploited for their agronomic benefit. Potentially, strain crossing could be used to combine beneficial traits but, until recently, AMF were considered to be asexual². Surprisingly, over the past decade, genomic evidence has accumulated suggesting that AMF should be capable of sexual reproduction^{3–6}. Here, we aim to investigate sexual reproduction in the model AMF species *Rhizophagus irregularis* with a method called Fluorescent In-Situ Hybridisation (FISH), in which fluorescently labelled probes are used to hybridize and visualize RNA transcripts or genomic DNA sequences inside fixed cells. This method allows us to directly visualize with fluorescent microscopy a key step in sexual reproduction, the fusion of nuclei originating from opposing mates (karyogamy), and the subsequent expression of meiotic genes that lead to genetically recombined offspring. So far, the first steps in the validation of the FISH method in *R. irregularis* are shown here, paving the way for exploring AMF's reproductive strategies in the near future, as a means to improve the application of AMF in agriculture.

Eco-evolutionary interactions in polymicrobial infections

Marjon de Vos, et al.

GELIFES — Groningen Institute for Evolutionary Life Sciences

Communities of bacteria derived from polymicrobial urinary tract infections (UTIs) together with commensal residents in the urobiome can be viewed as small ecosystems. By measuring pair-wise interactions we obtained a unique insight in the ecological interactions of these microbiome members. We find that many of these bacterial interactions affect the immediate tolerance to antibiotics, as well as their ability to evolve antibiotic resistance. This shows that microbial community composition affects the ecology and the evolution of infectious bacterial consortia.

The Barcode Trees of Life: Keystone References for Molecular Biodiversity Assessment

Rutger Vos, Naomi van Es, Noah Scheffer

Understanding Evolution, Naturalis Biodiversity Center

No abstract available

The impact of sexual selection on the evolution of adaptive response mechanisms

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In an era of rapid climatic change, understanding adaptation to changing environments is more important than ever. This has led to increased interest in different modes of adaptation, i.e. the different ways in which organisms may deal with environmental change, such as phenotypic plasticity, bet-hedging or adaptive tracking. Previous theoretical work has uncovered that both predictability and speed of environmental changes strongly affect which response mode is favoured by natural selection (Botero et al. 2015, PNAS). Furthermore, the authors found strong consistency across simulation replicates: the evolution of different response modes is highly replicable. However, it is unclear how the addition of sexual selection affects these conclusions. To explore this, we added sexual selection to the model developed by Botero and colleagues. We find that the addition of sexual selection strongly affects the outcome in at least three ways: Firstly, some response modes, such as plasticity, are favoured under a wider range of parameter combinations. Secondly, under sexual selection, new adaptive response modes arise that were not observed under natural selection alone. Finally, we find that the repeatability of the evolutionary trajectories of different replicates is reduced: when adding sexual selection to the mix, evolution loses predictability. In this talk, I will explore why sexual selection induces these shifts and consider the implications of these results.

Biosynthetic Pathway Discovery in Plants Based on Omics Data Integration

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The diversity of plant secondary metabolites provides a promising yet unexplored resource for the development of novel drugs and agrochemicals. In plants, genomic organization of biosynthetic pathways has evolved to a higher level of complexity compared to bacteria and fungi. Specifically, formation of biosynthetic gene clusters is a less common phenomenon in plant evolution, and genome duplications and polyploidy result in complex gene regulatory networks and functional redundancy. Hence, automated pathway annotation across plant species, as well as discovery efforts based on comparative approaches require the development of similarity metrics accounting for the complexity of plant genome architecture. To this end, integration of genomics, transcriptomics, and metabolomics data resources will be needed. However, paired datasets for gene expression, and corresponding plant metabolite profiles are unavailable for important crop species. Here, I will develop a phylogenetic metric in combination with a co-expression metric for the identification of orthologous pathway modules across crop species and wild relatives in the Brassicaceae. The metrics will be tested and validated on generated paired expression and metabolic profile datasets including time-series, and stress conditions. The resulting insights and predictions on biosynthetic pathway evolution will accelerate natural product discovery and provide new resources for synthetic biology and targeted plant breeding.

Color variation and consequences of temperature sensitivity in *Lygaeus simulans*

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Insects display plentiful and diverse color originating from their phenotypic plasticity. Warning or aposematic color serves as a poisonous and unprofitable signal to potential predators. While color variation is commonly found in insects, it may also result in costs to themselves such as reduced protection and fecundity. My project studies on a seed bug *Lygaeus simulans* with black-red warning colour. In 2012, a colour mutant was found that instead has black-yellow colouration. We found the mutant is temperature sensitive, changing color at 24 °C; and 26 °C; in embryo and nymph stages. We also investigate the consequences due to colour variation. In addition, insect color is consisted of a lot of structural pigments including melanins, carotenoids, and pteridines. The compounds are synthesized by metabolic enzymes encoded by genes. My project shall focus on the pigment compounds, enzymes and genes levels controlling the color trait.