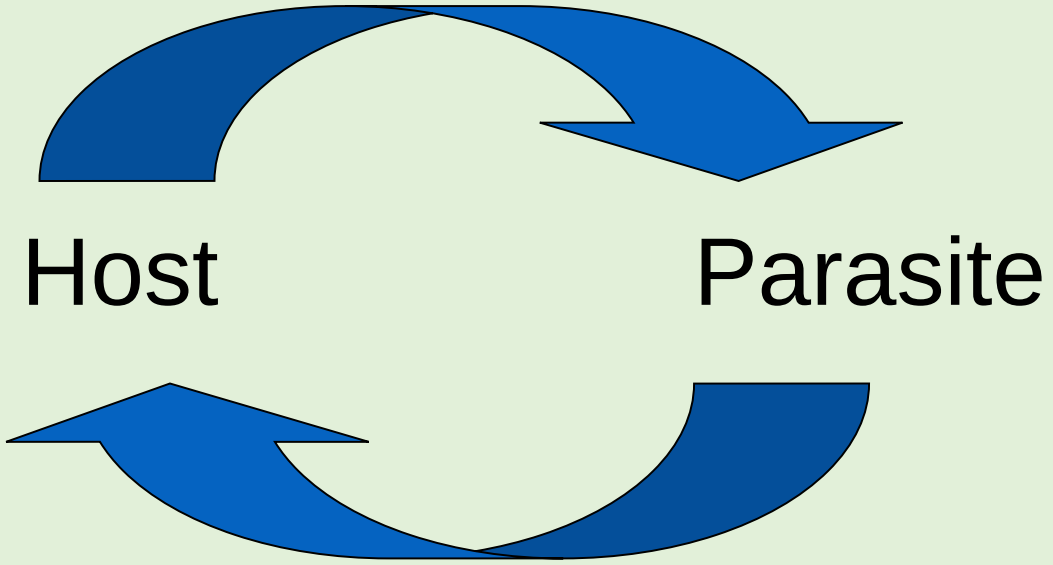
Project module / BSc topics in the Kurtz group

Background: Rapid coevolution of hosts and parasites
Evolutionary ecology of immune defenses



Red Queen Hypothesis:
Arms race between host and parasite
“In this place it takes all the running you can do, to keep in the same place.“

Project module / BSc topics in the Kurtz group

Approaches: Laboratory and field work

Red flour beetle
(Mehlkäfer)
Tribolium castaneum

Three-spined stickleback
(Dreistachliger Stichling)
Gasterosteus aculeatus

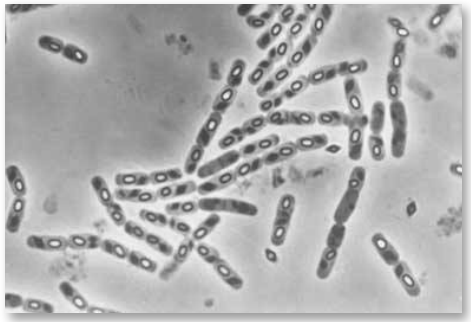
Mexican tetra ('cavefish')
(Mexikanischer Höhlenfisch)
Astyanax mexicanus

Supervisors:

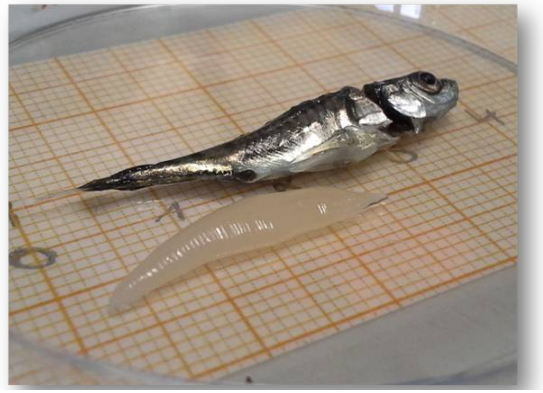





Parasites



Bacterium
Bacillus thuringiensis



Tapeworm
Schistocephalus solidus

Can the effects of virulence of a manipulative parasite alter community dynamics?

Supervisors: Shay Callahan and Dr. Jaime Anaya-Rojas

Model system: host = Three-spined sticklebacks (*Gasterosteous aculateus*)
pathogen = Tapeworm (*Schistocephalus solidus*)

Background: Trophically transmitted parasites have strong effects on their host; however, whether these effects are strong enough to alter ecological dynamics is still unknown.

Aim: We will measure the effects of *S. solidus* on three-spined sticklebacks and their effects on multiple aspects of the ecosystem, such as the benthic community (**student 1**), zooplankton community (**student 2**), and ecosystem functioning (**student 3**).

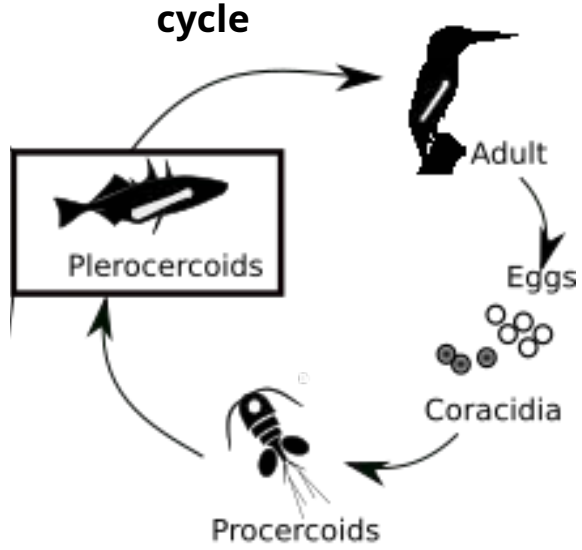
Methods: Mesocosm experiments, Fish rearing, phenotyping, animal identification, community ecology, and ecosystem measurements.

Literature:

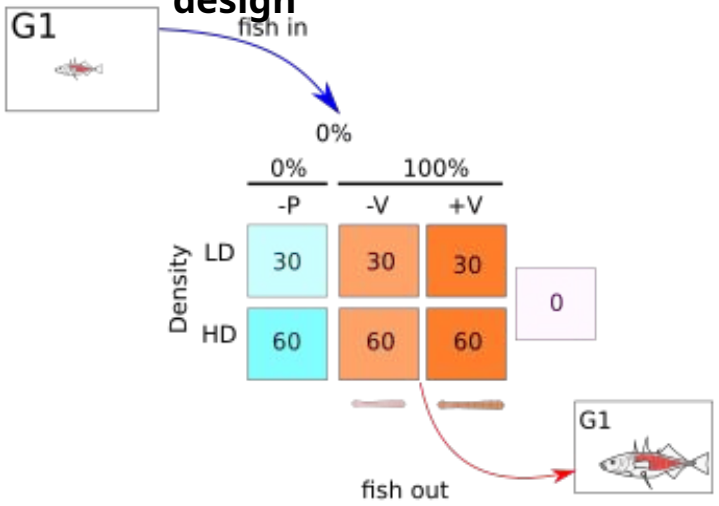
1.Anaya-Rojas, J. M. *et al.* *Ecology* e02744 (2019) doi:10.1002/ecy.2744.

2.Brunner, F. S., Anaya-Rojas, J. M., *et al Proc National Acad Sci* **114**, 3678–3683 (2017).

***S. solidus* life cycle**



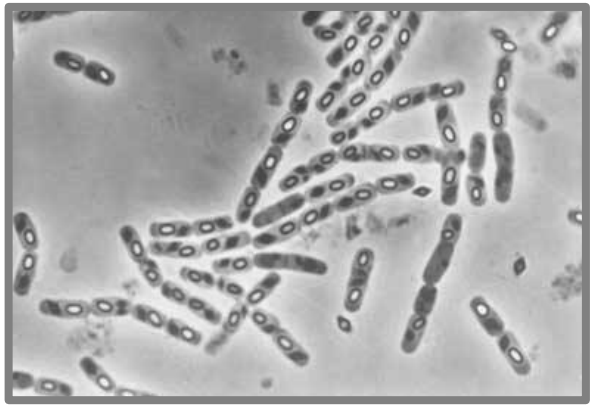
Experimental design



Do infection dynamics in the insect gut change after immune priming?

Supervisors: Moritz Baur, Dr. Nora Schulz

Model system: host = red flour beetle *Tribolium castaneum*
pathogen = obligate killer *Bacillus thuringiensis*



Background: Most insects are capable of immune priming, *i.e.*, improved survival upon secondary exposure, following a first non-lethal exposure to a pathogen.

Aim: We will use oral infections with bacterial spores, to determine whether previous oral immune priming alters host-parasite infection dynamics within the beetle's gut and changes spore germination rate, thereby potentially reducing bacterial replication. This will help us to understand how immune priming can alter infection outcomes.

Methods: microbiology techniques, insect rearing and dissection, molecular work (RNA extraction, qPCR)

Literature:

Milutinović et al. (2013). The Red Flour Beetle as a Model for Bacterial Oral Infections. *PLoS ONE, https://doi.org/10.1371/journal.pone.0107599*

Duneau et al. (2017). Stochastic variation in the initial phase of bacterial infection predicts the probability of survival in D. melanogaster *Elife*, https://doi.org/10.7554/eLife.28298

Are insect behavioral experiments reproducible across labs?

Supervisors: Dr. Nora Schulz (in collaboration with Dr. Vanessa von Kortzfleisch/ Prof. Dr. Helene Richter)

Background: Ongoing reproducibility crisis, in which the results of many scientific studies are difficult or impossible to reproduce. One major contributing factor to lacking reproducibility, besides experimenter and population might be the place where the experiment is carried out, the lab.

Model systems: red flour beetle, sawfly, grasshoppers

Aim: We will use three different insect models, to carry out behavioral experiments. Simultaneously, the same experiments will be performed in two other labs (Bielefeld, Jena). Besides testing whether all three experiments produce similar results across labs, this study will also improve our understanding of niche forming mechanisms in the three species.

Methods: Insect handling and manipulation, insect behavior tests, some field work (collecting specimens), advanced data analyses

Literature:

Crabbe et al. (1999) Genetics of Mouse Behavior: Interactions with Laboratory Environment. *Science,* DOI: 10.1126/science.284.5420.1670

Lo, R, Tewes et al. (2022) Immune Stimulation via Wounding Alters Chemical Profiles of Adult *Tribolium castaneum. J Chem Ecol, https://doi.org/10.1007/s10886-022-01395-x*

Chemical communication via cuticular hydrocarbon profiles in red flour beetles (1-2 students)

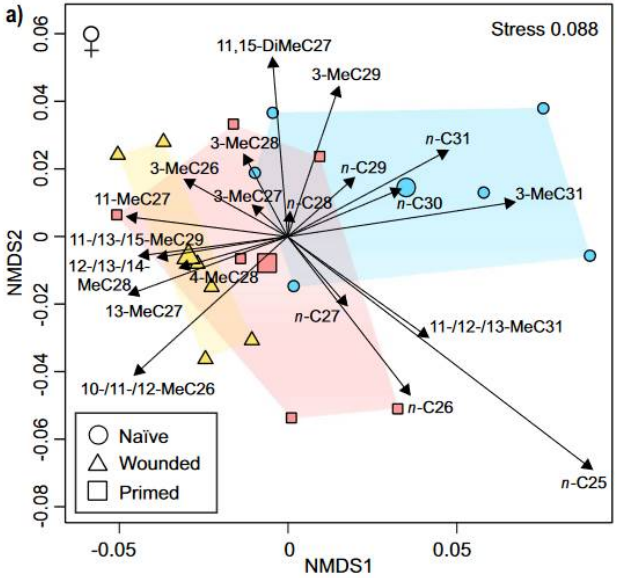
Supervisors: Dr. Nora Schulz (in collaboration with Dr. Jan Büllesbach)

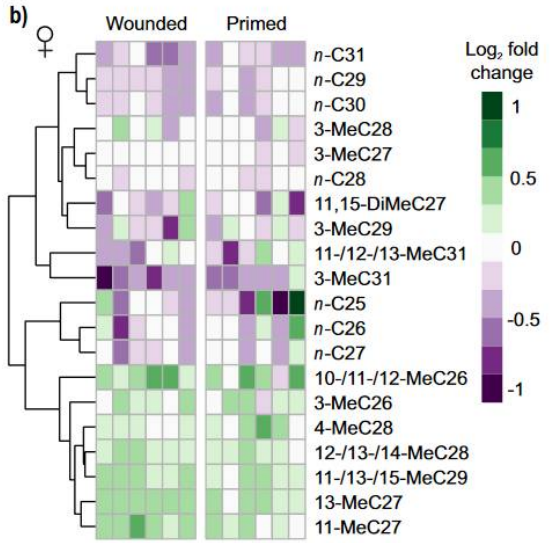
Background: Wounding/immune treatment changes CHC profiles of individuals.

Conspecifics change their gene expression after contact with wounded individuals.

Aim: We will try to identify the specific changes to CHC profiles after immune treatment and test how these changes alter conspecific behavior. Additionally, we will knockdown genes involved in CHC metabolism, to functionally test the role of CHCs in the recognition of wounded conspecifics

Methods: Establishing bioassay, knockdown via RNAi, GC-MS





Literature:

Lo, R, Tewes et al. (2022) Immune Stimulation via Wounding Alters Chemical Profiles of Adult *Tribolium castaneum. J Chem Ecol,* https://doi.org/10.1007/s10886-022-01395-x

Holze et al. (2021) Advances in deciphering the genetic basis of insect cuticular hydrocarbon biosynthesis and variation. *Heredity,* https://doi.org/10.1038/s41437-020-00380-y

Immune system of fire salamander larvae

Supervisors: Laura Schulte (Barbara Caspers Lab, Uni Bielefeld) and Robert Peuß

Background: Fire salamander females (*Salamandra salamandra*) typically deposit their larvae in first order streams. There, the conditions are very suitable for the larvae. Females also use different water bodies for larval deposition such as ponds. Here, the biotic and abiotic conditions are less suitable for larvae. Consequently, we found larvae from ponds to be more stressed than larvae in streams.

Aim: Larvae will be collected from the field (Kottenforst near Bonn) in spring 2023 and then transferred to the lab. Using Phytohemagglutinin (PHA), we will stimulate an immune response and then use gene expression analysis to measure the gene expression in body tissues over different time periods.

Methods: Field work, Methods for gene expression analysis (qPCR and RNAseq), Different immune assays to measure response to PHA

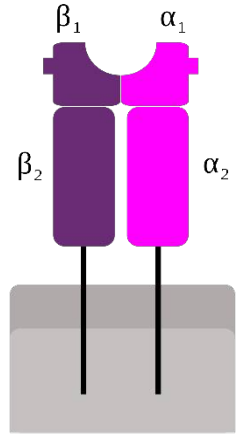
Literature:

Hahn LG, Oswald P, Caspers B. Behavioural responses to chemical cues of predators differ between fire salamander larvae from two different habitats. Journal of Zoology. 2022.

Immunogenomics of *Astyanax mexicanus*

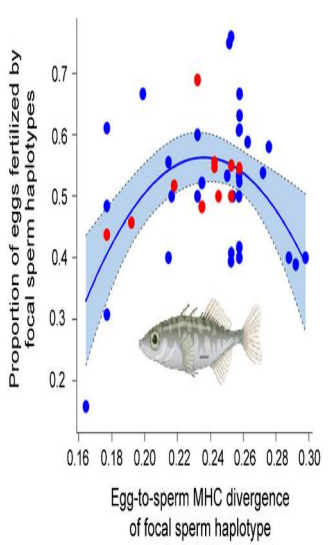
Supervisors: Robert Peuß (together with Michelle Borgers), in collaboration with Tobias Lenz, Uni Hamburg

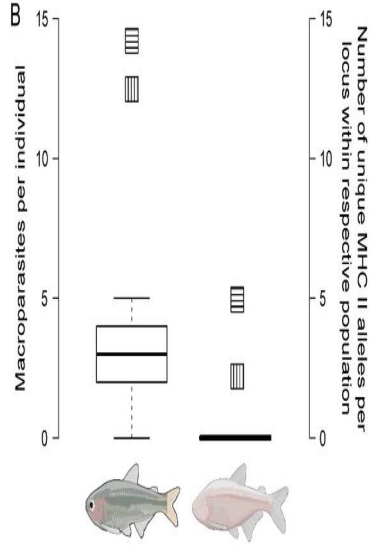
Background: The Mexican cavefish, *A. mexicanus*, adapted to different eco-systems (cave & river) that drastically differ in their biodiversity and parasite diversity. Here, we want to study the genomic basis of the immunological changes that evolved in the two different ecotypes, cavefish and surface fish.



Aim: Estimate the differences of the genomic diversity of the major histocompatibility complex II (MHC-II) of different *A. mexicanus* ecotypes as a result of genomic adaptation to different parasite regimes.

Methods: DNA-based techniques, PCR, Microsatellite analysis, Illumina sequencing





Literature:

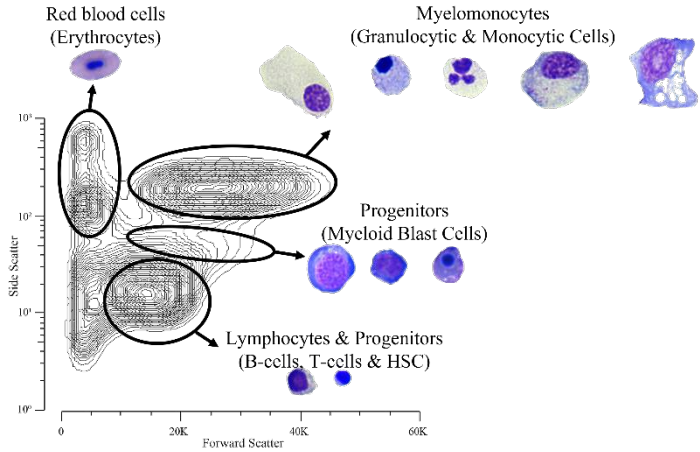
Peuß et al., Adaptation to low parasite abundance affects immune investment and immunopathological responses of cavefish. Nature Ecology and Evolution, 2020. https://doi.org/10.1038/s41559-020-1234-2

Immunological niche conformance in cavefish

Supervisors: Marc Bauhus and Robert Peuß

Background: The Mexican cavefish, *A. mexicanus*, adapted to different eco-systems (cave & river) that drastically differ in their biodiversity and parasite diversity. Adaptation to these ecosystems (or niche) resulted in the evolution of different immune phenotypes that seem to be unique to a certain ecosystem.

Aim: Analyze different cellular immune phenotypes to understand, whether and how adaptation to a distinct niche affects the immunological flexibility of host immunity.



Methods: Establishing primary immune cell cultures, Gene expression analysis, cellular immune assays (FACS, Phagocytosis)

Literature:

Peuß et al., Adaptation to low parasite abundance affects immune investment and immunopathological responses of cavefish. Nature Ecology and Evolution, 2020. https://doi.org/10.1038/s41559-020-1234-2

Project module / BSc topics in the Bornberg-Bauer group

Supervisors

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The evolution of sterile castes in termites

Supervisor: Mark Harrison

Background: Eusocial termites evolved from within the cockroaches around 150 million years ago

Distinct castes – workers, soldiers, kings and queens – are produced from the same genome via differential transcription. How these changes in transcription occurred within the termites is still unknown.

RNAseq of several termite and cockroach species with varying levels of sociality will be investigated to address different aspects of this question.

Project 1:The role of alternative splicing in the evolution of termite castes.

Method: R, DEXseq

Project 2: The role of TE regulation in the evolution of termite

Method: R, DESeq

References:

Reyes, Alejandro, Simon Anders, and Wolfgang Huber. "Analyzing RNA-seq data for differential exon usage with the DEXSeq package." (2012).

Love, Michael I., Wolfgang Huber, and Simon Anders. "Moderated estimation of fold change and dispersion for RNA-seq data with DESeq2." *Genome biology* 15.12 (2014): 1-21.

Harrison, Mark C., et al. "Hemimetabolous genomes reveal molecular basis of termite eusociality." *Nature ecology & evolution* 2.3 (2018): 557-566.

Price, J., et al. "Alternative splicing associated with phenotypic plasticity in the bumble bee Bombus terrestris." *Molecular Ecology* 27.4 (2018): 1036-1043.

Post, Frederik, et al. "More effective transposon regulation in fertile, long-lived termite queens than in sterile workers." *Molecular Ecology* (2022).

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Identifying caste-biased genes with Machine Learning

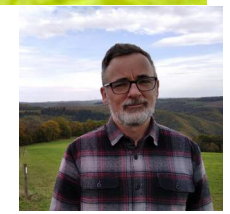
Supervisor: Mark Harrison

Background: In eusocial insect colonies (e.g. honey bees, ants, termites) vastly different castes are produced from the same genome via differential gene regulation, similar to different tissues within multicellular organisms

So far no common patterns of genes that are important for castes (caste-biased genes) have been found across different clades of eusocial insects.

Aim: In this project machine learning tools will be used to identify caste-biased genes in several species based on gene structure and sequence content.

Method: Python, SciKit-Learn



References:

Hao, Jiangang, and Tin Kam Ho. "Machine learning made easy: a review of scikit-learn package in python programming language." *Journal of Educational and Behavioral Statistics* 44.3 (2019): 348-361.

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Genome evolution of the subsocial cockroach *Cryptocercus meridianus*

Supervisor: Alina Mikhailova

Background: *Cryptocercus* genus is a group of wood-feeding subsocial cockroaches which is closely related to eusocial termites. They are proposed to be the best living model of the ancestral state of termites and provide insights into the evolution of sociality in cockroaches

Aim: Understanding differences in genomic properties between solitary cockroaches, subsocial cockroach *Cryptocercus meridianus* and eusocial termites

Method: Python3, analysis of k-mers and other genomic properties

References:
Legendre, Frédéric, and Philippe Grandcolas. "The evolution of sociality in termites from cockroaches: A taxonomic and phylogenetic perspective." *Journal of Experimental Zoology Part B: Molecular and Developmental Evolution* 330.5 (2018): 279-287.

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Genome evolution of the subsocial cockroach *Cryptocercus meridianus*

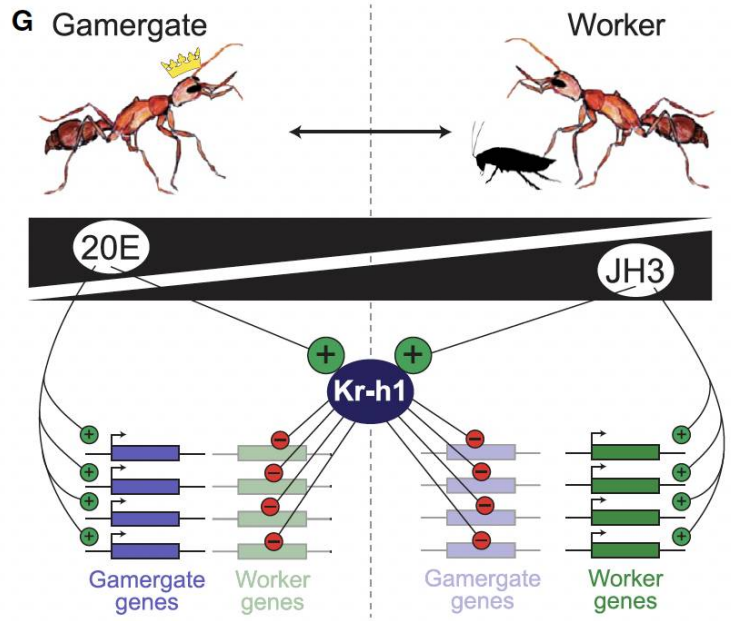
Supervisor: Alun Jones

Background:Comparative analysis of Kruppel. A TF involved in eusocial behaviour across hymenoptera and blattodea

Aim: Possible areas include; Selection, protein dynamics, Juvenile hormone interactions

Method: Wide scope for varying computational analysis and investigations.

References:



Proposed model in caste flexible ant (Gospocic et al 2021)

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Blattodea transcription factor complexity

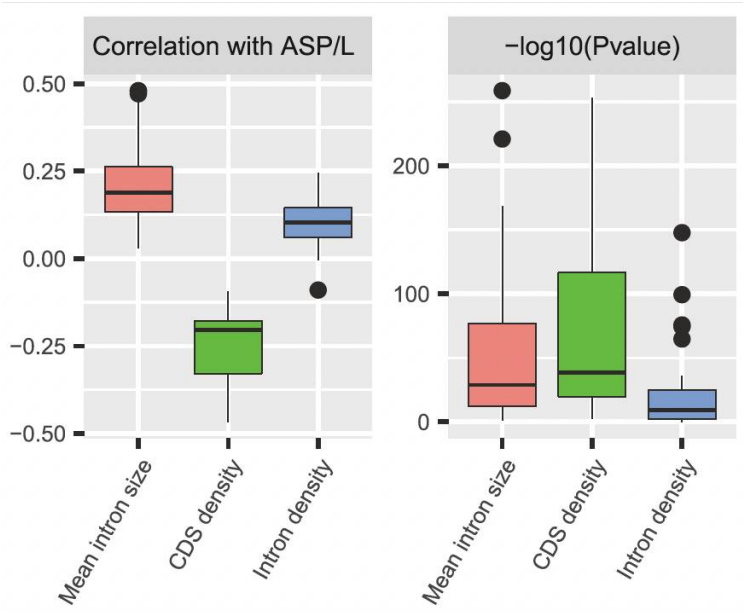
Supervisor: Alun Jones

Background:Comparative analysis of intron and isoform variation in blattodea TFs. Positive correlations with alternative splicing and organismal complexity

Aim: Aim to identify relationship with TF complexity and eusocial evolution

Method: Use of comparative phylogenetic methods

References:



Correlation and significance between organismal complexity and alternative splicing presence / level (Yang et al 2021)

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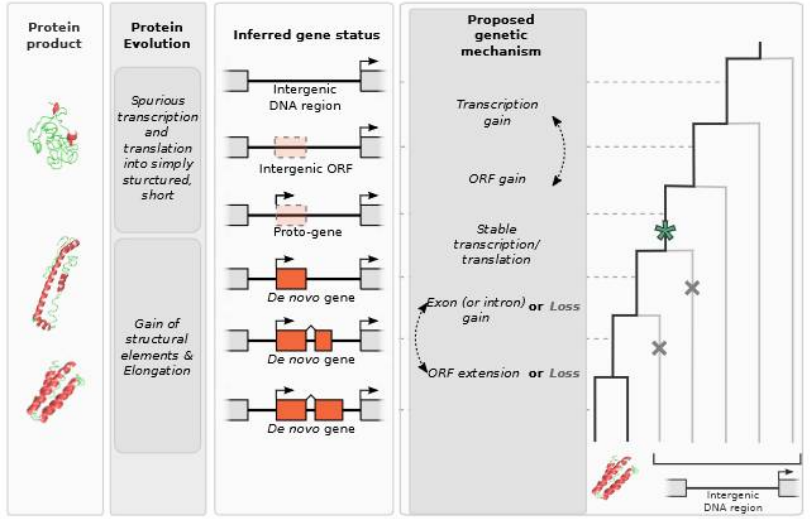
De novo Protein projects (all lab based) - Background

Supervisor: Andreas Lange and Margaux Aubel

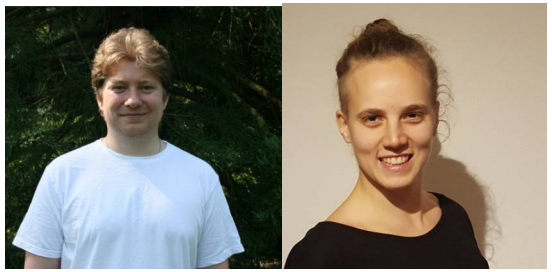
Background: Different species have different proteins encoded in their genome. Today we know that proteins do not only evolve by duplication and divergence of existing proteins but also arise from previously non-coding DNA. These proteins are called *de novo* proteins. Their properties are still poorly understood and their experimental analysis faces major obstacles.



Requirements:

- Interest in evolution at the level of individual proteins
- Interest in lab work on DNA and protein level and basic knowledge of PCR, DNA-cloning, protein expression & purification

References:
1. Lange A, Patel, PH, Heames B, Damry, A, Saenger, T, Jackson, CJ, Findlay GD, Bornberg-Bauer E Structural and functional characterization of a putative de novo evolved gene essential for male fertility in Drosophila
Nat Comm, 2021 https://doi.org/10.1038/s41467-021-21667-6
2. Bornberg-Bauer, E, Hlouchova, K, Lange A Structure and Function of Naturally Evolved de novo Proteins COSB, 2021



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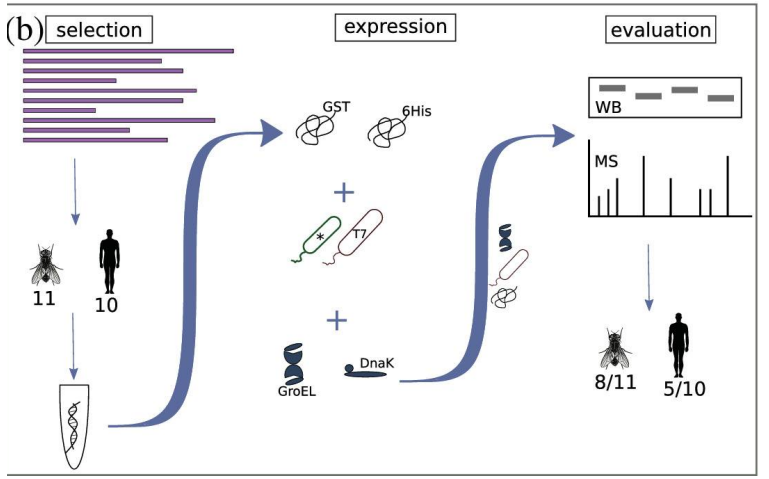
Expression, purification and analysis of putative de novo proteins (2 Students)

Supervisor: Andreas Lange and Margaux Aubel

Aim: In this project we aim to express, purify and analyse different putative de novo proteins from Homo sapiens or Drosophila melanogaster. Genes of interest will be cloned into respective vectors and proteins expressed in E. coli in combination with/without chaperones to enable soluble expression. Proteins will be purified using Affinity chromatography and first analysis will be conducted using SDS PAGE and Western Blots. Further experimental characterization will be performed to test folding and function, such as tat assay (folding), thermal shift assay (folding) and CD (structure).

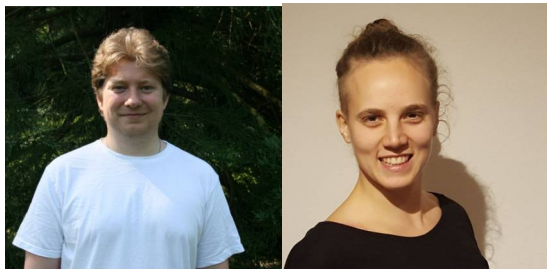


(a) Mechanism of chaperone assisted protein folding (b) Overview of the workflow on de novo protein expression: candidate proteins, expression using different tags (GST and His), different E. coli cells (star, T7), and different chaperones (GroEL and DnaK systems). The success of protein expression will be verified by Western blot (WB) and mass spectrometry (MS)

Methods:

- Molecular biochemistry (PCR, cloning, Sequencing & expression and purification of proteins
- Biochemical characterization of the proteins via SDS-PAGE & Western Blot

References: 1. Eicholt LA, Aubel M, Berk K, Bornberg-Bauer E, Lange A. Heterologous expression of naturally evolved putative de novo proteins with chaperones.Protein Science. 2022 https://doi.org/10.1002/pro.4371



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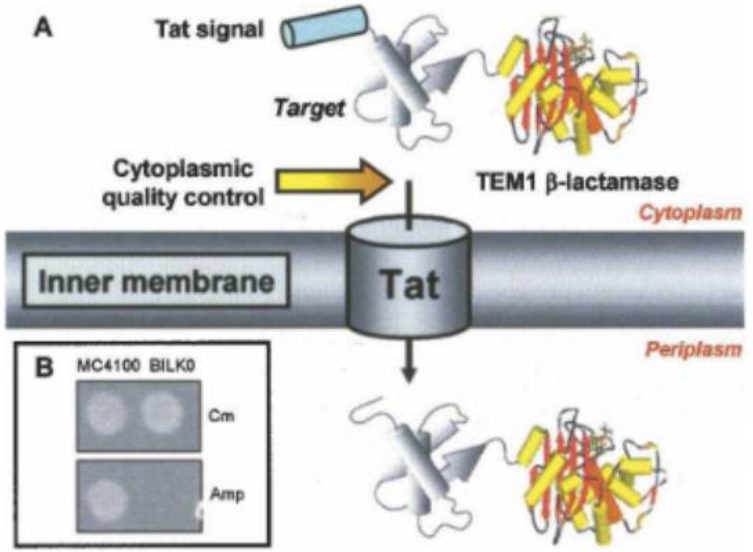
Expression, purification and analysis of putative *de novo* proteins (2 Students)

Supervisor: Andreas Lange and Margaux Aubel

Aim: Different kinds of *de novo* genes should be cloned into the pSALect vector using different restriction sites. In a follow up assay the possible folding of these *de novo* gene constructs should be controlled via ampicillin agar plates. The idea is that only cells, expressing the *de novo* protein + lactamase construct will grow.

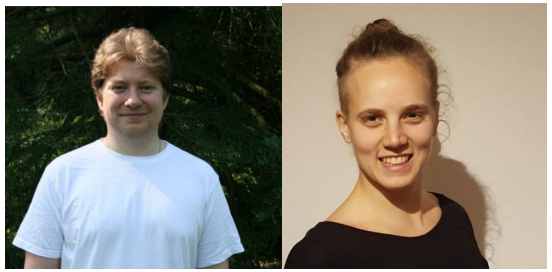


Exploiting the Tat pathway's folding quality control feature for monitoring protein solubility.

Methods:

- Molecular biochemistry (DNA-cloning, PCR, restriction digest, ligase, etc.) & plate based solubility assay
- Biochemical characterization of the proteins via SDS-gels

References:. Adam C. Fisher, Wookin Kim, and Matthew P. Delisa Protein Science, 20061



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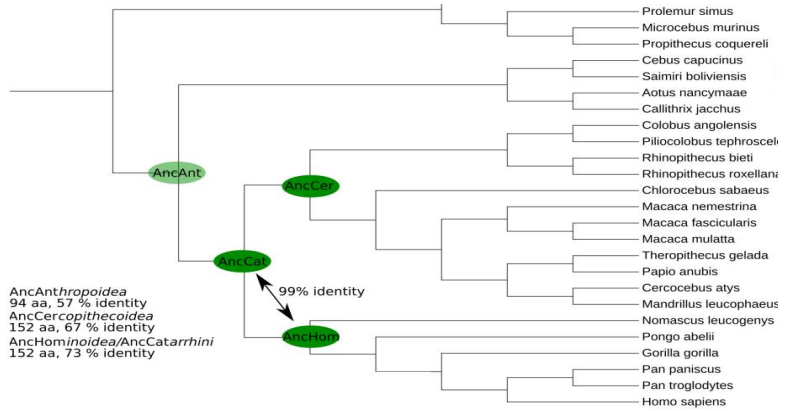
Ancestral reconstruction - Characterization of ancestral proteins of a possible *de novo* protein from *Homo sapiens* (1 Student)

Supervisor: Andreas Lange

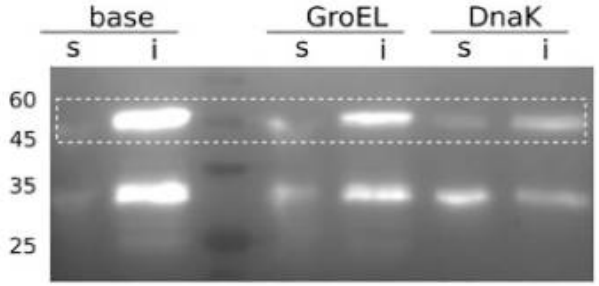
Aim: In this project we want to express and characterize different ancestral proteins of a putative *de novo* protein from *Homo sapiens*. Structural predictions of these ancestral *de novo* proteins show already some conserved regions. Within this work the ancestral proteins (B Cer, B Hom, and B Ant) of WT Human B shall be solubly expressed. After successful expression, the proteins will be purified and further characterized.

Methods:

- Expression and purification of proteins
- Biochemical characterization of the proteins via SDS-gels, maybe Circular Dichroism and Thermal Shift Assay



ASR tree of Human B and target ancestors



Expression of WT Human B

References: 1. Eicholt LA, Aubel M, Berk K, Bornberg-Bauer E, Lange A. Heterologous expression of naturally evolved putative de novo proteins with

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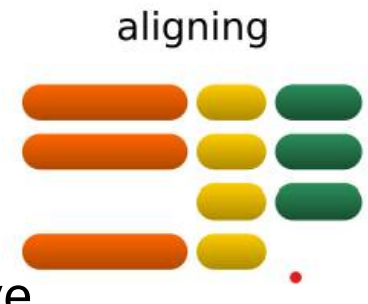
Domain arrangement alignment



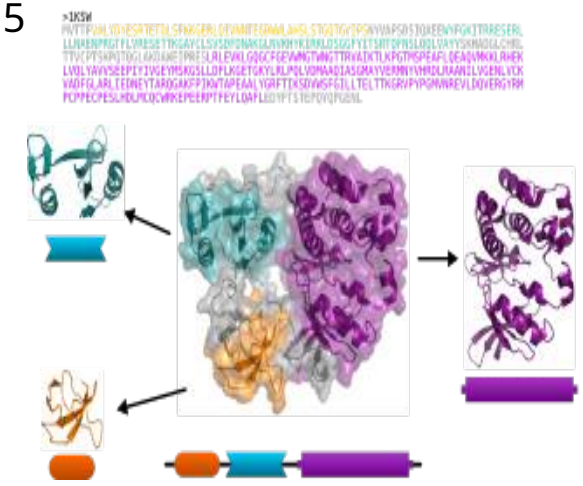
Supervisor: Carsten Kemena

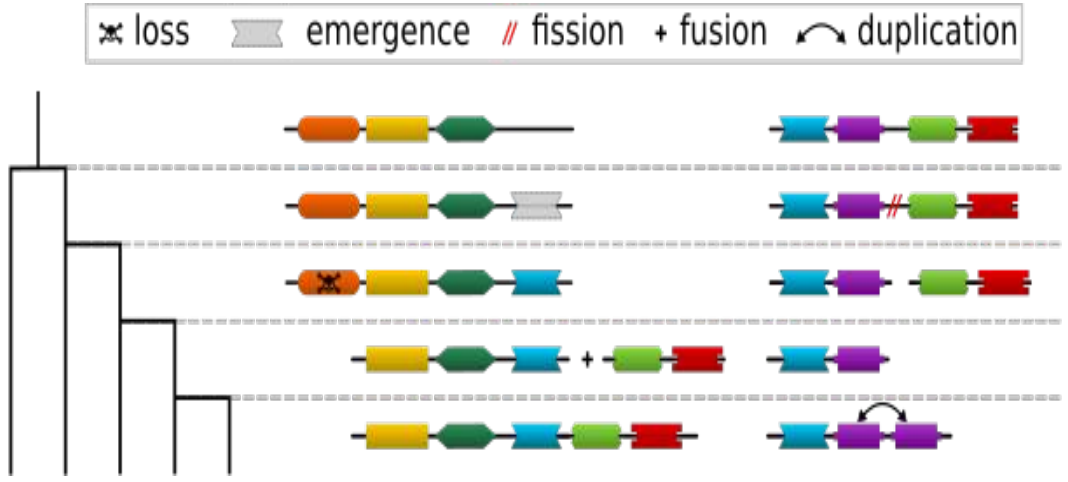
Background: Protein domains are reusable, functional units. A set of protein domains are called domain arrangements. Those domain arrangements change over time. Their analysis is important to improve the understanding of evolution and the functional change of proteins.

Aim: Development of an alignment program for domain arrangements.

Method: Write a new domain arrangement aligner based on MDAT. Make use of the C++ core library we developed.

References: Kemena *et al.* MDAT Aligning multiple domain arrangements, BMC Bioinformatics 2015





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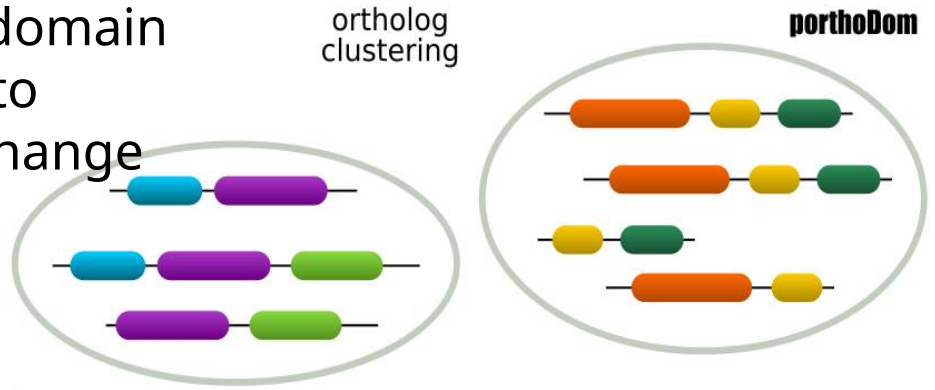
Protein ortholog clustering

Supervisor: Carsten Kemena

Background: Protein domains are reusable, functional units. A set of protein domains are called domain arrangements. Those domain arrangements change over time. Their analysis is important to improve the understanding of evolution and the functional change of proteins.



Aim: Development of a method for orthology detection based on protein domains.

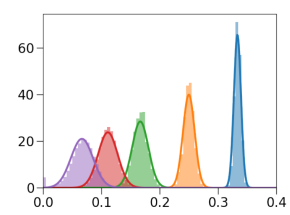
Method: Make use of the C++ core library we developed to seperate domain arrangements into potentially overlapping clusters. Sequence similarity of domains should be takein into account.

References: Persson *et al.* Domainoid: domain-oriented orthology inference, BMC Bioinformatics 2019

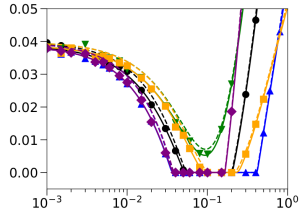
bornberglab.org

Theoretical Biology

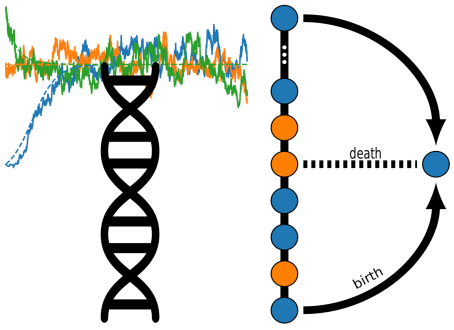
Pete Czuppon



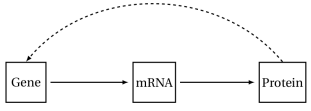
evolution



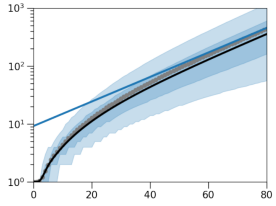
gene regulation



ecology



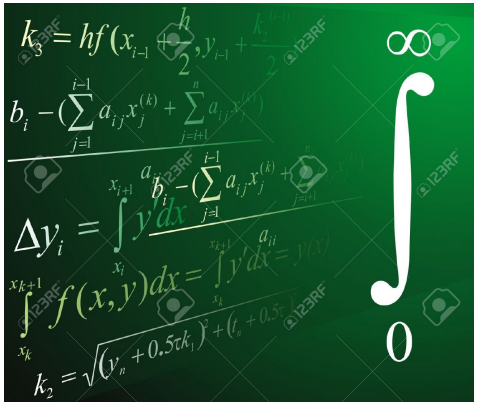
epidemiology



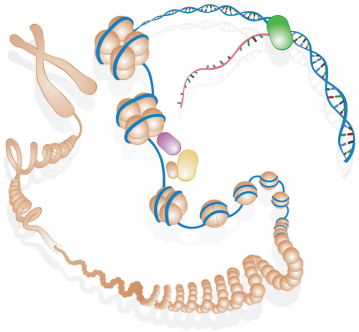
coding

&

maths



Potential projects



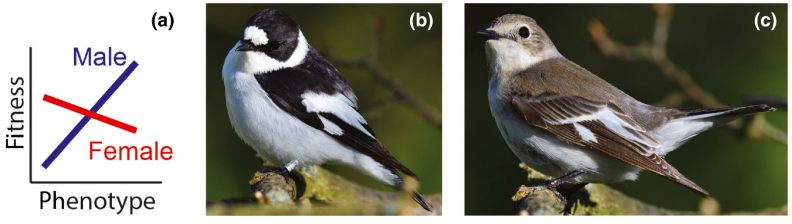
Transposable elements (TEs)

(self-replicating genetic elements)

→ study TE dynamics within the genome
(genome evolution)

Antibiotic resistance

→ study coexistence of antibiotic-resistant and -sensitive cells
(evolutionary epidemiology)



Sex-specific selection

→ study invasion of new alleles
(population genetics)

Project module/BSc topics in the Gadau group

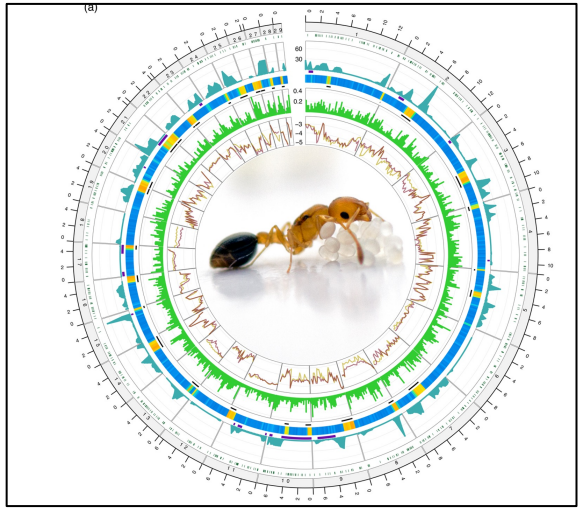
Background:
Evolution of sociality (and other things) in ants

Approaches:
lab work, field work, genomics, transcriptomics, evolutionary theory

Contact: gadauj@uni-muenster.de

Insect Evolutionary Genomics (Dr. Lukas Schrader)

Esther	Molecular biology & evolution	***Transposable elements*** *in evolution*
Simo	Population genomics	*The genomes of* ***invasive ants***
Sandra	Genomics & microCTs	***Olfactory systems*** *in ants*
Janina	Evolutionary genomics	***Horizontal gene transfers*** *in ants*
Josh	Morphology, transcriptomics	*Phenotypic robustness of* ***superorganisms***



Contact: Lukas.Schrader@wwu.de


Esther


Josh


Simo


Sandra

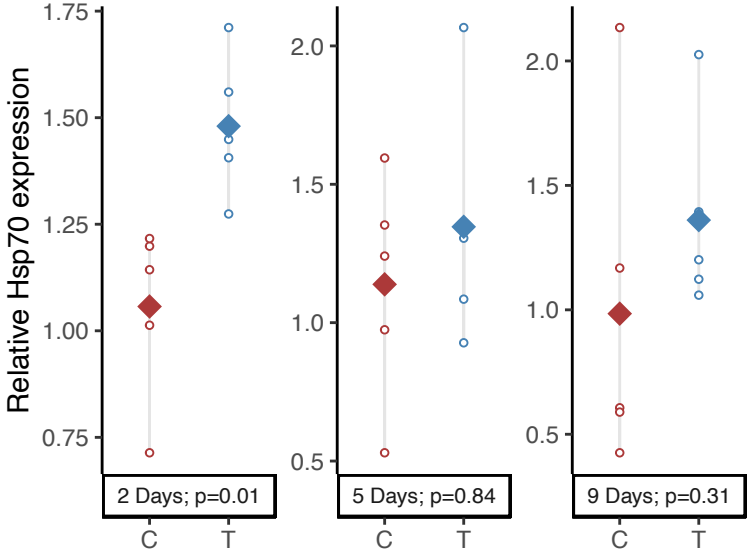

Janina

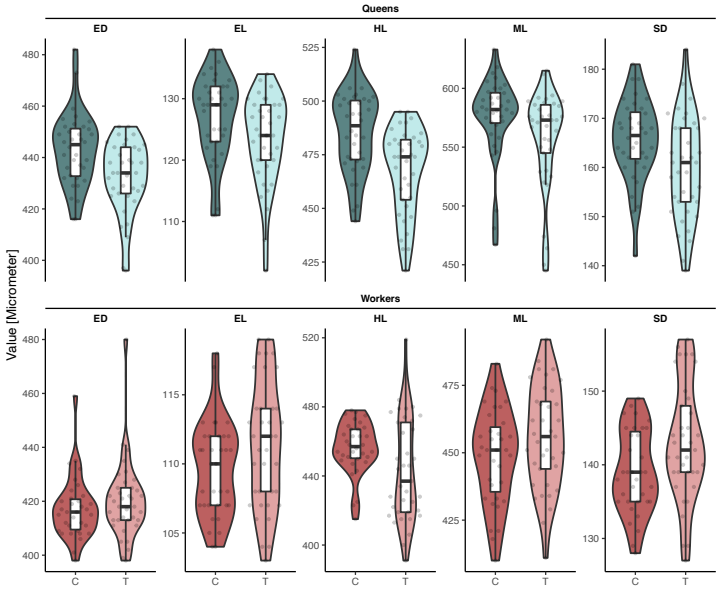

Lukas

Insect Evolutionary Genomics (Dr. Lukas Schrader)

P1: Fecundity in ants treated with a chemotherapeutic drug.

Background: *The drug 17-DMAG reduces the activity of HSP90, a key chaperone in eukaryotic cells. This can have severe effects for the organism's phenotype with some remarkable evolutionary implications.*





Aim: *Understanding how treating ant queens with the drug 17-DMAG impacts reprodcutive output of ant colonies.*

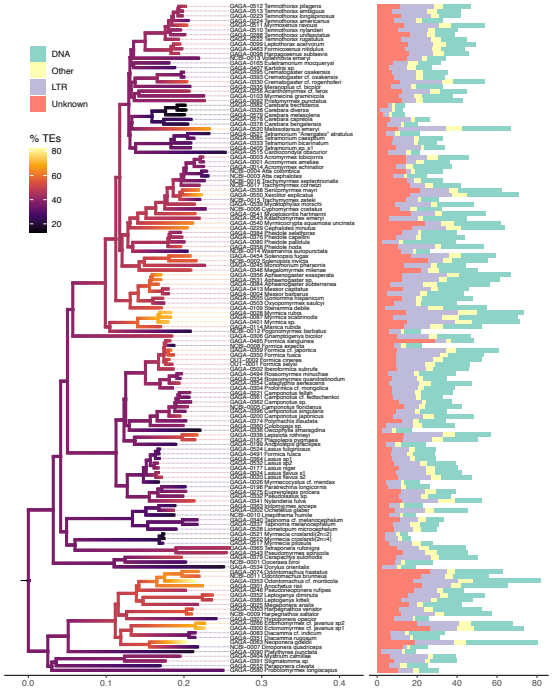
Methods: *qPCR, RNA extraction, ant care, ant morphology, coding in R, evolutionary thinking*

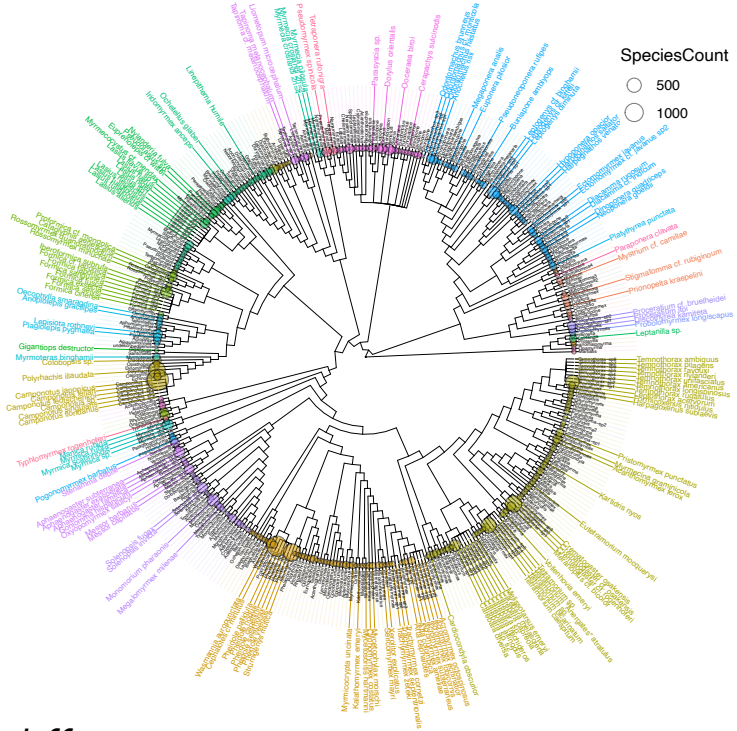
Contact: Lukas.Schrader@wwu.de

Insect Evolutionary Genomics (Dr. Lukas Schrader)

P2: Analyze the expression of transposons in RNAseq data of many different ant species.

Background: *Transposable elements (TEs, "jumping genes") are important drivers of genome evolution. The impact of TEs on ant genomes has been understudied so far.*





Aim: *Exploring the expression of active TEs in >50 different ant genera.*

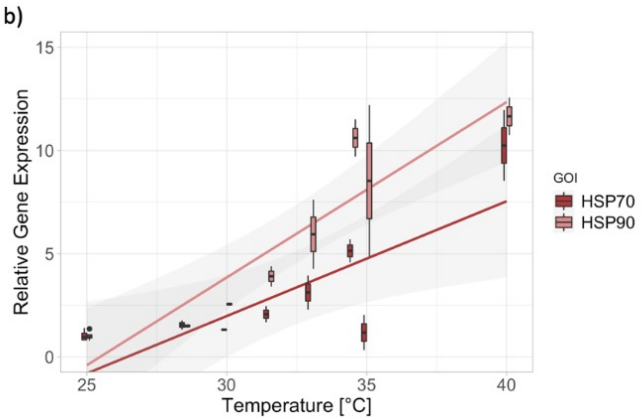
Methods: *data wrangling, gene expression analysis, coding in bash & R, evolutionary thinking*

Contact: Lukas.Schrader@wwu.de

Insect Evolutionary Genomics (Dr. Lukas Schrader)

P3: Establish and conduct a heat-shock experiments using infrared light.

Background: *Heatshock is a classic experimental approach to manipulate phenotypic traits in insects. However, applying such treatments to entire ant colonies is difficult, because the disturbance to the nest should be minimized.*



Aim: *Building an experimental setup to perform regular heatshock experiments on entire ant colonies. Apply this setup to study the effect of heatshocks on e.g. morphology, fecundity and behavior in ants.*

Methods: *"building stuff", experimental design, ant care, qPCR thinking*

Contact: Lukas.Schrader@wwu.de

Social Evolution in *Pogonomyrmex californicus*: "Epigenetic re-programming of queen behavior"

♀ Haplometrosis → Evolution/Maintenance of tolerance for cofounding/cohabitating queens → ♀♀♀ Pleiometrosis

Background

- Tolerant and aggressive queens are equally successful founding colonies
- Mutations -> *supergene*, genes for epigenetic modifications/chemical communication
- Expression differences for different social types in different social environments (phenotypic plasticity/social niche construction)
- Phenotypic plasticity modulated by epigenetic mechanisms?

Bachelor Project: Determine if aggressive behavior in *P. californicus* queens is regulated epigenetically.

Methods: Histone modifications (CBP,HDACs) to target regulatory enzymes and re-program behavior, Methylation profiles, Experimental behavioral studies (different social contexts), DNA-RNA extraction, statistical analysis, coding in R.

Coordination: PhD Tania Chavarria Pizarro (tchavarria@uni-muenster.de)
Project Manager: PhD Jürgen Gadau.