Universität Münster

Projektmodul & Bachelorprojects 2026

Prof. Dr. Erich Bornberg-Bauer	Molecular Evolution & Bioinformatics
Prof. Dr. Joachim Kurtz	Animal Evolutionary Ecology
Prof. Dr. Kai Müller	Evolution & Biodiversity of Plants
Prof. Dr. Jürgen Gadau	Molecular Evolution and Sociobiology

Retraining the ADOPT Model Using ESM2 Embeddings

Supervisors: Bharat Ravi b.ravi@uni-muenster.de

Background: Some proteins or protein regions do not fold into a fixed 3D structure but remain flexible or “disordered.” Understanding the determinants of disorder would be a key to understanding the evolution of these proteins.

ADOPT is a disorder prediction tool that is trained by first encoding protein sequences using the protein language model ESM1-b, and then using a linear model to map embeddings to disorder values.

Aim: To retrain ADOPT using ESM2 that can encode protein properties better than ESM1-b

Methods: *(Programming, Statistics, Machine Learning)*

- Generate per-residue embeddings using ESM2.
- Retrain the lasso regression model to predict experimental disorder scores.
- Compare results with the original ESM1b-based model

Literature (DOI):

10.1093/nargab/lqad041; 10.1126/science.ade2574; 10.1038/s41598-019-41644-w

Understanding protein structure evolution using evolutionary simulations

Supervisors: Bharat Ravi b.ravi@uni-muenster.de

Background: Some novel proteins can evolve without an ancestry (*de novo*) and are less likely to be structured. To understand how structure can emerge in proteins, evolutionary simulations as well as lab evolutuion can be performed.
This project involved analysis of simulation data for 350000 random sequences of different lengths and composition.

Aim: Perform statistical analysis of evolutionary simulation data using generalized linear models

Methods: *(Programming, Statistics, Machine Learning)*

- Understand the simulation data
- Fit models to understand the how some factors (length, composition) affect evolutionary outcomes
- Perform additional simulations if necessary (using existing program)

Literature (DOI):
10.1093/nargab/lqad041; 10.1126/science.ade2574

Genome annotation of fruitfly genomes using the deep learning based gene predictor Tiberius

Supervisor: Marie Kristin Lebherz (m.lebherz@uni-muenster.de)

Background: Genome annotation is important for many genomic analyses. Until recently, the best performing tools required extrinsic evidence (e.g. RNA sequencing data). Tiberius is a new deep-learning-based tool that can predict genes from the genome sequence alone with similar quality as evidence-based tools.

Aim: The aim of this project is to annotate a set of fruitfly genomes with Tiberius and check the quality of the resulting annotations.

Methods: The student will learn how to annotate genomes and use software to check the quality of the resulting annotations.

Literature

Gabriel, Lars, et al. "Tiberius: end-to-end deep learning with an HMM for gene prediction." *Bioinformatics* 40.12 (2024): btae685.

Improving Domain Annotation using secondary structure prediction

Supervisors: Carsten Kemena-Rinke (c.kemena@uni-muenster.de)

Background: Protein domains are used in many evolutionary analyses. It is therefore important to have a good annotation. Different methods exists to improve them.

Aim: Incorporate secondary structure prediction into the IDA program to improve protein domain annotation

Methods:
- C++ programming
- secondary structure prediction
- benchmarking

Literature

Payssan-Lafosse et al, The Pfam protein families database: Embracing AI/ML, NAR, 2025

Terrapon et al, Detection of new protein domains using co-occurrence: application to Plasmodium falciparum, Bioinformatics 2009

Structural properties of small peptides from"non-coding" RNA

Investigating the structure of miRNA-encoded peptides (miPEPs)

Supervisors: Claire Patiou, c.patiou@uni-muenster.de

Background:

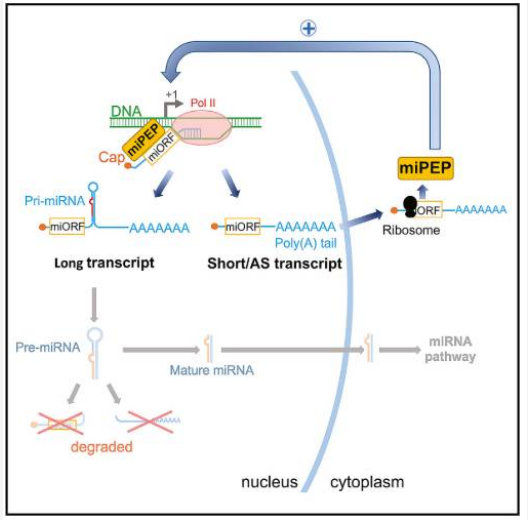
microRNA (miRNA) primary transcripts can encode peptides (miPEPs) that have recently beenuncovered as key regulators of plant miRNA expression. Yet, to this day, the structural characteristics of these peptides remains unknown. We have no information on their amino acid composition, hydrophobicity, domains, or structure.

Aim:

Determine whether miPEPs harbor specific structural properties that distinguish them from other types of polypeptides

Methods:

- Prediction of protein disorder by tools like IUPred
- Prediction of protein structure by AlphaFold2 or 3

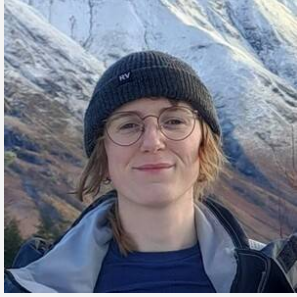


- Suggested mechanism fo the effect of miPEPs on miRNA expression

Literature

- Lauressergues, D. et al. (2022), Cell Reports, doi:10.1016/j.celrep.2022.110339.
- Prasad, A., Sharma, N. and Prasad, M. (2021), Trends in Plant Science, doi:10.1016/j.tplants.2020.12.004.
- Aubel, M., Eicholt, L. and Bornberg-Bauer, E. (2023), F1000Research, https://doi.org/10.12688/f1000research.130443.1.
- Middendorf, L. and Eicholt, L.A. (2024), Proteins: Structure, Function, and Bioinformatics, https://doi.org/10.1002/prot.26652.

Drosophila melanogaster testis transcription factors bidning sites prevalence



Supervisors: Apolline Petit a.petit@uni-muenster.de

Background:

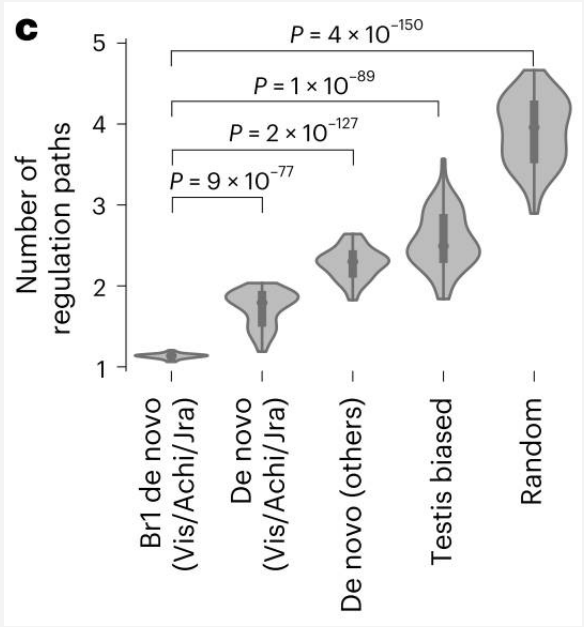
Inspired from Peng et al., 2025 “Gene regulatory networks and essential transcription factors for de novo-originated genes”. In this paper, they found that ⅓ *de novo* gene are regulated by 3 transcription factors (TFs), that are only expressed in the testis.

Aim:

Hypothesis: testis TFs have more prevalent binding site to facilitate regulation of new genes in those tissues.
Goal: determine if TFs specific to *D. melanogaster* testis have binding sites that can emerge more often by random than other tissue-specific TFs.

Methods:

Choose tissue-specific TFs. Use public database. Detect TFs binding sites with FIMO. Bash and R programming.



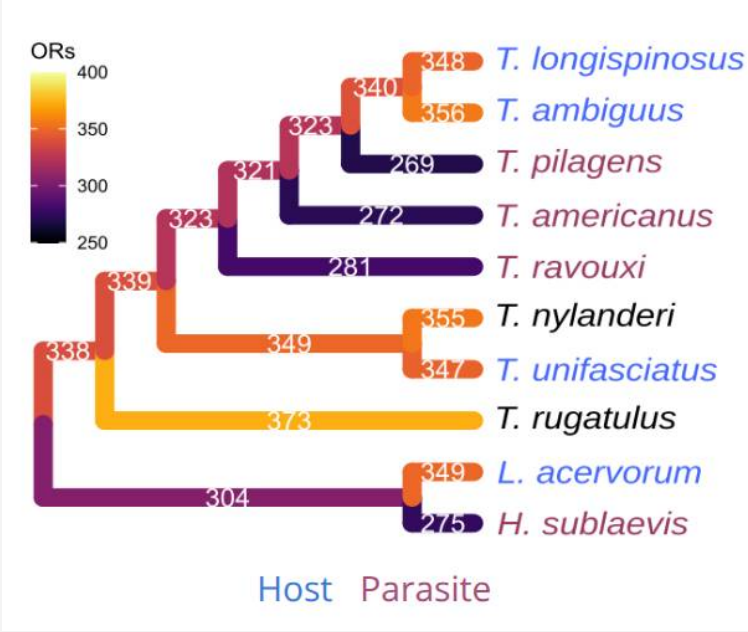
Literature
Peng, J., Wang, BJ., Svetec, N. et al. Gene regulatory networks and essential transcription factors for de novo-originated genes.
Nat Ecol Evol 9, 1487–1498 (2025). https://doi.org/10.1038/s41559-025-02747-y

Temnothorax rugulatus (ant) de novo genes expression

Supervisors: Apolline Petit a.petit@uni-muenster.de

Background:

There is numerous *de novo* genes found in the ants from the Temnothorax genus, in which there is multiple event of parasitic behavioral innovation. T. rugulatus is not a parasite nor a host from these parasites, in contrary to two other species already investigated by the team. The goal of this project is to identify if de novo genes are more or less numerous than in parasitic or host species from the same genus.



Aim:

Hypothesis: *T. rugulatus* have *de novo genes* expression patterns different from parasitic and host species from the same genus.
Goal: Identify if de novo genes are more or less numerous than in parasitic or host species from the same genus.

Methods:

Download and process ~130 RNAseq from public database. R scripts to detect *de novo* gene expression and in which tissues they are expressed. Co-expression analysis of de novo genes in R.

Literature

https://doi.org/10.1111/mec.17649
http://biorxiv.org/lookup/doi/10.1101/2024.12.31.630940

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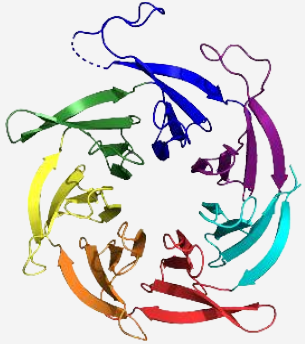
Analysis of Protein Repeats: Evolution of Cryptic Oligo-peptide Repeats

Supervisors: Matthew Merski mmerski@uni-muenster.de

Background: Oligo-peptide repeats are short (20-50 residues) stretches of highly conserved, repeated sequence. About 25-35% of all proteins contain repeats although many of these have gone unnoticed, even in proteins with known structures. We have identified thousands of clusters of proteins that contain these cryptic oligo-peptide repeats.

Aim: The student will focus on one of these clusters, studying, analyzing, and categorizing one of these repeat clusters. The repeat will be formally defined and its evolutionary relationship to other proteins will be determined.

Methods:
- multiple sequence alignment
- statistical analysis of protein sequence composition
- dot-plot analysis



Kelch repeat

TPR repeat

Literature
1) Schuler, A., Bornberg-Bauer, E. “Evolution of Protein Domain Repeats in Metazoa” Mol. Biol. Evol. 33, 3170 (2016)
2) Kajava, A.V. “Tandem repeats in proteins: from sequence to structure” J. Struct. Biol. 179, 279 (2012)
3) Merski, M. et al. “Self-analysis of repeat proteins reveals evolutionary conserved patterns” BMC Bioinformatics 21, 179 (2020)

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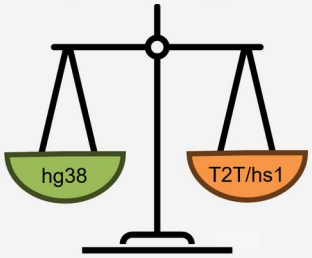
Assessing Assembly Quality's Impact on *De novo G*ene Identification

Supervisors: Sarah Lucas (s.lucas@uni-muenster.de)

Background: With the advancement of new sequencing technologies, more complete genomes are available for us to ask and answer biological questions. Because of this enhanced completeness, we expect this would allow greater power to detect *de novo* genes compared to older assemblies. This has not yet been formally evaluated.

Aim: For one chromosome in hg38 and hs1, compare how many *de novo* genes are identified using DENSE.



Methods: The student will learn some of the comparative genomic techniques including file manipulation, use of phylostratigraphy for *de novo* gene identification using DENSE, and if time permitting, methods to characterize the new *de novo* genes.

Literature: De Novo Genes – Zhao Annual Review of Genetics 2025; DENSE – Roginski GBE 2024; Human T2T - Nurk Science 2022; Ape T2T - Yoo Nature 2025

Laboratory evolution of de novo genes
Fluorescence measurement & Library Screening

Supervisors: **Jamil Serwanja** jamil.serwanja@uni-muenster.de

Background:

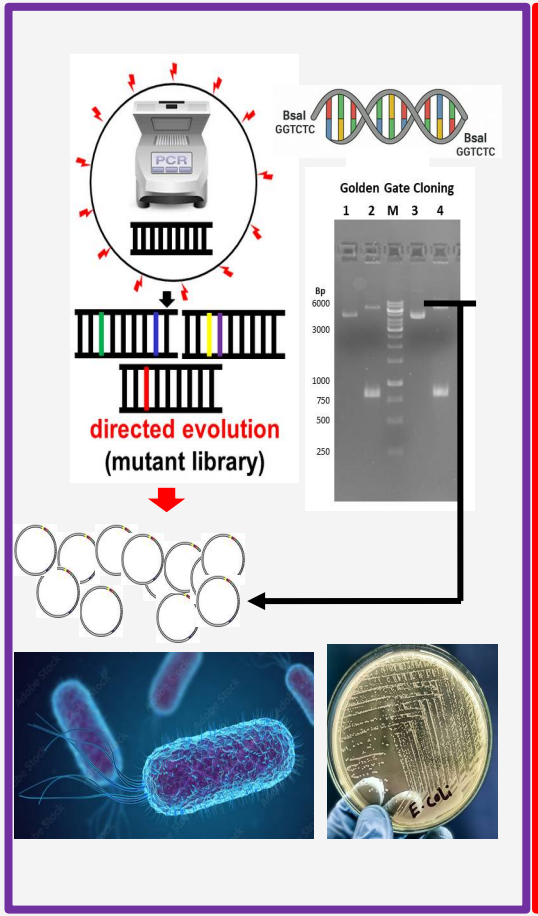
De novo genes arise from previously non-coding intergenic regions. *De novo* proteins have been predicted to have a high degree of disorder, are mostly insoluble and at times toxic leading to negative selection within the population.

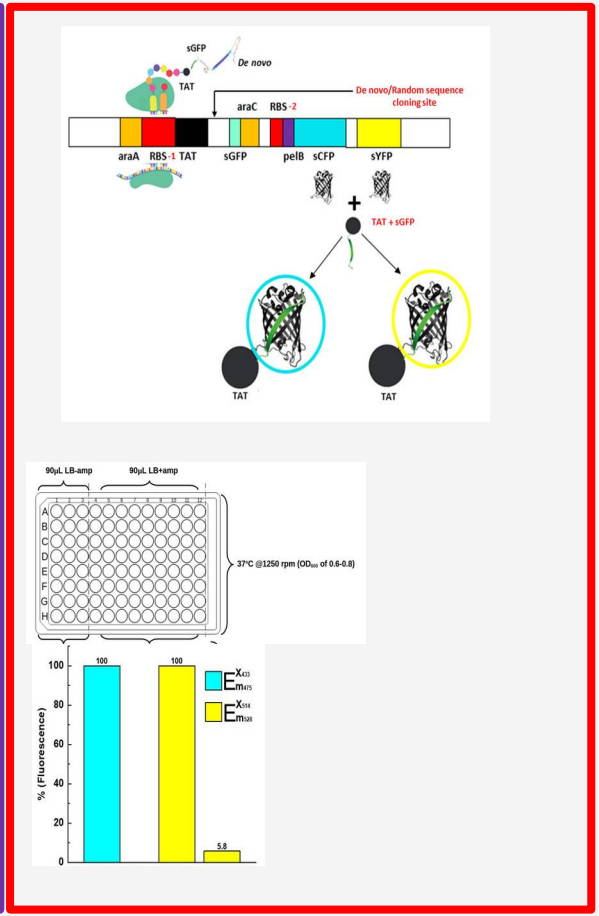
Aim:

The goal of the current project is to undertake a laboratory evolution of a selected *de novo* gene from an unstructured towards structured protein variant. By using evolved solubility as selection marker. This project will give crucial information as to how many mutation events could be necessary to attain structure among some *de novo* genes.

Methods:

-Molecular cloning by Polmerase Chain Reaction (PCR)
-Cell culture
-Library screening by Fluorescence measurement
-Sequence analysis (Multiple sequence alignments)





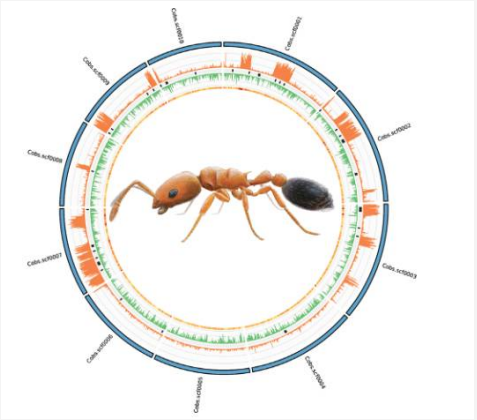
Transposable element diversity in ant genomes

Supervisors: Dr. Raziyeh Abdilzadeh (r.abdilzadeh@uni-muenster.de)

Background: Transposable elements (TEs) are mobile DNA sequences that make up a large fraction of eukaryotic genomes, including animals and plants. In many species, TEs account for a substantial proportion of the genome, for example, nearly half of the human genome is derived from transposable elements. Ant genomes provide an excellent comparative system due to their diversity in lifestyle and social organisation.

Aim: To compare TE classes and their genomic proportions across ant species using existing genome data.

Methods: Analysis of assembled ant genomes using existing RepeatMasker outputs, followed by summarisation and visualisation of transposable element class composition. All analysis scripts will be provided and explained.



Schrader, L., & Schmitz, J. (2019)

Literature:

- Wicker et al. 2007, A unified classification system for eukaryotic transposable elements: https://www.nature.com/articles/nrg2165
- Schrader et al. (2014), Transposable element islands facilitate adaptation to novel environments in invasive species https://www.nature.com/articles/ncomms6495

Projektmodul und BSc-Arbeiten in der AG Kurtz

Projektmodul

Studienarbeit

- "Research proposal" zur geplanten BSc-Arbeit: wissenschaftlicher Hintergrund (Literatur), Hypothesen, experimentelles Design, erste Daten…
- i.d.R. in engl. Sprache

Literatur-Seminar

- Vorstellen und Leiten der Diskussion zu einer Original-Forschungsarbeit
- aktive Teilnahme an allen Terminen

Aktive Beteiligung an der wissenschaftlichen Arbeit in der AG Kurtz

- Teilnahme an *group meetings* (Di. 9.11h)
- IEB Seminar (Di. 16-17h)
- Weitere Treffen zur Planung der Arbeit, etc.
- Start der Laborarbeit, Erlernen relevanter Methoden, etc.

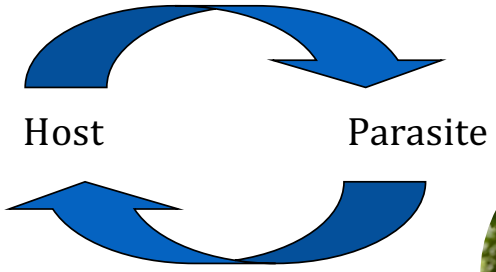
Projektmodul und BSc-Arbeiten in der AG Kurtz

BSc-Arbeit

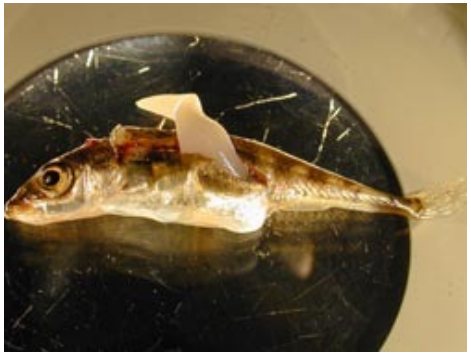
- Wissenschaftliche Arbeit (eigenständige Planung und Ausarbeitung der Experimente, Auswertung der Daten mittels Statistik, Vorstellen und Diskutieren der Pläne und Ergebnisse)
- Dies ist eine aktuelle Forschungsthematik, daher ist das Ergebnis offen
  (kann motivierend aber auch frustrierend sein)
- Selbständiges Arbeiten (Teamwork, unterstützt durch Techn. Mitarbeiter, MSc-Stud., Doktoranden, Postdoktoranden, Professor; i.d.R. jeweils ein unmittelbarer Betreuer)
- Verfassen der Arbeit mgl. in engl. Sprache, Struktur orientiert an Forschungs-Publikation, ca. 40-80 Seiten Umfang insgesamt
- Abschlussvorträge

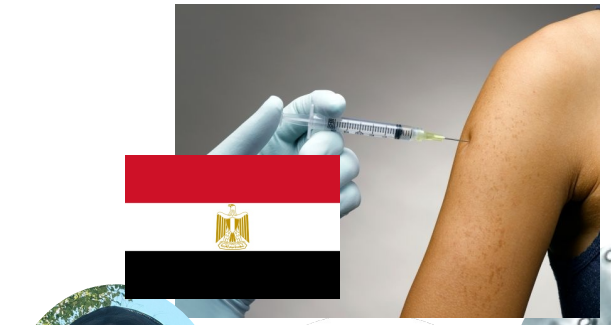
Kurtz group – our research in a nutshell

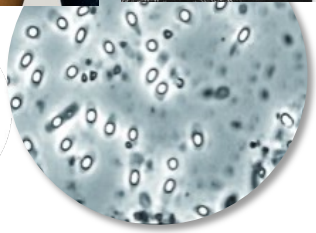
Host-Parasite Coevolution & Evolution of Immune Defence



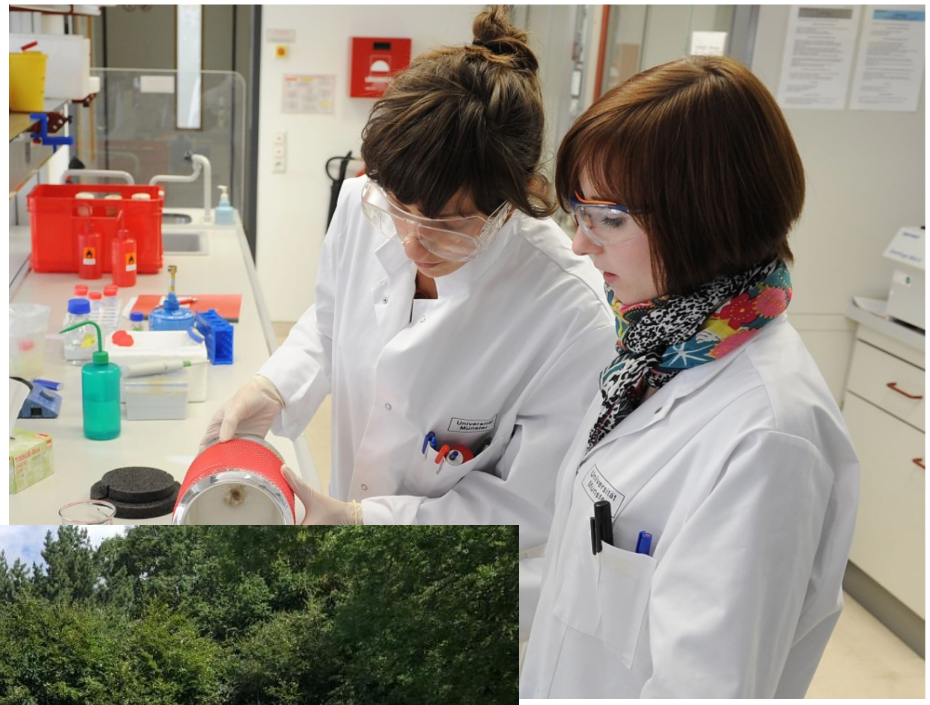
Red Queen Hypothesis:
Arms race between host and parasite
"In this place it takes all the running you can do, to keep in the same place."







Fieldwork



Labwork

From Bacteria to Fungi: Testing Cross-Resistance in Quinone-Constructed Niches

(1 student)

Supervisor: Dr. Ana Korša

Background:

- *Tribolium castaneum* secretes antimicrobial **quinones** that modify its environment and provide **external immunity**.
- This chemical **niche construction** benefits conspecifics and offspring and may **accelerate adaptation under pathogen pressure**, shaping host–pathogen evolution.

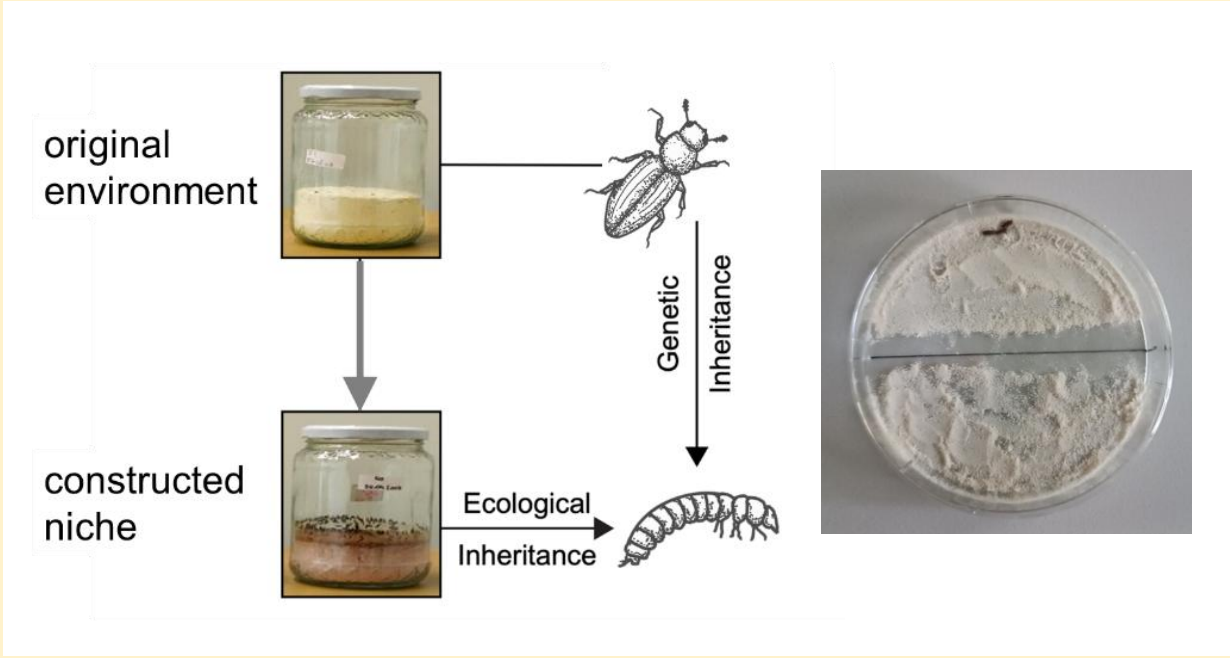
Model system:

Aims:

To test whether
(1) **non-producing larvae benefit from quinone-enriched environments** and whether
(2) beetle lines evolved under bacterial pathogen pressure show **cross-resistance to a novel fungal pathogen**.

Methods:

- insect rearing
- RNA interference
- bacterial and fungal infections
- life history traits measures



The effect of manipulative parasites on trophic specialization in Greenlandic sticklebacks

(2 students)

Supervisors: Maja Drakula and Dr. Jaime M. Anaya-Rojas

Model system: Three-spined sticklebacks (*Gasterosteus aculeatus*) & tapeworm (*Schistocephalus solidus*)

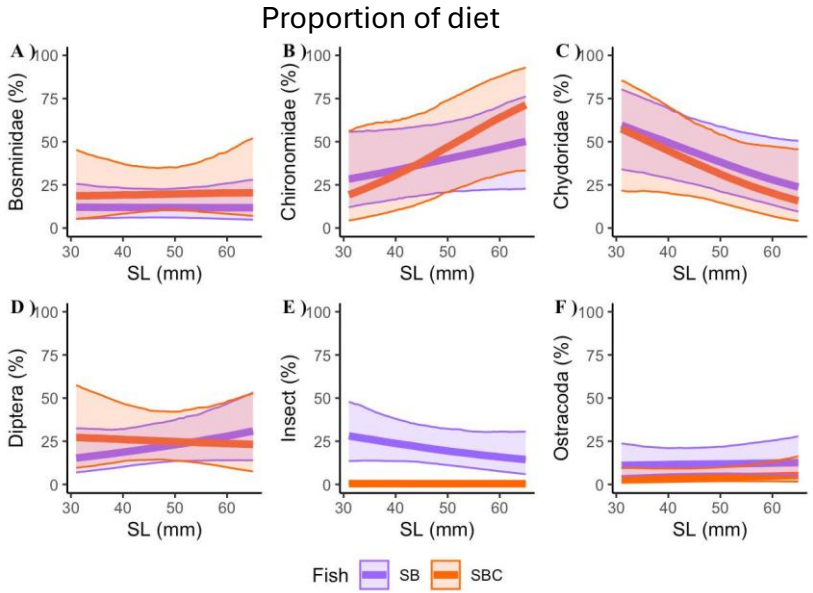
Background: **Trophically transmitted parasites** have strong effects on their host; however, whether these effects alter **ecological dynamics** is still unknown.

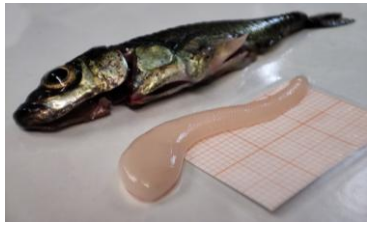
Aims (two projects):

1. Investigating the effect of parasites on **trophic specialization** in natural stickleback populations.
2. Analyzing **morphological variation** in sticklebacks based on the presence or absence of Arctic charr/*Schistocephalus solidus* in their habitat.

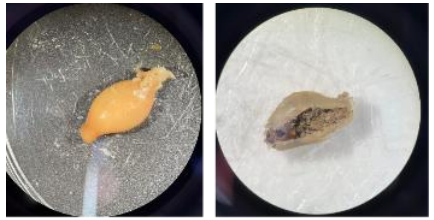
Methods:

- Dissections of stomachs
- Stomach content identification and analysis





Three-spined stickleback infected with *Schistocephalus solidus*



Dissected stomachs of three-spined sticklebacks

Dad's immune "memory" in beetles: sperm signal or female-mediated effect?

SUPERVISOR: Dr. Nora Schulz | nora.schulz@uni-muenster.de

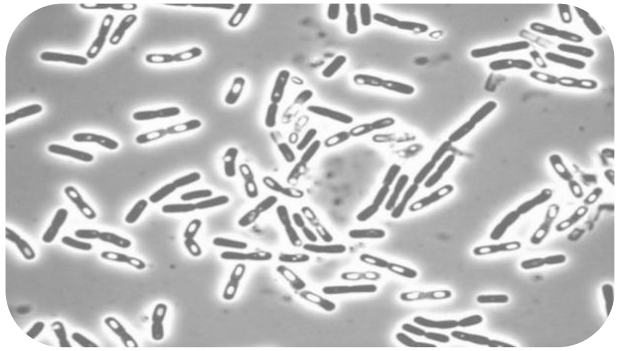
BACKGROUND

Insects can show a form of immune "memory": after an initial immune challenge, they may survive later infections better (**immune priming**).

This benefit can sometimes be passed to the next generation (**transgenerational immune priming, TGIP**) — even from **fathers**, despite no pregnancy or parental care.

How do fathers transmit this effect? sperm-borne (germline, epigenetic) or female-mediated transmission (via ejaculate effects/behavioral manipulation)

MODEL SYSTEM



AIMS

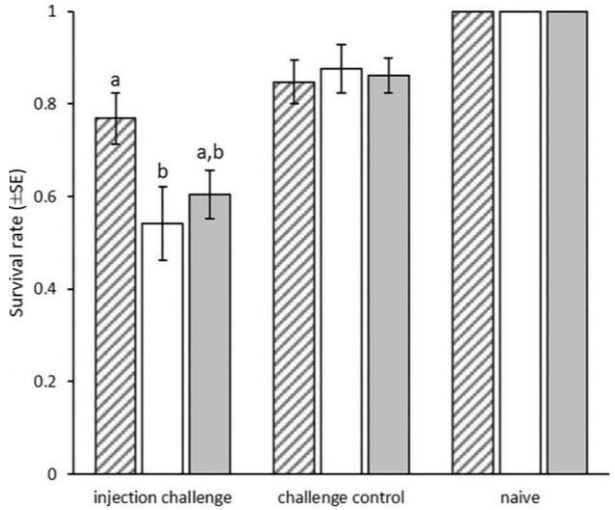
Quantify and distinguish the two transmission routes by:

- validating paternal TGIP
- quantifying sperm precedence
- testing route-specific patterns

(compare genetic and "step-genetic" offspring)

METHODS

- Insect rearing
- Priming & infection assays
- Mating assays
- Paternity scoring
- Data analysis and visualization in R



Establishing RNAi for *Dnmt1* in the rice weevil: tissue expression and reproductive function

SUPERVISOR: Dr. Nora Schulz | nora.schulz@uni-muenster.de

MODEL SYSTEM

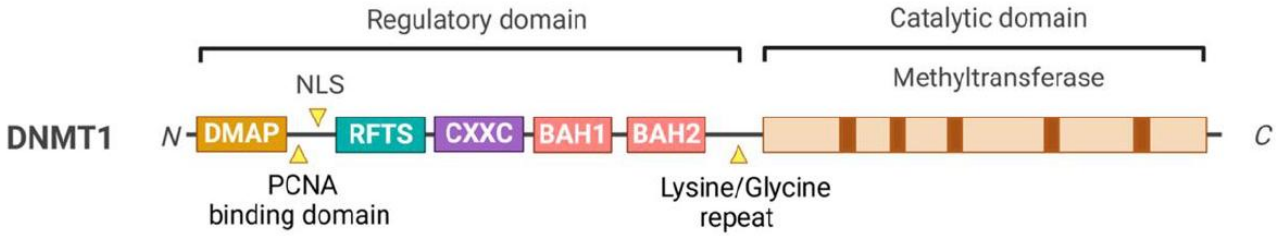
BACKGROUND

RNA interference is a powerful approach to knock down gene function in insects, but delivery efficiency can be highly species- and tissue-dependent.

DNA methyltransferase 1—responsible for DNA methylation maintenance—is repeatedly implicated in reproduction across many insects and other animals, often showing strong gonadal expression and knockdown-associated fecundity phenotypes.

AIMS

Establish an effective RNAi protocol in adult *S. oryzae*
Map *Dnmt1* expression in reproductive tissues and whole bodies
Test functional relevance for reproduction



METHODS

- Insect rearing
- RNAi injections
- Tissue dissection
- RNA extraction and qPCR
- Fecundity assay
- Data analysis and visualization in R

Studying the role of circadian clock genes in *Tribolium castaneum by RNAi-induced gene silencing*

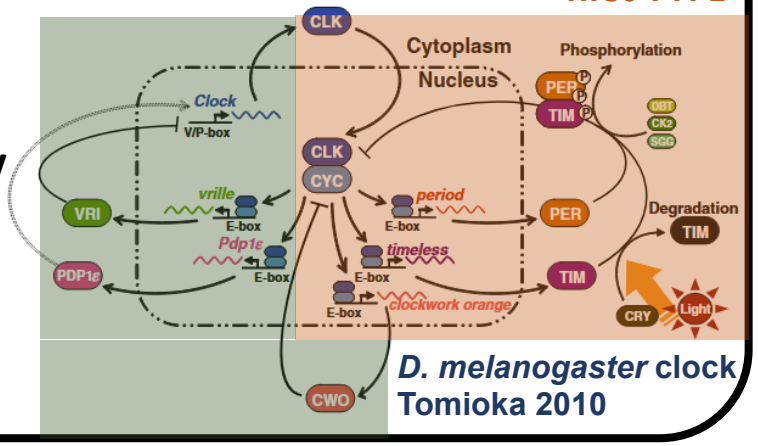
Supervisor: Tobias Prüser

Background

Circadian clocks are **molecular pacemakers**, creating **~24h rhythms**, thereby allowing organisms to anticipate recurring environmental changes.

While the principal mechanisms are conserved, insects show surprising **evolutionary flexibility** in these pacemakers.

Recent work in the model beetle *Tribolium castaneum* focused on **the first Transcription–Translation Feedback Loop (TTFL)** of the circadian clock, while the role of **other clock genes** remained unclear.



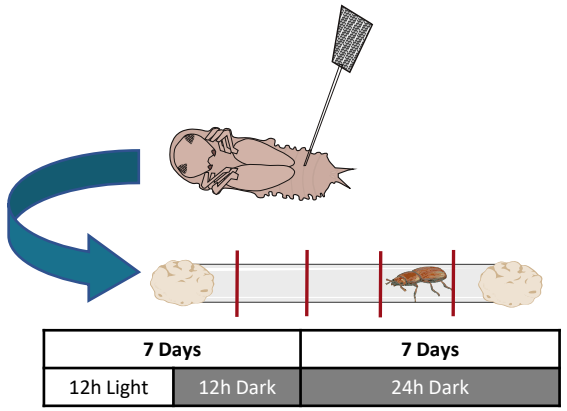
Aim

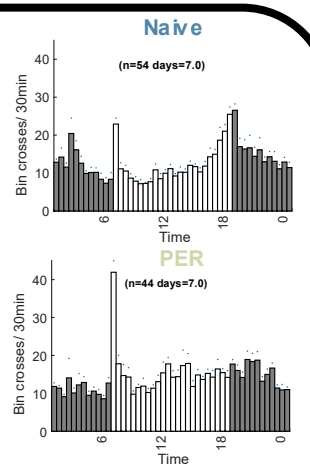
Testing the role of two clock genes, selected together with you, by:

- RNAi-mediated knock-down
- Evaluating anticipation behaviour and the ability to maintain rhythmic behaviour in constant environments

Methods

- Insect rearing
- RNAi injections
- RNA extraction and qPCR
- Locomotor activity assays
- Data visualization and analysis using MATLAB and R



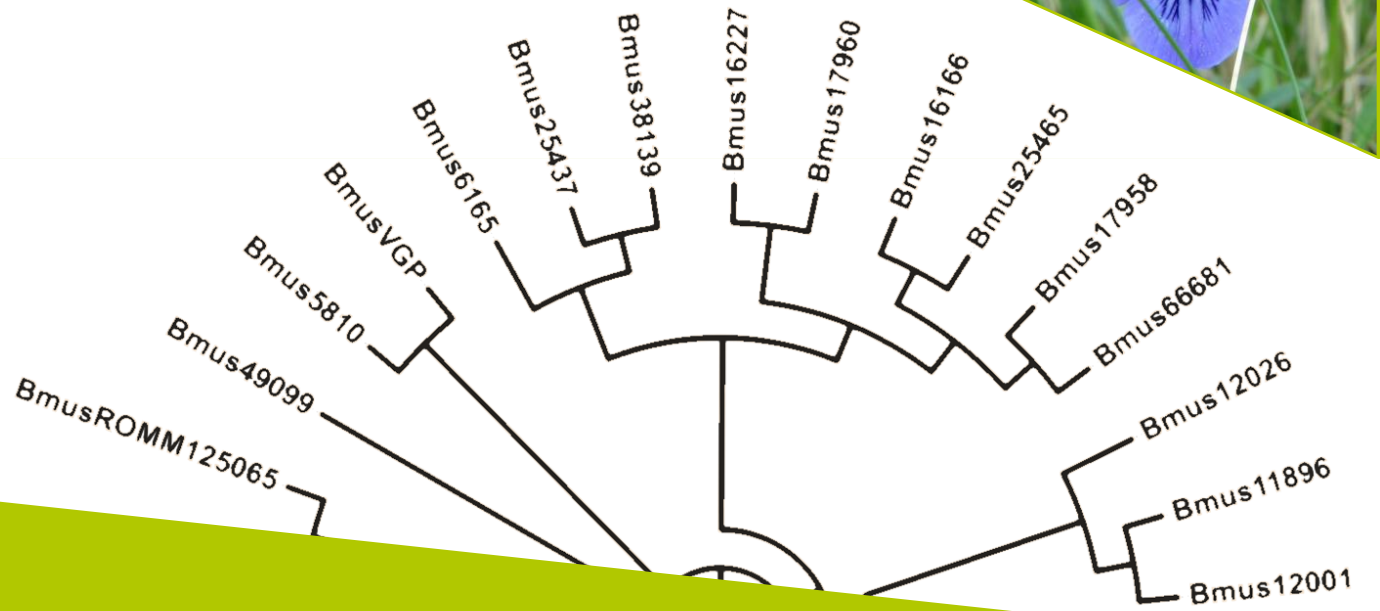


Loss of evening anticipation after Period KD

Universität Münster

Evolution & Biodiversity of Plants

Prof. Kai Müller



AG Müller

Evolution and Biodiversity of Plants

BOTANISCHER GARTEN
UNIVERSITÄT MÜNSTER

Evolution

Catopsis berteroniana
(SCHULT. & SCHULT.F.) MEZ

Pinguicula lusitanica L.

Genlisea aurea A.ST.-HIL.

Evolution

Catopsis berteroniana
(Schult. & Schult.f.) Mez

Pinguicula lusitanica L.

Genlisea aurea A.St.-Hil.

Biodiversity

Utricularia bremii
Heer ex Koell.

Andromeda polifolia L.

Viola l. calaminaria
Lej.

Viola guestphalica
Nauenb.

Evolution

Pinguicula lusitanica L.

Genlisea aurea A.St.-Hil.

Biodiversity

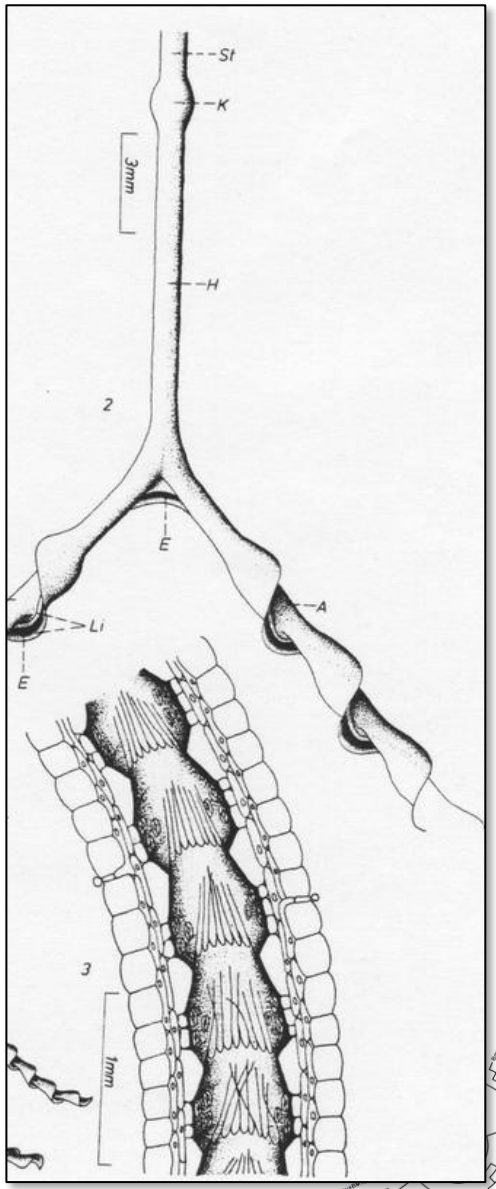
Utricularia bremii Heer ex Koell.

Project 1:

Evolution of microbe communities in carnivorous plants

- Comparison between *Genlisea* community and other CPs (e.g. *Nepenthes, Broccinia reducta, Drosera etc.)*
- DNA extraction, amplification of barcodes specific for bacteria, fungi, algae

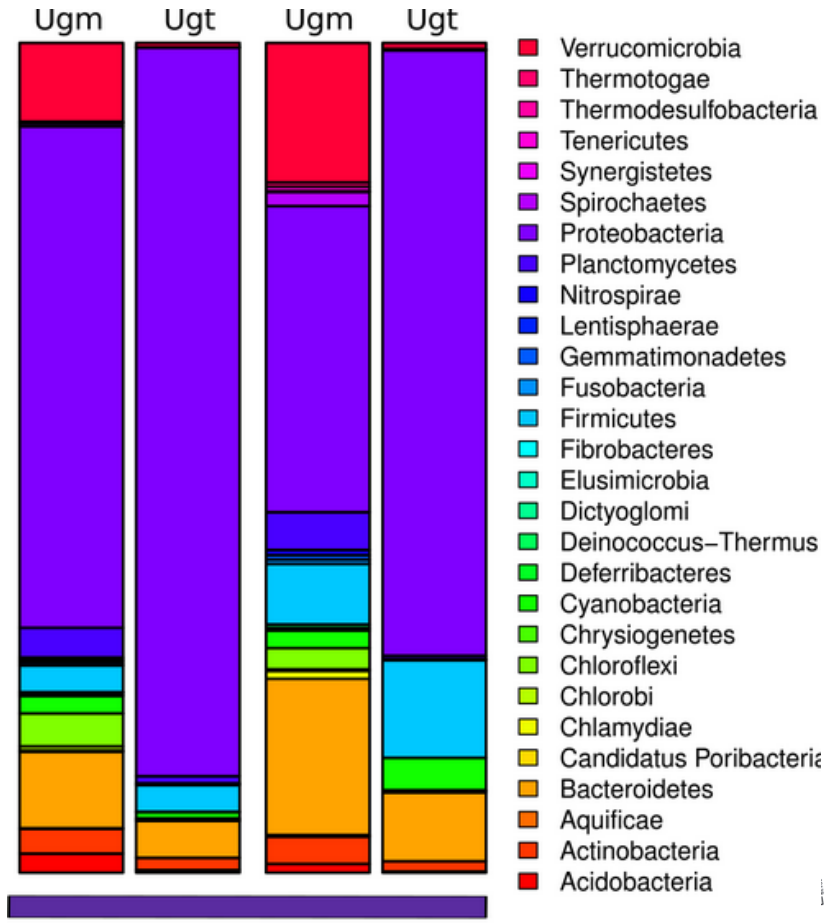
Genlisea aurea A.ST.-HIL.



Project 1:

Project tasks:

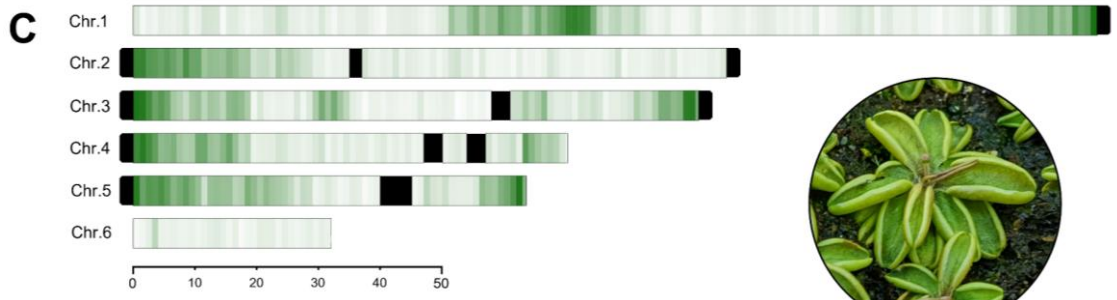
- Bioinformatic evaluation using databases
- Comparing species diversity within bacteria, fungi and algae
- Relate species composition to digestive system



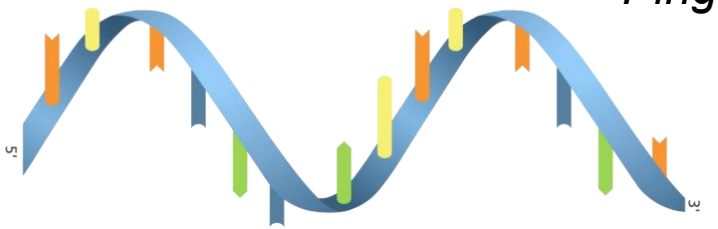
Project 2:

Finding carnivory-related genes in butterworts

- *Pinguicula lusitanica* genome to study early evolution in Lamiales
- Transcriptome data available
- Annotate genes and find genes related to carnivory



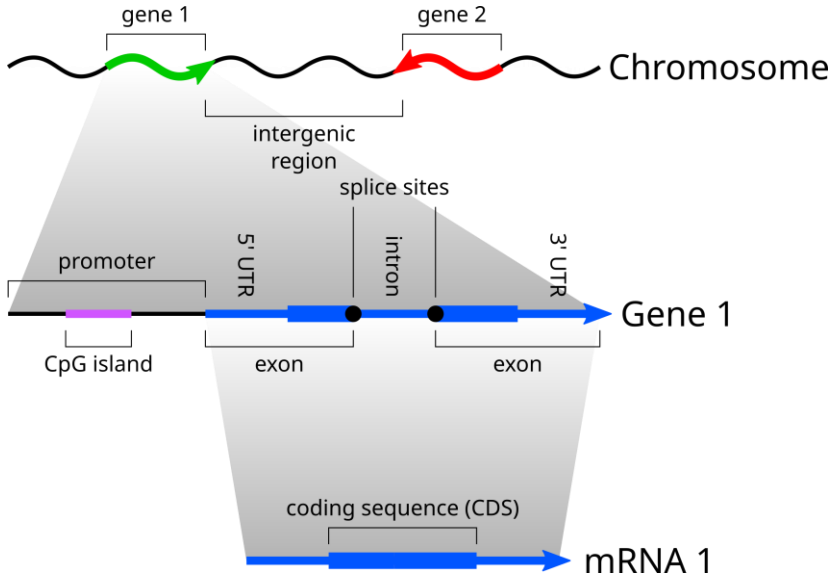
Pinguicula lusitanica L.

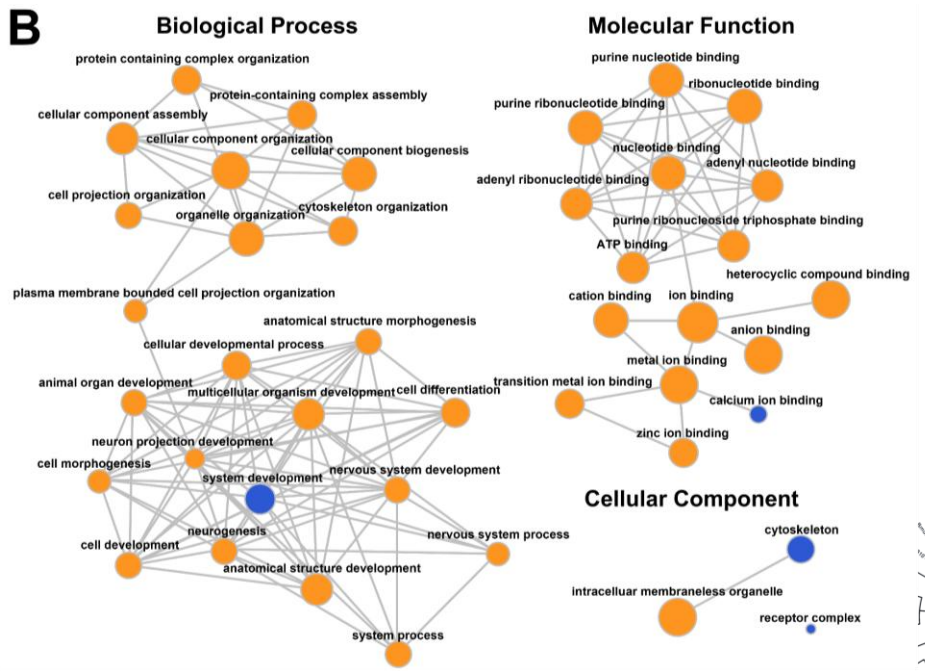


Project 2:

Project tasks:

- Annotate genome to receive high-quality gene models
- Test for positive selection and gene family expansion
- Gene enrichment analysis and functional link to carnivory



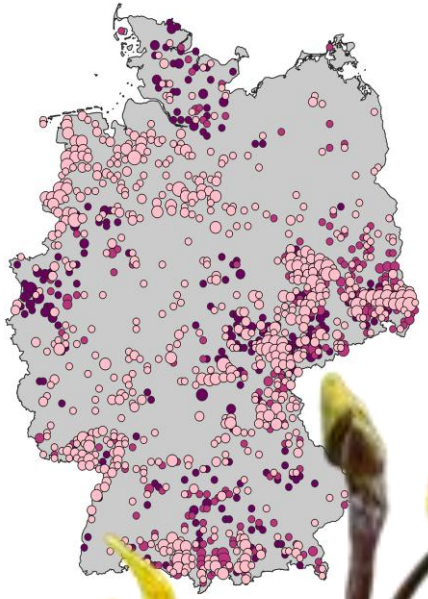


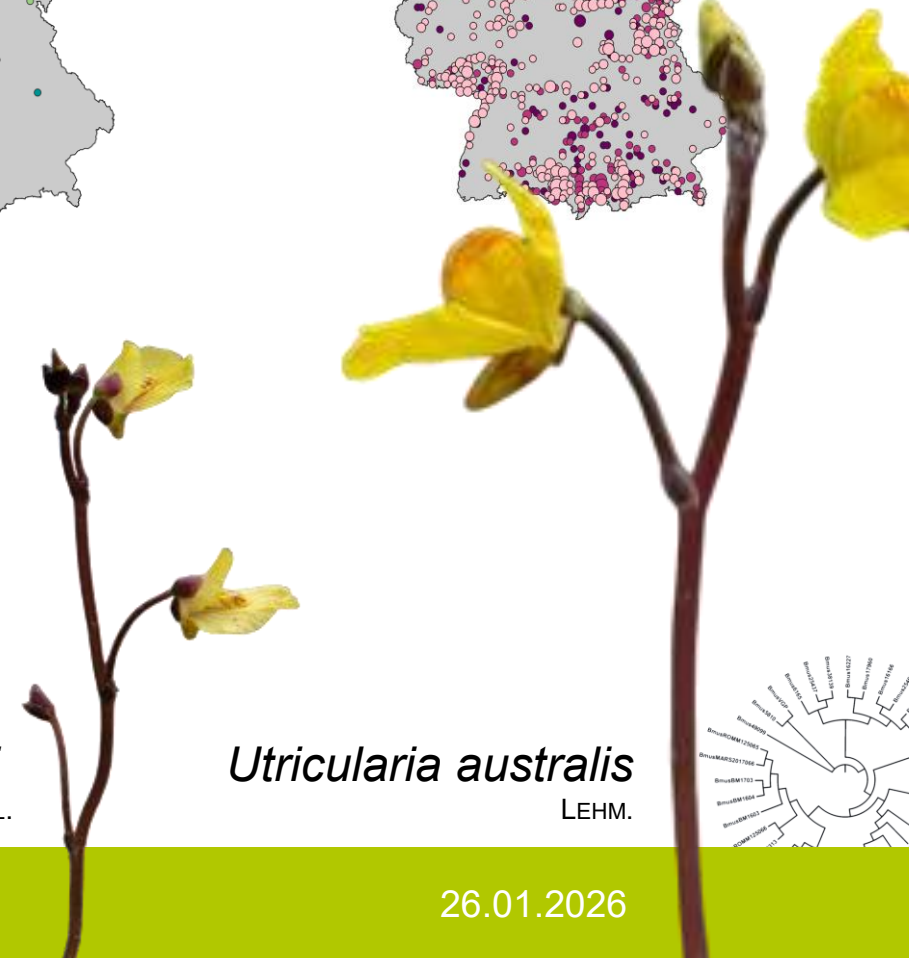
Project 3:

Characterizing the microbial communities and prey composition inside *Utricularia*

- *U. australis* outcompetes *U. bremii*, the reason is unknown
- Population genomic data available
- A lot of non-plant DNA…

→ endophytes, symbionts, prey





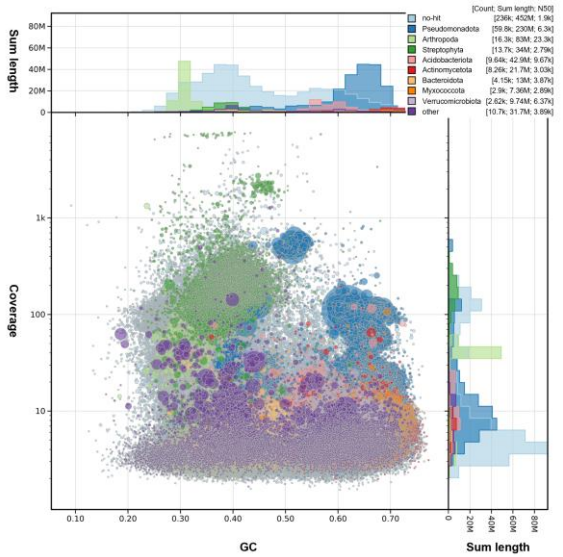
Utricularia bremii Heer ex Koell.

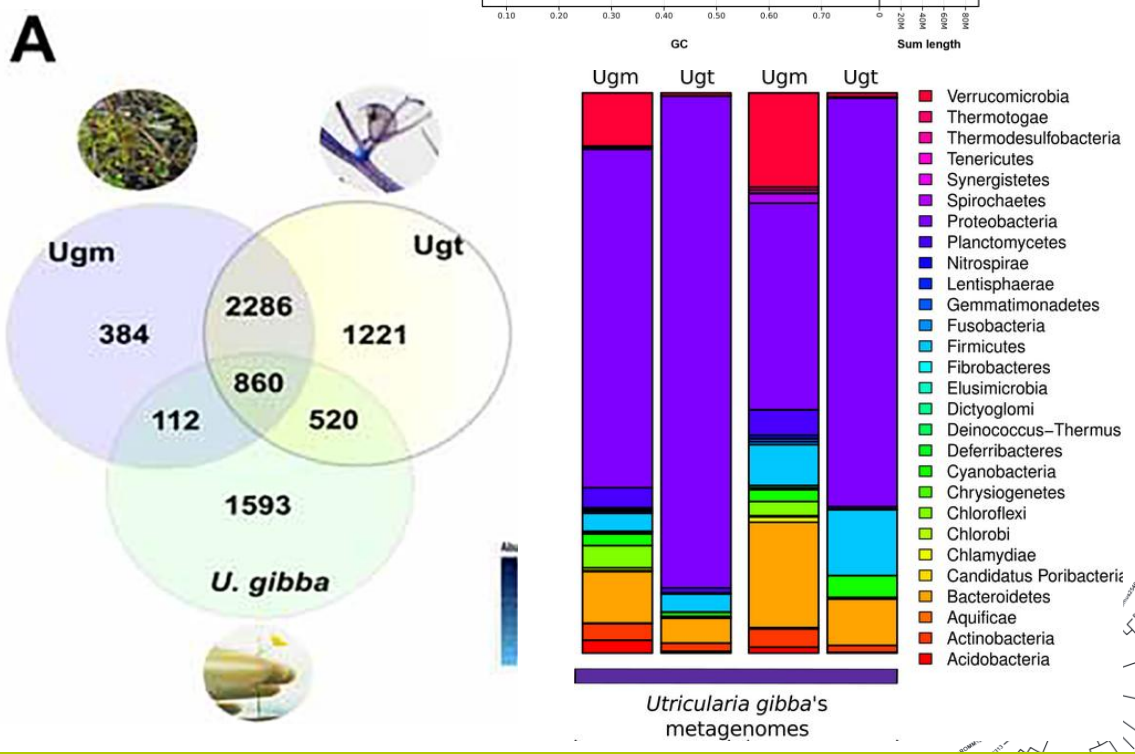
Utricularia australis Lehm.

Project 3:

Project tasks:

- Extraction and comparison of barcode regions to compare species diversity
- Pan-genomes recruitment and functional gene comparison to compare gene diversity





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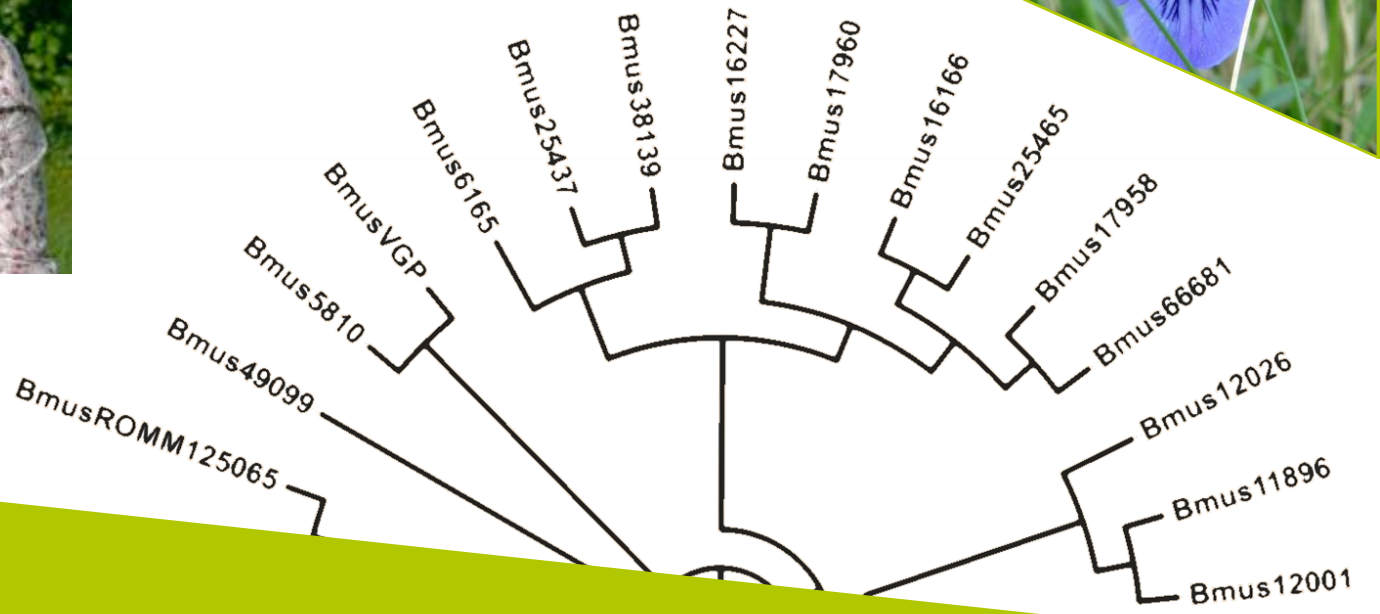
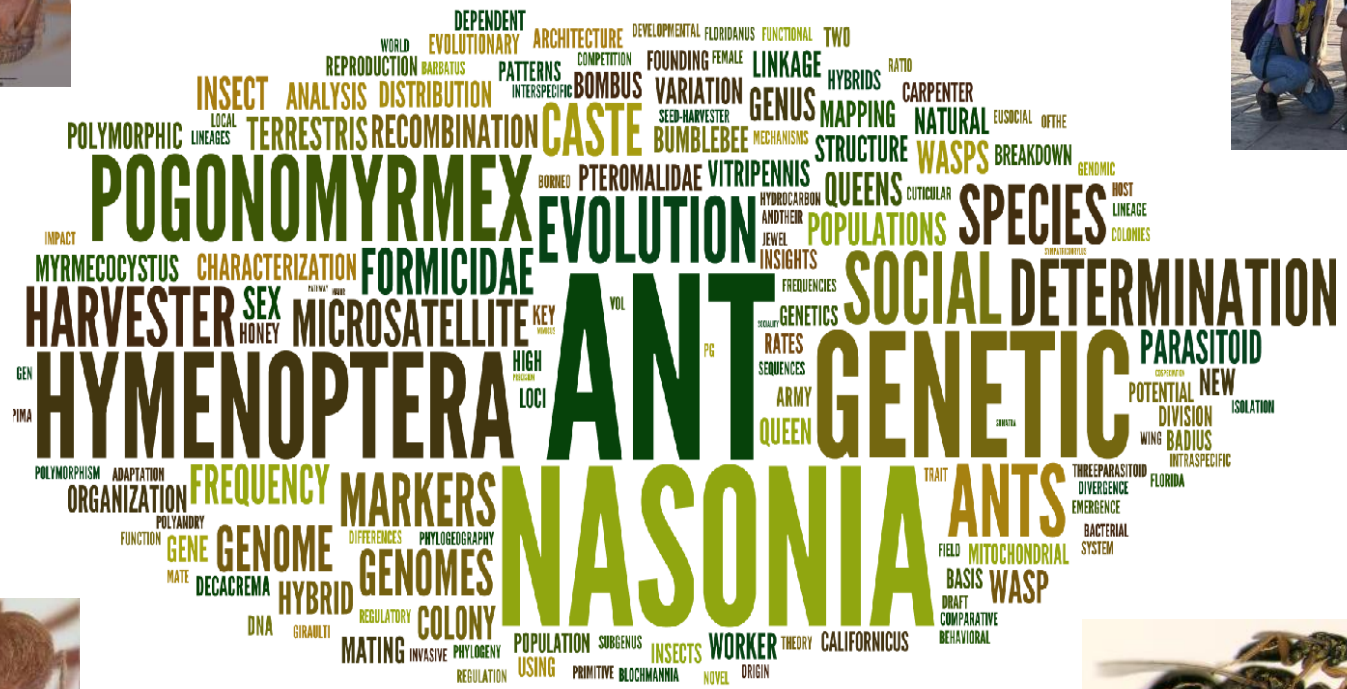


Molekulare Evolution and Sociobiologie

Prof. Dr. Jürgen Gadau, Dr. Lukas Schrader

Wir untersuchen genetische und epigenetische Architektur adaptiver Merkmale und Artbildung.



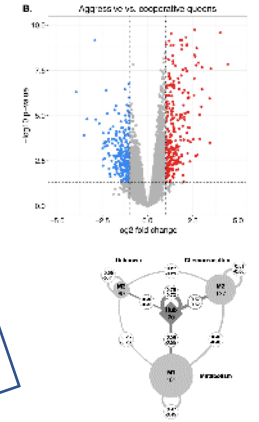
Genetic, epigenetic and genomic architecture of adaptive traits in social and solitary Hymenoptera

Genomstruktur und Aufbau

Genetische und epigenetische Genomregulation

Aggression
Sozialverhalten
Kommunikation
Genetischer Konflikt

Phänotyp



Genotyp

GATCCC
GATTCC

DNA-Methylation
$C^{m}pG$

Antbiodiversity + Impact of Plant Protection Products on ants!

Potential Areas for a Projektmodul and Bachelorthesis

1. Establishing dsRNAi in the ant *Cardiocondyla obscurior/Camponotus* spp. (Schrader)
2. Bioinformatics (requires some previous knowledge) – functional genomics/comparative genomics (Schrader)
3. Effects of pesticides and herbicides on ant colonies – determining different Life History traits for model-parametrization (RISKANT – testing a Multiagent-Modell to estimate effects of toxins on ant colonies at all levels.) (Gadau/Pohl)
4. Epigenetic - DNA methylation in ants (function and behavioral effects on division of labor) and mechanisms (inheritance and environmental plasticity) (Gadau)
5. Social evolution in *P. californicus/Lasius niger* – in connection with epigenetic effects (DNA methylation) (Gadau)