

Abstract Book

2022 Conference of the Netherlands Society for Evolutionary Biology

Tuesday, June 28th 2022

Akoesticum, Ede, The Netherlands



Sponsors



Organizing committee

Jeroen Meijer, Sijmen Schoustra, Koen Verhoeven, Marjon de Vos

Program June 28 2022

- 8:45 Arrival with coffee/tea
- 9:15 Welcome & Introduction *Auditorium*
- 9:25 **Katja Peijnenburg** (Naturalis, UvA) *Auditorium*
- 9:55 **Jaap Kaandorp** (Universiteit van Amsterdam) “Modelling embryogenesis and biomineralization in sea anemones, jelly fish and corals”, *Auditorium*
- 10:30 Coffee/tea break
- 11:00 **Parallel sessions** of contributed talks
 Session I *Auditorium*
 Session II *Tuinzaal*
- 12:15 Lunch with network opportunities
- 13:30 **Eric Snijder** (Leiden University Medical Center) “That good old ‘novel’ coronavirus” *Auditorium*
- 14:00 NL Evo Biology 2021 prize winner *Auditorium*
- 14:20 Coffee/tea break
- 14:50 **Parallel sessions** of contributed talks
 Session III *Auditorium*
 Session IV *Tuinzaal*
- 15:50 General Assembly *Tuinzaal*
- 16:30 **Tim Hammer en Mirthe Dokter – FIGHT** (Cultural Intermezzo) *Auditorium*
- 17:10 **Poster session** *Tuinzaal*
- 18:30 Poster Prize winner & Closing remarks *Tuinzaal*
- 18:35 Dinner, with optional round table discussions

Keynote speakers

[Dr. Katja T.C.A. Peijnenburg \(Naturalis Biodiversity Center\)](#)

Group leader Plankton Diversity and Evolution

Associate professor University of Amsterdam

Katja Peijnenburg is an evolutionary biologist and oceanographer interested in the diversity of marine zooplankton. She wants to know: which and how many species live in the open ocean? What processes drive the evolution of marine plankton?

[Dr. Jaap Kaandorp \(Universiteit van Amsterdam\)](#)

Associate professor, Computational Science Lab

“Modelling embryogenesis and biomineralization in sea anemones, jelly fish and corals”

Rather than being directed by a central control mechanism, embryogenesis can be viewed as an emergent behavior resulting from a complex system in which several sub-processes on very different temporal and spatial scales (ranging from nanometer and nanoseconds to cm and days) are connected into a multi-scale system. In our research we have been focusing on the embryogenesis of basal organisms like the non-calcifying sea anemone *Nematostella vectensis* and the hydrozoan *Clytia hemisphaerica* and the calcifying coral *Acropora millepora*. We have developed methods for analysing spatio-temporal gene expression patterns, methods for spatio-temporal modelling and inferring gene regulatory networks from gene expression data (qPCR data and in-situ hybridizations) and a cell-based mechanical model of early embryogenesis. In the coral we have developed a model of calcification physiology controlling biomineralization. Currently we are investigating how the different levels of organization (gene regulation controlling embryogenesis, cell mechanics and biomineralization) can be coupled into a multi-scale model of embryogenesis.

[Prof. Dr. Eric J. Snijder \(Leiden University Medical Center\)](#)

Professor of Molecular Virology

That good old 'novel' coronavirus

Eric Snijder is professor of molecular virology and head of the Section Research of the Department of Medical Microbiology of Leiden University Medical Center (LUMC). His research focuses on the replication, evolution and virus-host interactions of positive-stranded RNA viruses, in particular coronaviruses and their relatives, which he has studied for more than 35 years.

Program parallel sessions

Session I Auditorium (chair: Jeroen Meijer)

- 11:00 **Lars Zandbergen** (GELIFES) Higher-order ecological interactions within pathogenic communities
- 11:15 **Anne Kupczok** (Wageningen University & Research) High-resolution metagenomics uncovers strain relationships and gene content evolution in two co-colonizing symbionts of deep-sea mussels
- 11:30 **Yiuval Mulla** (University of Cologne) Beyond predator-prey: phages in bacterial communities
- 11:45 **Marjolein Bruijning** (Princeton University) Selection for imprecise vertical microbiome transmission in variable environments
- 12:00 **Meike Wortel** (UvA) Together we reach the top: How ecological interactions can make fitness landscapes more connected

Session II Tuinzaal (chair: Koen Verhoeven)

- 11:00 **Sebastian Lequime** (GELIFES) Endogenous viral elements in shrew genomes provide insights into Flaviviridae ancient history
- 11:15 **Frederic Lens** (Naturalis Biodiversity Center) The evolution of insular woodiness
- 11:30 **Paula Ramos-Silva** (UvA) Pteropod shell proteomes reveal distinct biomineralization toolkits in the formation of crossed lamellar and helical microstructures
- 11:45 **Judith Risse** (NIOO-KNAW) Bill length variation in great tits (*Parus major*): Are there any fitness consequences?
- 12:00 **Marian Bemer** (WUR) The role of MADS-box genes in the evolution of flowering and fruit development

Session III Auditorium (chair: Sijmen Schoustra)

- 14:50 **Natalie E. van Dis** (GELIFES) Genomic basis of rapid adaptation to climate change in the winter moth
- 15:05 **Duur K. Aanen** (WUR) Why do some fungi grow fast and others slowly?
- 15:20 **Maurijn van der Zee** (Leiden University) Ecdysone under selection in fast developing beetle eggs
- 15:35 **Hilde Schneemann** (University of Cambridge) The diverse effects of phenotypic dominance on hybrid fitness

Session IV Tuinzaal (chair: Marjon de Vos)

- 14:50 **Liedewij Laan** (TU Delft) Epigenetic feedback on noisy protein dosage boosts evolvability
- 15:05 **Thomas Blankers** (UvA) Repeatability of experimental evolution in the nematode *C. elegans*
- 15:20 **Jana Riederer** (GELIFES) The evolution of condition-dependent mutation rates
- 15:35 **Mark Lammers** (University of Münster) Inbreeding constrains the potential for rapid adaptation and reduces phenotypic plasticity

Round Table Discussions

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

Table 1: **Liedewij Laan** “Work/life balance”

Table 2: **Tycho Malmberg** “Evolution at the job market”

Table 3. **Kim Ferguson** “Data Archiving & Networked Services (DANS-KNAW)”

DANS-KNAW is the Dutch national centre of expertise and home to one of the largest repositories for research data in Europe. We can help you find and re-use existing data, as well as give advice in making your data FAIR (Findable, Accessible, Interoperable, Reusable) and Open. Got questions about research data management? We'll help you find the answers.

Abstracts contributed talks

Session I

Higher-order ecological interactions within pathogenic communities

Lars Zandbergen, Freya Eriksen, Marjon de Vos

Microbial eco-evolutionary medicine, GELIFES Groningen University

Microbes interact with each other in various ways within an ecosystem. When investigating interactions with more than two interacting members, complexity is added to a system in the form of higher-order interactions. Higher-order interactions can potentially alter the response to a biotic or abiotic environment encountered by an organism. Even though higher-order interactions play an important role in microbial ecology and evolution, they are still poorly understood and are mostly investigated theoretically. We showed the presence of higher-order interactions by measuring interactions between uropathogenic bacteria in environments with increasing levels of complexity, starting from pairwise interactions. We found that pairwise bacterial interactions could often not predict the higher-order interactions with respect to population size and growth rate. Our findings show the importance of higher-order interactions in small pathogenic communities, and the need for a better consensus on the quantification of higher-order ecological interactions.

High-resolution metagenomics uncovers strain relationships and gene content evolution in two co-colonizing symbionts of deep-sea mussels

D. Romero Picazo, T. Dagan, A. Werner, R. Ansorge, J. M. Petersen, N. Dubilier, A. Kupczok

Bioinformatics group, Wageningen University & Research

One of the driving forces of genome evolution in bacteria that live in symbiosis with eukaryotes is the way the bacteria colonize and disperse among individual hosts. However, how the colonization dynamics affects genome divergence and gene content evolution of horizontally transmitted bacteria is poorly characterized. Here we analyzed multiple deep-sea mussel *Bathymodiolus brooksi* individuals from a single cold seep, which are co-colonized by two horizontally transmitted chemosynthetic symbiont species, sulfur-oxidizing and methane-oxidizing gammaproteobacteria. Using high-resolution metagenomics, we reconstructed core genome-wide strain sequences and population pangenomes including core and accessory genes. We found that three population diversity measures varied among mussel individuals in a correlated way: core genome nucleotide diversity, gene content diversity, and diversity in strain composition. Compared to core genes, accessory genes were enriched in functions involved in genome integrity. By analyzing sequence similarity, we found no evidence for recent horizontal gene transfer (HGT) between both symbionts. Thus, the pangenomes of both mussel symbionts evolved mainly by vertical inheritance of genes within each symbiont population. We conclude that the association with individual hosts over their lifetime of many years leads to genetically isolated symbiont subpopulations, constraining the frequency of HGT in the evolution of horizontally transmitted symbionts.

Beyond predator-prey: phages in bacterial communities

Yuval Mulla, Viera Kovacova, Michael Laessig, Tobias Bollenbach

Institute for biological Physics, University of Cologne

Co-cultures of a bacterium-infecting virus (phage) and its host are a powerful model system for predator-prey co-evolution. However, in nature the phage-bacterium relationship is far more complex. Most phages can integrate their DNA into the bacterial host, linking their evolutionary

success. Moreover, specific bacteria actively hijack the phage machinery for horizontal gene transfer. However, we lack systematic experimental studies, as such events do not occur in mono-cultures and it is notoriously difficult to obtain stable multi-species co-existence due to resource competition. We have developed an assay consisting of separately cultured bacteria, but with phages periodically surging through the entire bacterial metapopulation. We have used this assay to evolve hundreds of clinically relevant bacteria and roughly equally many phages. We use this assay in combination with high throughput sequencing and phenotypic assays to map phage-host networks and track gene flow between bacteria. Our work reveals how phages govern evolution in bacterial communities, such as the spread of virulence and antibiotic resistance genes.

Selection for imprecise vertical microbiome transmission in variable environments

*Marjolein Bruijning, Lucas P. Henry, Simon K.G. Forsberg, C. Jessica E. Metcalf, Julien F. Ayroles
Ecology and Evolutionary Biology, Princeton University*

How and when the microbiome modulates host adaptation remains an evolutionary puzzle, despite evidence that the extended genetic repertoire of the microbiome can shape host phenotypes and fitness. One complicating factor is that the microbiome, unlike host genetic material, is often transmitted imperfectly across host generations. I will talk about how such imperfect vertical transmission could be adaptive in varying environments. Using an evolutionary model, I demonstrate that decreasing vertical transmission fidelity can increase microbiome variation, and thus phenotypic variation, across hosts in a population. When the most beneficial microbial genotypes change unpredictably from one generation to the next (for example, in variable environments), hosts can maximize fitness by increasing the microbiome variation among offspring, as this improves the chance of there being an offspring with the right microbial combination for the next generation. This is an example of a diversified bet hedging strategy. I then illustrate how selection on vertical transmission is further shaped by the environmental predictability, by microbiome changes during host development and by the contribution of other factors to host trait variation. These results provide a basis to understand the evolutionary pathways that potentially led to the wide diversity of microbe transmission patterns found in nature.

Together we reach the top: How ecological interactions can make fitness landscapes more connected

*Meike Wortel, Philip Ruelens, Eline de Ridder, Marco Lezzerini, Bodine de Slegte, Arjan de Visser
Microbiology, Swammerdam Institute for Life Sciences, University of Amsterdam*

Fitness landscapes map genotypes to fitness, visualizing possible evolutionary paths. These landscapes are studied both at the conceptual level and made explicit by measuring the fitness of nearby genotypes to create empirical fitness landscapes. Since the mapping of the genotype to fitness depends on the environment, approaches have included the environment (e.g. seascapes and deformability). These methods do assume a new genotype removes the old genotype. However, certain changes of the environment, such as the production of cross-feeding components or the removal of toxins from the environment, allow strains to coexist. Therefore, we introduce 'eco-fitness landscapes', which include ecological mechanisms of coexistence. We use an empirical fitness landscape of cefotaxime resistance in *E. coli* with a TEM1 gene coding for a beta-lactamase, which can break down the antibiotic. The breakdown decreases cefotaxime concentrations, which allow for growth of more susceptible strains. We measured properties affecting these dynamics, such as growth rates and antibiotic clearance rates, of eight different mutants, and show experimentally that coexistence is possible. Using this experimental data in a mathematical model we can create an

empirical 'eco-fitness landscape' and predict how evolutionary trajectories are affected by coexistence. Including ecology in fitness landscapes may lead to more realistic predictions and a different view on the reachability of fitness optima.

Session II

Endogenous viral elements in shrew genomes provide insights into Flaviviridae ancient history

*Yiqiao Li, Magda Bletsa, Philippe Lemey, Sebastian Lequime
GELIFES, University of Groningen*

As viral genomic imprints in host genomes, endogenous viral elements (EVEs) shed light on the deep evolutionary history of viruses, ancestral host ranges, and ancient viral-host interactions. EVEs are thus genomic fossils to compensate for the absence of physical fossil traces of viruses. Flaviviridae are an important family of viruses, including well-known human pathogens, such as Zika, dengue, or hepatitis C viruses. Most EVEs derived from Flaviviridae have been identified in arthropods, but none, to date, in the genome of mammals, even though the family encompasses numerous mammal-infecting members. Through a comprehensive in silico screening of a large dataset of available mammalian genomes, our study (Li et al. <https://doi.org/10.1101/2022.02.11.480044>) identified two novel Flaviviridae-like EVEs in the reference genome of the Indochinese shrew (*Crociodura indochinensis*), a first in mammals. Homologs of these novel EVEs were subsequently detected in an additional 27 shrew species, including 26 species representing a wide distribution within the Crocidurinae subfamily and one in the Soricinae subfamily on different continents. Based on this wide distribution, we estimate that the integration event occurred before the last common ancestor of the subfamily, about 10.8 million years ago, attesting to an ancient origin of Flaviviridae.

The evolution of insular woodiness

*Frederic Lens, Alexander Zizka
Functional Traits, Naturalis Biodiversity Center*

Insular woodiness (IW)—the evolutionary transition from herbaceousness towards woodiness on islands—is one of the most iconic features of island floras. Since pioneering work by Darwin and Wallace, a number of IW drivers have been proposed: (1) competition for sunlight requiring plants with taller and stronger woody stems, and (2) drought favouring woodiness to safeguard root-to-shoot water transport. Alternatively, IW may be the indirect result of increased life-span related to (3) favourable aseasonal climate, and/or (4) lack of large native herbivores. However, information on the occurrence of IW is fragmented, hampering tests of these potential drivers. Here, we identify 1,097 insular woody species on 375 islands, and infer at least 175 evolutionary transitions on 31 archipelagos, concentrated in only six angiosperm families. Structural equation models reveal that the insular woody species richness on oceanic islands correlates with aseasonal favourable climate, followed by increased drought and island isolation (approximating competition). When continental islands are also included, reduced herbivory pressure by large native mammals, increased drought and island isolation are most relevant. Our results illustrate different evolutionary trajectories leading to rampant convergent evolutionary patterns towards IW, and further emphasize archipelagos as natural laboratories of evolution.

Pteropod shell proteomes reveal distinct biomineralization toolkits in the formation of crossed lamellar and helical microstructures

*P. Ramos-Silva, G. MC Janssen, A. G. Checa, E. Goetze, P. A. van Veelen, K. TCA Peijnenburg
Department of Freshwater and Marine Ecology, Institute for Biodiversity and Ecosystem Dynamics,
University of Amsterdam*

Shelled pteropods, known as sea butterflies, are a group of small gastropods that spend their entire lives swimming and drifting in the open ocean. They build thin, transparent shells of aragonite that

have been shown to dissolve and have reduced thickness with decreasing ocean pH. Thus, pteropods are considered as bioindicators to monitor the impacts of ocean acidification. Pteropod shells are strikingly diverse and have exceptional mechanical properties. Pteropods build shells made of crossed lamellar microstructures, as is common in molluscs, but also shells made of nanofibers that form 3D helical structures. The helical nanofibers are unique to pteropods. The genetic toolkit involved in pteropod biomineralization, and notably the proteins occluded in their shells, remain unknown. By combining shell proteomics with transcriptomics, we identify the biomineralization toolkit in three pteropod species with distinct shell microstructures: *Limacina helicina antarctica* (crossed lamellar), *Heliconoides inflatus* (simple helical) and *Diacria costata* (complex helical). Using a comparative proteomics approach, we observe a core set of proteins shared between species, but also many lineage-specific novelties. We shed light on the molecular basis underlying pteropod shell diversity, providing new molecular markers that enable both functional and evolutionary studies aimed at understanding the origin and evolution of pteropod biomineralization.

Bill length variation in great tits (*Parus major*): Are there any fitness consequences?

Judith E. Risse, Mirte Bosse, Jacintha Eilers, Marcel E. Visser
Animal Ecology, NIOO-KNAW

Bird bills vary greatly in shape and size and this variability is strongly associated with feeding ecology and species differentiation. Studies show that bill length and shape is a true polygenic trait. In great tits bill length varies across populations with differences between UK and Dutch birds. These differences were shown to be due to selection for larger bills in the UK population, associated to human bird feeding. We hypothesized the Dutch population too would experience selection of larger bills and aimed to catch 'evolution in the act'. We studied potential fitness consequences of bill length, the underlying genetic variation and the associated developmental processes using a multi-disciplinary approach. Our data consist of multi-year observations of bill length, phenotypic and life history traits in four long-term study populations of the great tit, embryonal bill gene expression data from a selection experiment, and whole genome sequencing data from phenotypic extreme wild individuals. Results show that bill length is a heritable trait varying between sites and years but without any fitness consequences or evidence of selection. The genetic data hints at involvement of the developmental pathways previously implicated, however with variation in different gene. strengthening the view that bill length is a polygenic trait. Thus, in contrast to our expectations, bill size is not under selection and, despite it being heritable, is not expected to evolve to larger bills.

The role of MADS-box genes in the evolution of flowering and fruit development

Xiaobing Jiang, Kai Thoris, Michiel Vandenbussche, Marian Bemer et al.
Biosystematics and Plant Developmental Systems, WUR

The evolution of the flower and fruit have led to the rise of the angiosperms, of which there are approximately 300,000 species on earth today. Molecular and genetic research has revealed that the genes that regulate important features such as inflorescence- and fruit development are to a large extent conserved. However, shifts in their expression patterns and in the interactions between the genes/proteins has resulted in the large phenotypic diversity that we see in these features today. The MADS-box gene family, encoding transcription factors, has largely expanded at the beginning of angiosperm evolution and has become very important for the regulation of flowering and fruit development. We are focusing on the MADS-box gene family to study the molecular basis of conservation and divergence of inflorescence- and fruit characteristics. This includes investigating the molecular basis of different flowering habits in the Brassicaceae and Solanaceae, and the comparison of regulatory networks underlying dry- and fleshy fruit development in these families.

Session III

Genomic basis of rapid adaptation to climate change in the winter moth

*Natalie E. van Dis, Judith E. Risse, Agata Pijl, Roelof A. Hut, Marcel E. Visser & Bregje Wertheim
GELIFES, Groningen University*

Climate change threatens many species with extinction. To persist, populations will need to genetically adapt, but we know little about what determines adaptive potential in wild populations. The winter moth is one of the few species for which we have evidence that it has genetically adapted to climate change. In just a decade, the response of its egg development rate to temperature has genetically changed such that eggs now take longer to develop under the same temperatures. We combine RNAseq and whole genome sequencing approaches to characterize the genomic basis of this rapid adaptation to climate change. By sampling RNA in a temperature experiment with wild eggs, we explore which genes are involved in regulating the temperature sensitivity of embryonic development rate. We then use the resequencing of historically collected population samples from the same wild populations to determine which genomic regions have changed between 2000 and 2020. By also sequencing multiple timepoints in between 2000 and 2020, we investigate how allele frequencies of candidate genomic sites have changed in relation to selection pressure strength and population dynamics. Combining the candidate genes identified by RNAseq with the candidate genomic regions that have changed under selection will give unprecedented insight into what determines the speed of adaptation in the wild.

Why do some fungi grow fast and others slowly?

*Duur K. Aanen
Plant Sciences Group, Wageningen University*

There is a striking dichotomy in growth mode between moulds (filamentous ascomycetes), and mushrooms (filamentous basidiomycetes): moulds typically grow fast, are short-lived and produce asexual spores, while mushrooms grow slowly, are among the longest-lived organisms known and rarely produce asexual spores. I propose that this difference is due to a fundamental difference in growth strategy between the two. On the one hand, mould growth is like a 'pyramid-scheme': a colony depends on an exponentially increasing number of hyphae to provide it with a constant supply of a growth-limiting nutrient such as nitrogen. So essentially, colony growth depends on "living on credit", provided by offspring hyphae. However, this is only possible as long as there is space to grow exponentially, so in other words, 'the pyramid scheme crashes' when space is filled. On the other hand, mushrooms follow a sustainable growth strategy, not depending on exponential growth but on linear growth. However, linear growth does not provide sufficient influx of the growth-limiting nutrient to supply the entire colony at a constant rate, predicting that generally only the colony edge is alive in mushrooms. I discuss the evidence for this model and the implications for mutation rate and the rate of evolution.

Ecdysone under selection in fast developing beetle eggs

*Shixiong Cheng, Joost van den Heuvel, Elisa Mogollon Perez, Chris Jacobs and Maurijn van der Zee
Institute of Biology, Leiden University*

Climate change exerts strong selection on insect developmental speed, due to mismatches with host plant or prey availability. Here, we investigated the genetic basis of embryonic developmental speed by selecting replicate outbred populations of the beetle *Tribolium castaneum* for fast or slow development during 20 generations. The response of selection was spectacular, and the selection lines

started to diverge in developmental speed during dorsal closure. Using pooled Illumina and nanopore resequencing, combined with RNAseq, qPCR and a small RNAi screen, we uncovered two main targets of selection. One is a 230 bp deletion upstream of CYP18A1, the cytochrome that degrades active ecdysone. This deletion contains a binding site for the architectural protein Tramtrack affecting chromatin conformation. Using CRISPR-Cas9 technology, we recreated this allele in the homogeneous genetic background of the Georgia lab strain, and demonstrate that this deletion advances the ecdysone peak inducing dorsal closure. This allele in the fast lines explains 50% of the time difference with the unselected lines. With this study, we have revealed natural genetic variation in ecdysone signaling that may be highly relevant in response to global warming, for instance to match caterpillar hatching with host plant bud burst.

The diverse effects of phenotypic dominance on hybrid fitness

Hilde Schneemann, Asli D. Munzur, Ken A. Thompson, John J. Welch
Department of Genetics, University of Cambridge

When isolated populations of plants or animals come back into contact and interbreed, the fitness of their hybrids will determine whether or not the populations remain distinct. Especially important are the initial first-generation hybrids, with one parent from each original population. I will present a mathematical model of the fitness of first-generation hybrids, paying particular attention to dominance (i.e. interactions between the maternally-inherited and paternally-inherited copies of the same gene). I will show that dominance effects have no special tendency to function well together, having not been exposed to natural selection on their combined effects. As a result, dominance will often reduce hybrid fitness. Sometimes, however, dominance can lead to novel trait combinations that enhance hybrid fitness in novel environments. This prediction matches empirical reports of hybrids flourishing in habitats to which their parents are poorly adapted. I will end with some comments on the interaction between and uniparental inheritance (where certain regions of the genome come from one parent alone) and discuss how we might empirically assess their importance in hybridisation.

Session IV

Epigenetic feedback on noisy protein dosage boosts evolvability

Werner Karl-Gustav Daalman and Liedewij Laan

Bionanoscience, TU Delft

Epistasis and gene expression noise are ubiquitous phenomena which are linked when fitness depends on protein dosage. To understand how their linkage affects evolutionary trajectories, we constructed a minimal epistasis and noise (MEN) model, where one heritable protein in two possible dosage states sets the progeny of otherwise equal cells. For realistic parameters based on experimental data of noise and mutational effects in yeast, our model sketches the following picture. Firstly, expression noise strongly expands the non-neutral mutational pool (up to 12-fold). Secondly, noise inflicts a fitness penalty, particularly for essential genes. However, this is mostly mitigated by an emergent epigenetic feedback, as lucky cells with a good dosage generate more daughters with subsequently a more favourable initial dosage by protein inheritance. For essential gene mutations, this feedback can rescue viability or delay extinction by a few-fold in extreme cases. In short, this feedback smoothens the ruggedness of the fitness landscape associated with epistasis. Consequently, dosage feedback may form an important epigenetic addition to mechanisms that boost the evolvability of organisms.

Repeatability of experimental evolution in the nematode *C. elegans*

Thomas Blankers, Karen Bisschop, ... , Martijn Egas, Jacintha Ellers, Astrid T. Groot, Marcel Visser
Evolutionary and Population Biology, University of Amsterdam

Evolutionary biology is a cornerstone in addressing major challenges for society, such as the evolution of antibiotic resistance, new diseases, and species extinctions. However, this requires the field to transition from inference to forecasting. A key question is how predictable evolution is and which factors influence this predictability. We predicted that factors that reduce genetic diversity in a population will also cause evolution in these populations to be more dependent on drift and thus less predictable. We experimentally evolved the nematode *Caenorhabditis elegans* in a novel environment, simultaneously at six research institutes. We asked whether fitness (population growth) and genomic evolution were repeatable within and across institutes and whether repeatability was affected by demographic factors (population bottleneck, gene flow among subpopulations) and by reproductive mode. We found that populations generally evolved higher fitness over time. However, there was substantial variation, especially among replicate populations evolving at different research institutes. Repeatability of fitness evolution was higher than genetic evolution, but replicate populations shared more divergent genes than expected by chance. Demographic factors had predictable effects on genetic diversity, but these effects did not always translate to increased or reduced repeatability of evolution. These findings show that the predictability of evolution is highly context dependent.

The evolution of condition-dependent mutation rates

Jana Riederer, Timo van Eldijk, Franjo Weissing, Sander van Doorn
GELIFES, University of Groningen

Mutation provides novelty, and thus the raw material for selection to act on. Previous evidence has shown that increased mutation rates can indeed lead to higher evolutionary rates and faster adaptation. However, when organisms are well adapted, most mutations are likely to be maladaptive

– depending on the current degree of adaptation, increased mutation rates may thus be either beneficial or harmful. Particularly interesting in this context is stress-induced mutagenesis: a condition-dependent upregulation of mutation rates under stress. As stress may be a signal for maladaptation, stress-induced mutagenesis may allow mutations to occur predominantly in times of maladaptation, i.e. when they are more likely to be adaptive. Whilst this has received much attention in empirical work, comparatively few theoretical models have explored this topic. Here, we use individual-based simulations to investigate the evolution of condition-dependent mutation rates in fluctuating environments, where environmental change repeatedly leads to maladaptation and thus to stress. We show that condition-dependent mutation rates are indeed adaptive in this scenario – however, they only evolve under specific circumstances. We explore how this relates to initial conditions, selection strength, genome structure and patterns of environmental change. Overall, we discuss the relevance of condition-dependent mutation rates for evolvability, i.e. for the capacity for adaptive evolution.

Inbreeding constrains the potential for rapid adaptation and reduces phenotypic plasticity

Mark Lammers, Lukas Schrader, Jürgen Gadau

Institute for Evolution and Biodiversity, University of Münster

Phenotypic plasticity allows individuals to exploit a larger variety of environments. When a novel environment (e.g. new host species) emerges, more plastic individuals may succeed to use its resources. Subsequent generations may rapidly adapt to the novel environment, e.g. through genetic accommodation if the population is genetically diverse. Population dynamics of the aphid-parasitoid system are characterized by boom-and-bust dynamics in nature. Collapse of an aphid population forces parasitoid wasps to disperse and attack other hosts. Consequently, the wasps' life-history alternates between local inbreeding followed by dispersal, a lifestyle hypothesized to select for phenotypic plasticity but reduce genetic diversity. We inbred *Aphidius ervi* purging >98% of heterozygosity, maintaining the outbred laboratory population in parallel. All lines were subjected to experimental evolution, rearing them either on a novel, smaller host, or on the original host. The outbred population but only few highly inbred lines successfully reproduced on the novel host showing signs of adaptation. However, long-term survival of inbred lines was only observed on the original host. All populations had constrained plasticity after the host switch: they could no longer subdue another three host species to which all lines were naive.

Cultural Intermezzo

Tim Hammer and Mirthe Dokter – FIGHT

<https://www.mirthedokter.nl/>



The animal kingdom is full of frolicking lions, screaming koalas and scratching cats. But what animal can give a human couple the right inspiration for a fair duel? Discover it in FIGHT: a comical performance on a scientific basis.

A teaser can be found on:

https://www.youtube.com/watch?v=Zt91E2JX_WY

Posters

Ginger snail project – revealing the inheritance mode of shell colour polymorphism in *Lymnaea stagnalis*

Yumi Nakadera, Matthijs Ledder, Alexandra Staikou, Joris M. Koene
ALIFE, Vrije Universiteit Amsterdam

Snail shell colour polymorphism is a classic study system for evolutionary genetics. However, the genetic mechanism of determining shell morphs remains to be fully elucidated. Here we propose a new model system to reveal the genomics of shell polymorphism. Recently, our research group discovered a unique shell colour polymorphism in the great pond snail *Lymnaea stagnalis*. Part of the snails from a Greek population show a distinct red shell colour (nicknamed as ginger snail), while the shell colour of this species is usually beige. In order to evaluate if this shell colour polymorphism is useful for genomic investigation, we compared the inheritance mode of this shell colour as well as several life history traits (e.g., reproduction, behaviour) between ginger and wild type snails that were all offspring of the Greek parent population. The life history traits of ginger snails are very similar to wild types, and the mode of inheritance of the ginger phenotype seems to fit simple, single locus Mendelian inheritance. Therefore, we believe that this new variant of *L. stagnalis* provides a promising opportunity for further exploration of the genetic basis of shell polymorphism.

Juicy genome information: Comparative genomics of accessory gland proteins in gastropod molluscs

Yumi Nakadera, Coen M. Adema & Joris M. Koene
Ecology & Evolution, Amsterdam Institute for Life and Environment (A-LIFE), Vrije Universiteit Amsterdam

As modulators of reproductive biology, accessory gland proteins (ACPs) are essential ingredients of an ejaculate, the complex cocktail of spermatozoa and other substances. In molluscs, study of ACPs has focused mainly on two gastropod species, *Lymnaea stagnalis* and *Cornu aspersum* (formerly *Helix aspersa*). ACPs trigger behavioral and physiological changes in recipient snails, thought to benefit reproductive success after mating. To address the underlying fundamental questions about ACP function and -evolution in these hermaphrodite snails, it is crucial to identify ACP homologs in additional gastropods. With genomic Next-Gen Sequencing (NGS) data at our disposal, we applied previously obtained peptide sequences to characterize full gene sequences for *L. stagnalis* ACPs and *C. aspersum* love dart allohormone. Subsequent computational sequence similarity searches against NGS data to take inventory of ACP-encoding sequences among select hygrophilid and stylommatophoran gastropods indicated that some ACPs are present in many species, while others are species-specific. These initial intra- and interspecific comparisons, i.e. exploration of micro- and macro-evolutionary patterns, provide ample direction for follow-up studies at the genomic/transcriptomic level, but also at the functional level. We will present plans to proceed and propose some key species and comparisons that we anticipate will help to broaden knowledge of snail ACPs.

Are ship-timber beetles the oldest insect farmers of fungi?

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Fungiculture has evolved in three insect groups; ants, beetles and termites. Fungus-growing beetles, collectively called ambrosia beetles, are the only group that evolved fungiculture more than once, probably more than 12 times. It has recently been proposed that the oldest example of fungiculture

may be found in the ship-timber beetles (family Lymexylidae). Members of this family appear in amber dating back 125 million years ago. However, details on the evolutionary origin are lacking, since fungus-growing has been demonstrated in only a few species and details on fungal associations are lacking in most species. We would like to identify the origin or origins of fungiculture in the ship-timber beetles. We will do this by screening representative species of all extant lymexylid genera for their ability to cultivate fungi and by reconstructing a time-calibrated phylogeny. Female adults of fungus-growing species within this group carry the fungus in special pouches, called mycangia, located near the apex of the ovipositor. We will screen both extant lymexylid beetles and extinct beetles preserved in amber for the presence of mycangia, a strong indication for their ability to grow fungi. To detect mycangia, we will use X-ray micro-CT, a novel technique for this group. This research will disclose a heavily understudied, and potentially the oldest example of insect fungiculture, which also has economic significance as this family contains important pest species.

Adaptation of species communities on adaptive landscapes

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Adaptive landscapes are a way to visualize to what extent combinations of alleles, genotypes or species are adapted to a given environment. Depending on the nature of the environment, multiple adaptive peaks may exist. Changes in alleles, genotypes or species can allow movement towards adaptive peaks. Here we use such adaptive landscapes to project adaptation of species communities. The position in the landscape is determined by the community composition at the level of species, levels of community functionality determine the heights of adaptive peaks. We used microbial communities from a traditional fermented milk product from Zambia, mabisi, that harbours natural microbial communities consisting of around 10 distinct microbial types. Six comparable but different natural microbial communities from a traditional fermented food were each split into five identical replicates, which underwent 16 repeated propagation cycles in a novel, common environment. We compared bacterial species composition at the start and the end of the experiment. We found that differences in starting community led to significant differences in final community composition during prolonged propagation in the common new environment. Our results suggest that multiple adaptive peaks exist in our landscape and that replicate species communities approached different peaks due to species sorting, while series of communities founded as different initial species communities approached different peaks. Next steps

Eco-evolutionary interactions and the spread of antimicrobial resistance in pathogenic microbial communities

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As pathogens and other microbes become progressively resistant to antibiotics, there is a growing world-wide concern that their use for treating and preventing diseases is rapidly becoming less effective and unsustainable. An important mechanism in the evolution of antibiotic resistance is horizontal gene transfer (HGT), as it is one of the most effective ways of transferring information between bacteria. Until now, HGT has experimentally mainly been studied in single bacterial populations. Yet, bacterial pathogens often do not live in isolation. It is therefore important to understand the role of HGT in the spread of antimicrobial resistance in a community context. This will be crucial for elucidating the nature of polymicrobial infections, given that ecological interactions and the microbial context can greatly impact bacterial growth and antibiotic efficacy. In this project, we

investigate the community conjugation rates of pathogens isolated from polymicrobial urinary tract infections (UTIs). My research will provide fundamental knowledge on HGT in infectious communities by identifying eco-evolutionary principles that govern the rate of HGT and the spread of antimicrobial resistance in polymicrobial communities.

Exploration of microbial community dynamics and functionality in traditional fermentation of milk Shepherd Nehanda, Supervisors: Dr. S. Schoustra, Prof. E. J. Smid, Prof. B. Zwaan & Dr. J. Chileshe
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Background: Microbial communities coexist and interact in a given niche. However, fundamental understanding of how microbial consortium are constructed and function as a community, remains largely unexplored. Fermented foods offer tractable niches to elucidate this phenomenon. Here, we apply mabisi, a Zambian traditional fermented milk product as a study model.

Objectives: To determine the effect of varied substrate selection on microbial community dynamics and metabolic activity. Also, to explore whether varied microbial ecosystem drive different potential for riboflavin and folate functional properties.

Methodology: Conduct both a field and laboratory evolution experiment by propagation of mabisi fermenting microbes in 5 different milk derived substrates (raw bovine milk, F100, S26, low fat and full cream milk). In addition, conduct a field sampling of mabisi from 48 different producers in western province, Zambia. Thereafter, perform DNA analysis to profile microbial communities, detect and sequence vitamin B2 & B9 genes, and GCMS analysis for proxy metabolic profiling (carboxylic acids, esters, alcohols, aldehydes, etc) on mabisi samples.

Expected outcome: This will help elucidate ecological impact of substrate selection on microbial community dynamics & metabolic activity, provide basis for understanding practical potential of mabisi microbiota for broad application, and identify microbial ecosystems with optimal B group vitamin potential.

Eco-evolutionary interactions in polymicrobial infections

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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.

Cooperation and competition across the evolutionary transition to multicellularity

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From organic compounds in a primordial soup to the remarkable diversity of modern organisms, the evolution of life has been driven by pivotal moments of cooperation and competition. In what instances are individuals driven to cooperate, rather than compete? The most paradigmatic of these

dynamics are observed in Major Evolutionary Transitions (METs), where transitions in individuality require the formation of a cooperative group with sufficiently minimal within-group conflict to overcome competition between groups. While key drivers of METs remain unknown, some transitions are reproducible in the laboratory. Previous work used settling selection to drive the transition to multicellularity in the yeast system, *S. cerevisiae*, allowing for real-time analysis of the causes and consequences of multicellularity. Yet, populations rarely evolve in isolation, raising the question: How does interspecific competition impact the origin of multicellularity? In this study, we explored the evolution of multicellularity in co-cultures of two yeast species, *S. cerevisiae* and *K. lactis*, examining how competition influenced the emergence of cooperative multicellular groups. We found that while *K. lactis* evolved multicellularity first, interspecific competition did not lead to exclusion of *S. cerevisiae*. When rare, each species could invade the other, illuminating how the interplay of cooperation and competition across this MET altered the eco-evolutionary landscape between species.

The effects of sex-biased mortality on the evolution of biparental care

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In many sexually reproducing species, offspring mortality is reduced by parental care. However, parents caring for offspring limit their mating opportunities. This not only results in a trade-off between care and matings, but also causes a conflict of interests between the parents. This may lead to evolution of biparental or uniparental care. A widely cited claim is that negative feedback between operational sex ratio and opportunity costs of care causes selection for equal biparental care. To examine the generality of this claim, here we simulate a general time-in time-out model allowing evolution of parental care. We found that biparental care evolved due to individual variation in care, not through a negative feedback. Furthermore, uniparental care - be it maternal or paternal - may evolve due to sex-biased mortality differences when the mortality is a direct cost, e.g. mortality when performing parental care, or the cost of a sexual ornament directly signalling care. Overall, the claims on how parental care evolves appear not general. We discuss how this impacts sexual selection when parental care is signalled.

Temporal flexibility and consistency of daily rhythms within and between individuals in wild Great Tits *Parus major*

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Organisms make use of circadian clocks to organise their daily activities. These clocks are genetically determined but are modified by environmental cues to match environmental conditions. Consistent daily rhythms (chronotypes) facilitate the anticipation for predictable situations such as the start and end of the day. In contrast, temporal flexibility allows the individual to cope with unpredictable short-term changes in the environment. Here, we aim to assess the consistency of behavioural and physiological chronotypes as well as their temporal flexibility to daylength, ambient temperature and breeding stage in a wild Great Tit population. Next, we correlated these chronotype characteristics to fitness and this way assess selection on parental daily rhythms. We monitored the daily rhythms of 26 breeding pairs on the island of Vlieland and tagged 23 males and 23 females with a temperature-sensitive radio transmitter. Additionally, data from temperature loggers to record incubation rhythms and registration of nest visits during chick provisioning were collected. From these data we extracted onset and offset as measure for daily timing of different activities (i.e. overall activity, incubation and

chick provisioning, and body temperature) and linked these to fitness using data from brood monitoring. This allows us to explore selection on temporal flexibility and consistency of different chronotypes in a wild population.

The importance of being plastic: evolutionary and ecological correlates of phenotypic plasticity

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Phenotypic plasticity allows individuals to cope with different environmental conditions without the need for genetic adaptation. Consequently, plasticity affects the nature and strength of selection on traits. Plasticity enables individuals to experience novel selection pressures, for example through migration, possibly leading to genetic adaptation. At the same time, plasticity may shield the genotype from selection, impeding genetic adaptation. Plasticity, therefore, can have opposing effects on evolutionary change and population divergence.

The visual system of cichlid fish is a suitable model trait to study the relationship between plasticity and evolutionary change, because of the high species richness and the variation among species in visual habitat. Furthermore, plasticity in the expression of genes involved in the cichlid' visual system is well established. Here, we test whether visual plasticity is correlated to the degree of ecological specialisation and clade species richness. We quantify plasticity in the expression of these genes in species from species-poor and species-rich clades, inhabiting different visual habitats in nature, by exposing individuals to different light conditions and determining light-induced variation in gene expression. Preliminary results indicate that expression indeed differs among light treatments, in multiple species. We expect our study to provide a better understanding of the impact of phenotypic plasticity on divergent evolution.

Modelling reaction norms with few assumptions

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Reaction norms describe the phenotypic expression of a genotype over a range of environments. In evolutionary theory, these are typically modelled using very specific shapes, such as straight lines or logistic (S-shaped) curves. This may lead to wrong conclusions when the assumptions being made are too restrictive. Here we present a novel method to model smooth non-linear reaction norms with very few a priori assumptions about shape, using restricted cubic splines – a type of function defined piecewise by polynomials. We present an example of an optimal non-linear reaction norm obtained analytically, where a hypothetical single celled organism is able to vary its metabolic investment into processing different nutrients which themselves vary in digestibility. To simulate this example reaction norm, we use a restricted cubic spline based on k independent gene values. Each simulation consisted of a starting population of 1,000 individuals with a horizontal reaction norm defined by 5, 10 or 20 genes, which were then allowed to evolve freely for 300,000 generations. All populations achieved a shape very similar to the optimal reaction norm, independently of the number of genes used. Moreover, a lower number of genes does not lead to faster adaptation. Here we show that modelling smooth non-linear reaction norms is possible without constricting their shape.

The effect of diversity on community function in natural microbial communities

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The interconnection of species and genetic diversity with ecosystem function is a central topic in ecology, yet it is still unclear how this relationship changes over time. Investigating diversity-function relationships over evolutionary time scales ideally combines the complexity of natural communities and environments with the control and quick generation times of evolution experiments.

My research uses natural microbial communities of Mabisi – a traditionally fermented milk beverage from Zambia – as a model system for studying the interacting roles of evolution and diversity on community function. By serially transferring Mabisi microbial communities of four starting levels of diversity levels for approximately 110 generations, I have focused on investigating the effect of diversity on functional properties and diversity on the repeatability of ecological trajectories. Initial results demonstrate sustained functional differences in metabolic profiles between two groupings of initial community diversity.

Furthermore, an underlying motivation of my research is conceptualising communities as “superorganisms” and reinterpreting the level of selection (i.e., individual, species, community). It is a difficult yet exciting ambition in microbial biology to detect and interpret the consequence of genetic changes within a species evolving amongst a multispecies community; experimental evolution in a future “Mabisi inspired” synthetic system could provide an innovative approach.

Evolutionary paths to high-level ampicillin resistance

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The widespread use of beta-lactams has resulted in a growing prevalence of highly resistant pathogens. Indeed, clinical isolates can have very high resistance to beta-lactams, most prominently to ampicillin where resistance levels could even exceed 1,000 µg/ml. Yet, in striking contrast, bacteria evolved in laboratory settings, typically plateau on much lower levels of resistance. Here, evolving *Escherichia coli* on the Microbial Evolution and Growth Arena (MEGA) plate, we found that large population sizes circumvent the previously observed saturation of resistance under ampicillin selection, selecting for mutants comparable with clinically observed resistance. Whole-genome sequencing of resistant isolates revealed that this high ampicillin resistance was acquired via a combination of single-point mutations and an increasingly focused gene amplification of the beta-lactamase enzyme AmpC. Importantly though, blocking AmpC-mediated resistance only slightly reduced the adaptive potential: strains deleted for *ampC* were able to evolve high-level resistance through combinations of genetic changes in genes involved in multidrug resistance such as efflux pumps, transcriptional regulators, and porins. Our results reveal that combinations of distinct genetic mutations, accessible at large population sizes, can drive high-level resistance to ampicillin even independently of beta-lactamases.

Composition or environment: what matters more?

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PSG GEN, WUR

Variation in the diversity of species and their interactions contribute to ecosystem functionality and stability. Ecological theory predicts that ecosystem stability relies on balanced networking between species and the environment. In our project, we study mabisi, a Zambian spontaneously fermented milk product, as a model system to understand mechanisms driving community stability. Alongside various lactic acid and acetic acid bacteria, mabisi harbors yeasts and viruses. In a serial propagation experiment all these microbes co-existed as a functionally stable ecosystem with some variation in

microbial composition. To the contrary, little is known about the role of the growth environment in supporting the stability of the microbial mabisi community. In a further experiment, the microbial mabisi community has been fermented in different environment types, namely, goat, lactose free and skim milk. We expected the microbial community composition to shift depending on the growth environment. Results indicate that sugar and fat content affect community composition and functionality less than more different environment (goat milk). To plan further experiments, we are developing a mathematical model of mabisi with key 5 species and several environmental components. Our results highlight that a combination of experimental evolution, mathematical modelling and meta-omics assemble into a promising approach to deepen our understanding of the stability of (microbial) ecosystems.

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